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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 43.7968 seconds
(without alignments)
256.908 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 611

Sequence: 1 MSPGTVCGLLLGLMLDL.....LGKFLQDILWEAKEAPADK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611	100.0	117	1 A59316	ghrelin precursor
2	518	84.8	117	1 B59316	ghrelin precursor
3	88.5	14.5	115	1 A33323	motilin precursor
4	86	14.1	119	1 MSPG	motilin precursor
5	79	12.9	1234	2 T30160	hypothetical prote
6	75.5	12.4	410	2 C84205	hypothetical prote
7	73.5	12.0	709	2 D82825	conserved hypothet
8	72.5	11.9	115	2 J65511	motilin precursor
9	72.5	11.9	482	1 S93904	platelet-derived e
10	72.5	11.9	922	2 G83109	probable two-compo
11	72	11.8	147	2 T09722	histone H2B1 - upl
12	71	11.6	299	2 B36134	RepC protein - Esc
13	70	11.5	840	2 F90788	probable outer mem
14	70	11.5	840	2 G85648	probable usher pro
15	69	11.3	411	2 S47436	flagellar antigen
16	69	11.3	792	2 JC7122	protein kinase (EC
17	69	11.3	2273	2 I46477	calcium channel BI
18	69	11.3	2424	2 I46480	calcium channel BI
19	68.5	11.2	133	1 S24315	motilin precursor
20	68.5	11.2	340	2 S53763	homeotic protein H
21	68.5	11.2	533	2 AC0414	probable exported
22	68	11.1	330	2 A82292	beta-hexosaminidas
23	68	11.1	409	2 D87426	cyclopropane-fatty
24	67.5	11.0	270	2 E87408	hypothetical prote
25	67.5	11.0	416	2 I38428	T-complex protein
26	67.5	11.0	938	2 A13417	[glutamate-ammonia
27	67	11.0	233	2 T41263	hypothetical prote
28	67	11.0	2212	2 A41098	calcium channel pr
29	66.5	10.9	385	2 F70591	probable kefB prot

30	66.5	10.9	485	2 C75460	hypothetical prote
31	66.5	10.9	575	2 F86639	hypothetical prote
32	66.5	10.9	992	2 T08772	hypothetical prote
33	66.5	10.9	1018	2 T43168	hypothetical prote
34	66.5	10.9	1171	2 AB0130	DNA-directed DNA p
35	66	10.8	247	2 S58394	myelin/oligodendro
36	66	10.8	770	2 I49508	ISGF3 p91-related
37	66	10.8	770	2 A54444	DNA-binding protol
38	66	10.8	922	2 D75615	exonuclease ABC c
39	65.5	10.7	262	2 D71068	probable pseudouri
40	65.5	10.7	334	2 S39870	transaldolase (EC
41	65.5	10.7	491	2 H97088	protein containing
42	65.5	10.7	627	2 T19542	hypothetical prote
43	65.5	10.7	692	2 B55546	flagellar biosynth
44	65.5	10.7	692	2 AE0745	flagellar biosynth
45	65.5	10.7	1065	2 E69795	acriflavin resista

ALIGNMENTS

RESULT 1

A59316

ghrelin precursor - human

N:Alternate names: preproghrelin

C:Species: Homo sapiens (man)

C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000

C:Accession: A59316

R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A:Reference number: A59316; MUID:20067959; PMID:10604470

A:Accession: A59316

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-117 <KOJ>

A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BAAB9371.1; PID:g6691572

A:Experimental source: tissue stomach endocrine cells

A:Note: submitted to Genbank, June 1999

C:Comment: Ghrelin secreted by the stomach stimulates the release of spmatotropin (gr

C:Superfamily: motilin

C:Keywords: hormone; lipoprotein; stomach

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-51/Product: ghrelin #status predicted <MAT>

F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 611; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 9.1e-55;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPGTVCGLLLGLMLDLAMAGSFLSPHQRVQQRKESKPPAKLPRLAGWLRLPE 60

Db 1 MSPGTVCGLLLGLMLDLAMAGSFLSPHQRVQQRKESKPPAKLPRLAGWLRLPE 60

QY 61 DGGQEGAEDELEVRNAPFDVGIRLGVQVQOHSQALGKFLQDILWEAKEAPADK 117

Db 61 DGGQEGAEDELEVRNAPFDVGIRLGVQVQOHSQALGKFLQDILWEAKEAPADK 117

RESULT 2

B59316

ghrelin precursor - rat

N:Alternate names: preproghrelin

C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000

C:Accession: B59316

R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A:Reference number: A59316; MUID:20067959; PMID:10604470

A:Accession: B59316

A:Status: not compared with conceptual translation

Query Match 14.1%; Score 86; DB 1; Length 119;
Best Local Similarity 26.0%; Pred. No. 0.13;
Matches 20; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

QY 26 SFLSPHORVQQRKESKPPAKLPQALAGWLRPEDGGQAEDELEVRFNAPDVGIK 85
DB 29 SFTYGLQRMQEKRNKQKSLSVQQAASEELGPLDSEPTKEERVVVKLLAPVDIGIR 88

QY 86 LSGVQYQOHSQALGKFL 102
DB 89 MDSRQLEKYRATLERLL 105

RESULT 5
T30160
hypothetical protein C37A2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T30160
R:Le, T.T.; Kemp, K.; Scheet, P.
submitted to the EMBL Data Library, April 1997
A:Description: The sequence of C. elegans cosmid C37A2.
A:Reference number: Z20746
A:Accession: T30160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1234 <LET>
A:Cross-references: EMBL:U97194; PIDN:AB52447.1; GSPDB:GN00019; CESP:C37A2.2
A:Experimental source: strain Bristol N2; clone C37A2
C:Genetics:
A:Gene: CESP:C37A2.2
A:Map position: 1
A:Introns: 46/1; 124/1; 159/1; 231/1; 508/3; 740/3; 891/1; 931/1; 975/1; 1014/3; 1083/3

Query Match 12.9%; Score 79; DB 2; Length 1234;
Best Local Similarity 27.6%; Pred. No. 9;
Matches 32; Conservative 20; Mismatches 44; Indels 20; Gaps 6;

QY 2 PSPGTVCSLLLGLMWLDLMAAGSSFLSPHORVQQRKESKPPAKLPQALAGWLRPED 61
DB 422 PQPG---SLGPNGLGPTTAPGSPQPMNQRIQQQQQA-APASNSP-LLVNLISNOQ 476

QY 62 GQQAEGAEDLEVRFNAPDVGIKLSGV----QYQOHSQALGKFLQDILMEPAKFA 113
DB 477 PPQY-----QYMPGPGSAQGLSMQIAAQIQQQQHQQ-----YQQRILQQQQQQA 521

RESULT 6
C84205
hypothetical protein Vng0468c [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84205
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
Leitchauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: C84205
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-410 <STO>
A:Cross-references: GB:AE004437; NID:g10580073; PIDN:AAG19007.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG0468C

Query Match 12.4%; Score 75.5; DB 2; Length 410;
Best Local Similarity 30.3%; Pred. No. 6;
Matches 23; Conservative 9; Mismatches 37; Indels 7; Gaps 2;

QY 29 SPEHORVQQRKESKPPAKLPQALAGWLRPEDGGQAEDELEVRFNAPDVGIKLSG 88

DB 78 SPHEYFVQD-----QPGAVLEFAEPKQWL--VAAGEQQAQYRFEARVNNPTTEGGEIVG 130
QY 89 VOYQOHSQALGKFLQD 104
DB 131 VKYDGEVYGDIIID 146

RESULT 7
D82825
conserved hypothetical protein XF0277 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82825
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: AB2515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: D82825
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-709 <SIM>
A:Cross-references: GB:AE003881; GB:AE003849; NID:g9105093; PIDN:AAF83090.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpton, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Sanceilli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0277

Query Match 12.0%; Score 73.5; DB 2; Length 709;
Best Local Similarity 23.5%; Pred. No. 18;
Matches 36; Conservative 14; Mismatches 52; Indels 51; Gaps 6;

QY 5 GTVCSL-----LLGLMWLDLMAAGSSP----- 27
DB 422 GALASLIGFARLYLGAHNLSDVGLGMFLGIFMLLVGIAYRRRLTHELOVNPFLSWLFYGT 481

QY 28 -----LSPEHORVQQRKESKPPAKLPQALAGWLRPEDGGQAEDELEVRFN 78
DB 482 FSIAIVVAPRHLEOKLTKFEPPPPS---PRAIAEGHWK-NDWRQLPARRNEFDDEARW 537

QY 79 PFDVGIKLSGVQYQOHSQALGKFLQ-DILWEEA 110
DB 538 PLNVQVAGSLVPLQHQLELTQGWRRQPQTGWKEA 570

RESULT 8
JC6511
motilin precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 19-Jan-2001
C:Accession: JC6511
R:De Clercq, P.; Depoortere, I.; Peeters, T.
Gene 202, 187-191, 1997
A:Title: Isolation and sequencing of the cDNA encoding the motilin precursor from she
A:Reference number: JC6511; MUID:98087436; PMID:9427564
A:Accession: JC6511
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <DEA>

Db 113 VDK 115

C;Accessio

C;Accession: B36134
P;Dorrington P A : Pawlings D P
C;Date: 30-NOV-1990 *sequence_revision 30-NOV-1990 *text_change 00-OCT-1999

J. Bacteriol. 172, 5697-5705, 1990
A:Title: Characterization of the minimum replicon of the broad-host-range plasmid pTF-FC
A:Reference number: A36134; MUID:91008941; PMID:2120189
A:Accession: B36134
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <DOR>
A:Cross-references: GB:I73777; GB:M35249; NID:g154646; PIDN:AAA27382.1; PID:g154648
C:Genetics:
C:Genome: plasmid

Query Match 11.6%; Score 71; DB 2; Length 299;
Best Local Similarity 25.8%; Pred. No. 12;
Matches 25; Conservative 15; Mismatches 37; Indels 20; Gaps 4;
QY 32 HORVOORKESK--KPPAKLQPRALAGWLRPEGGQAE-----GAEDE-LEVRN 77
DB 200 IIRINNAEVRKLETPARLLHRLCGWIDPGSGKAEIDTLCGYVMPDAANDAMKKRQ 259
QY 78 APFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAP 114
DB 260 TARKALVELAAVGTVNEYAKCK-----WEISRPNP 290

RESULT 13
F90788
probable outer membrane usher protein ECs1278 [imported] - Escherichia coli (strain O157
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: F90788
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90788
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-840 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA034701.1; PID:g13360738; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs1278
C:Superfamily: outer membrane usher protein fimD

Query Match 11.5%; Score 70; DB 2; Length 840;
Best Local Similarity 25.9%; Pred. No. 48;
Matches 30; Conservative 15; Mismatches 43; Indels 28; Gaps 5;
QY 3 SPGTVCSSLLLGLMLDLAMAGSFLSPHQVRQORKEKSKPPAKLQPR-----LAG 55
DB 127 AFG-ITSQTQLSQLRLDLSVPQSOLIS-----RPRGYVPPSELDTGASLAFMYNIAN 177
QY 56 WLRPEDGGQAEAELEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAK 111
DB 178 YYNVAYSGONAHQSRLWASFN-----GINLGAWQYRQ-----LSNMTWDNDK 221

RESULT 14
G85648
probable usher protein Z1536 [imported] - Escherichia coli (strain O157:H7, substrain ED
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: G85648
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouasis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85648
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-840 <STO>

A:Cross-references: GB:AE005174; NID:g12514401; PIDN:AAG55651.1; GSPDB:GN00145; UMGF:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z1536
C:Superfamily: outer membrane usher protein fimD

Query Match 11.5%; Score 70; DB 2; Length 840;
Best Local Similarity 25.9%; Pred. No. 48;
Matches 30; Conservative 15; Mismatches 43; Indels 28; Gaps 5;
QY 3 SPGTVCSSLLLGLMLDLAMAGSFLSPHQVRQORKEKSKPPAKLQPR-----LAG 55
DB 127 AFG-ITSQTQLSQLRLDLSVPQSOLIS-----RPRGYVPPSELDTGASLAFMYNIAN 177
QY 56 WLRPEDGGQAEAELEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAK 111
DB 178 YYNVAYSGONAHQSRLWASFN-----GINLGAWQYRQ-----LSNMTWDNDK 221

RESULT 15
S47436
flagellar antigen - Trypanosoma brucei (fragment)
C:Species: Trypanosoma brucei
C:Date: 13-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 03-Nov-2000
C:Accession: S47436
R:Imboden, M.; Mueller, N.; Hemphill, A.; Mattioli, X.Y.Z.; Seebeck, T.
submitted to the EMBL Data Library, August 1994
A:Description: Repetitive proteins from the flagellar cytoskeleton of African Trypano
A:Reference number: S47436
A:Accession: S47436
A:Molecule type: mRNA
A:Residues: 1-411 <IMB>
A:Cross-references: EMBL:Z36281; NID:g530358; PID:g530359
A:Experimental source: strain stock TREU 1285
C:Superfamily: cytoadherence-accessory protein hmw1

Query Match 11.3%; Score 69; DB 2; Length 411;
Best Local Similarity 30.2%; Pred. No. 27;
Matches 26; Conservative 16; Mismatches 28; Indels 16; Gaps 4;
QY 33 QRVOQRKESKPPAKLQPRALAGWLRPEDGGQAEAELEVRFNAPFDVGIKLSGVQYQ 92
DB 317 EALEELEEPQQAPEAQPEAVA-----PE-GDIAVEALEELEEPQQAPE-----AEAQ 362
QY 93 QHSQALGKFLQDIL--WEEAKEAPAD 116
DB 363 PEAQPEGDIATVEALEELEEPQQAPE 388

Search completed: September 11, 2003, 17:26:21
Job time : 46.7968 secs

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; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (23)...(23)
US-09-853-253-6

Query Match 100.0%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 9e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 3

US-09-853-253-4
; Sequence 4, Application US/09853253
; Patent No. US2002005156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-4

Query Match 100.0%; Score 23; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 4

US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East

; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Query Match 100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 5

US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US2002005156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-2

Query Match 100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
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DB 52 ALAGWLRPEDGQAEAELEEV 74

RESULT 6

US-09-989-722-268

Sequence 268, Application US/09989722

Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gunney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC63

CURRENT APPLICATION NUMBER: US/09/989,722

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

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PRIOR FILING DATE: 1997-11-24

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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.5e-15; Mismatches 0; Indels 0; Gaps 0;

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 Db 52 ALAGWLRPEDGGAEGAELEV 74

RESULT 7

US-09-989-723-268

; Sequence 268, Application US/09989723

; Patent No. US20020072092A1

; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gottard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: KJavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C62
 ; CURRENT APPLICATION NUMBER: US/09/989, 723
 ; PRIOR FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 23; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.5e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
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Db 52 ALAGWLRPEDGGQAGAEDELEV 74

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RESULT 8
 US-09-989-279-268
 ; Sequence 268, Application US/09989279
 ; Patent No. US20020072496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 52 ALAGWLRPEDGGQAGAEDEV 74

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; Sequence 268. Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
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Query Match 100.0%; Score 23; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.5e-15; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0;

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RESULT 10

US-09-989-731-268
; Sequence 268, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC70
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CURRENT FILING DATE: 2001-11-20
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Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186

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; PRIOR FILING DATE: 1998-07-01
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 ; PRIOR FILING DATE: 1998-07-02
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.5e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 13

US-09-990-442-268
 ; Sequence 268, Application US/09990442
 ; Patent No. US20020132252A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gottard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC8
 ; CURRENT APPLICATION NUMBER: US/09/990,442
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
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 ; PRIOR FILING DATE: 1998-02-25

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 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.5e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
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 Db 52 ALAGWLRPEDGGQAGAEDELEV 74
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RESULT 14
 ; Sequence 268, Application US/09991163
 ; Patent No. US20020132253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C17
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
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RESULT 15
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; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993.604
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:37 ; Search time 8.73262 Seconds
(without alignments)
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Title: US-09-853-253-5
Perfect score: 23
Sequence: 1 ALAGWLRPEDGGQAEAGAEDEV 23

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	8	34.8	483	2 T04453	hypothetical prote
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4	7	30.4	344	2 A48990	transcription regu
5	7	30.4	910	2 B83451	aconitate hydratase
6	7	30.4	1239	1 Q0BE10	BOLFI protein - hu
7	6	26.1	69	2 C87574	cold-shock domain
8	6	26.1	142	2 AB0401	probable membrane
9	6	26.1	175	2 E82118	conserved hypothet
10	6	26.1	178	2 A03230	quiescence-specifi
11	6	26.1	180	2 T46695	hypothetical prote
12	6	26.1	189	2 A91082	hypothetical prote
13	6	26.1	189	2 B85927	hypothetical prote
14	6	26.1	198	2 D63070	imidazoleglycerol-
15	6	26.1	223	2 A08666	HL-60-induced diff
16	6	26.1	237	2 T30002	hypothetical prote
17	6	26.1	265	2 A95298	hypothetical prote
18	6	26.1	267	1 CTPGP	corticotropin / li
19	6	26.1	284	2 B25624	tropomyosin I, tho
20	6	26.1	284	2 A25624	tropomyosin I, emb
21	6	26.1	288	2 A55737	PD-1 protein - hum
22	6	26.1	289	2 T48894	lipoprotein mtsA,
23	6	26.1	289	2 H83433	hypothetical prote
24	6	26.1	290	2 H71852	hypothetical prote
25	6	26.1	299	2 T35144	glutamate transpor
26	6	26.1	302	2 T48871	catechol 1,2-dioxy
27	6	26.1	308	2 F72508	probable hydrogena
28	6	26.1	313	2 E82762	conserved hypothet
29	6	26.1	315	2 F64129	probable phosphogl

transcription repr
30S ribosomal prot
probable prolipop
hypothetical prote
sam-dependent meth
cysteine proteinase
hypothetical prote
hypothetical prote
alcohol dehydrogen
cysteine proteinase
phosphoribosylamin
molybdopterin bios
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical membr

ALIGNMENTS

RESULT 1

A59316
ghrelin precursor - human
N:Alternate names: preproghrelin
C:Species: Homo sapiens (man)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C:Accession: A59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: A59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-117 <KO>
A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BAA89371.1; PID:g6691572
A:Experimental source: Tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gr
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0% Score 23; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAEAGAEDEV 23
|||||
DB 52 ALAGWLRPEDGGQAEAGAEDEV 74

RESULT 2

T04453
hypothetical protein F4D11.80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04453
R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Hohelsel, J.; Mewes,
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15360
A:Accession: T04453
A:Molecule type: DNA
A:Residues: 1-483 <BEV>
A:Cross-references: EMBL:AL022537
A:Experimental source: cultivar Columbia; BAC clone F4D11
C:Genetics:
A:Map position: 4
A:Introns: 17/3; 44/1; 94/1; 141/3; 206/2; 247/2; 345/3; 395/1; 434/2

A;Note: F4D11.80

Query Match 34.8%; Score 8; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAED 20
 |||||||
DB 302 QAEGAED 309

RESULT 3

JH0572
hypothetical protein - Streptomyces lividans (fragment)
C;Species: Streptomyces lividans
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-1999
C;Accession: JH0572
R;Lichenstein, H.S.; Busse, L.A.; Smith, G.A.; Narhi, L.O.; McGinley, M.O.; Rohde, M.F.;
Gene 111, 125-130, 1992
A;Title: Cloning and characterization of a gene encoding extracellular metalloprotease f
A;Reference number: JH0571; MUID:92192468; PMID:1547948
A;Accession: JH0572
A;Molecule type: DNA
A;Residues: 1-302 <LIC>
A;Cross-references: GB:M89476; NID:g153411; PIDN:AAA26804.1; PID:g153412
A;Experimental source: strain TK24
A;Note: the authors translated the codon GTA for residue 260 as Asp
C;Superfamily: Pseudomonas putida regulatory protein catR

Query Match 30.4%; Score 7; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
 |||||||
DB 100 ALAGWLR 106

RESULT 4

A48990
transcription regulator LysR family homolog Snpr - Streptomyces lividans
C;Species: Streptomyces lividans
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C;Accession: A48990
R;Butler, M.J.; Davey, C.C.; Krygsmann, P.; Walczyk, E.; Malek, L.T.
Can. J. Microbiol. 38, 912-920, 1992
A;Title: Cloning of genetic loci involved in endoprotease activity in Streptomyces livid
A;Reference number: A48990; MUID:93099553; PMID:1464066
A;Contents: 66
A;Accession: A48990
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-344 <BUT>
A;Note: sequence extracted from NCBI backbone (NCBIN:121210, NCBIIP:121213)
C;Superfamily: Pseudomonas putida regulatory protein catR

Query Match 30.4%; Score 7; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
 |||||||
DB 104 ALAGWLR 110

RESULT 5

B83451
aconitate hydratase 1 PA1562 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83451
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bf

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83451
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-910 <STO>
A;Cross-references: GB:AE004584; GB:AE004091; NID:99947516; PIDN:AA04951.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: acnA; PA1562
C;Superfamily: iron-responsive element-binding protein

Query Match 30.4%; Score 7; DB 2; Length 910;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
 |||||||
DB 65 ALAGWLR 71

RESULT 6

Q0BE10
BOLFI protein - human herpesvirus 4 (strain B95-8)
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
C;Accession: A43041; A03752; S32995
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi
A;Reference number: A93065; MUID:85035713; PMID:6092825
A;Accession: A43041
A;Molecule type: DNA
A;Residues: 1-1239 <BAN>
A;Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24841.1; PID:g1334855
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.
Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region
C;Superfamily: human herpesvirus 4 BOLFI protein

Query Match 30.4%; Score 7; DB 1; Length 1239;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AEGAED 20
 |||||||
DB 696 AEGAED 702

RESULT 7

C87574
cold-shock domain family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C;Accession: C87574
R;Nierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87574
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <STO>
A;Cross-references: GB:AE005673; NID:g13424199; PIDN:AAK24591.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC2623

C:Superfamily: major cold shock protein; cold shock domain homology

Query Match 26.1%; Score 6; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PEDGGQ 13
|||||
Db 20 PEDGGQ 25

RESULT 8

AB0401
Probable membrane protein YPO3302 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0401
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Lil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0401
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92534.1; PID:g15981232; GSPDB:GN00175
C:Genetics:
A:Gene: YPO3302
C:Superfamily: hypothetical protein HI0489

Query Match 26.1%; Score 6; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAGWLR 7
|||||
Db 104 LAGWLR 109

RESULT 9

E82118
conserved hypothetical protein VC2111 [imported] - Vibrio cholerae (strain N16961 serogr conserved
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82118
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
A:Accession: E82118
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-175 <HEI>
A:Cross-references: GB:AE004284; GB:AE003852; NID:g9656649; PIDN:AAF95256.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2111
A:Map position: 1

Query Match 26.1%; Score 6; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GOAEGA 17
|||||
Db 54 GOAEGA 59

RESULT 10

A30230
quiescence-specific protein precursor - chicken
N:Alternate names: Ch21 protein
C:Species: Gallus gallus (Chicken)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 15-Nov-1996
C:Accession: A30230; A42581; A36595; A35491
R:Bedard, P.A.; Yannoni, Y.; Simmons, D.L.; Erikson, R.L.
Mol. Cell. Biol. 9, 1371-1375, 1989
A:Title: Rapid repression of quiescence-specific gene expression by epidermal growth
A:Reference number: A30230; MUID:89261749; PMID:2498647
A:Accession: A30230
A:Molecule type: mRNA
A:Residues: 1-178 <BED>
R:Dozin, B.; Descalzi, F.; Briata, L.; Hayashi, M.; Gentili, C.; Hayashi, K.; Quarto
J. Biol. Chem. 267, 2979-2985, 1992
A:Title: Expression, regulation, and tissue distribution of the Ch21 protein during c
A:Reference number: A42581; MUID:92147639; PMID:1737754
A:Accession: A42581
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-95, 'L', 97-178 <DOZ>
A:Experimental source: tibia hypertrophic cartilage
A:Note: sequence extracted from NCBI backbone (NCBIN:80796, NCBIP:80797)
R:Cancedda, F.D.; Dozin, B.; Rossi, F.; Molina, F.; Cancedda, R.; Negri, A.; Ronchi,
J. Biol. Chem. 265, 19060-19064, 1990
A:Title: The Ch21 protein, developmentally regulated in chick embryo, belongs to the
A:Reference number: A36595; MUID:91035433; PMID:2229062
A:Accession: A36595
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 21-95, 'L', 97-178 <CAN>
A:Cross-references: GB:M37611
R:Cancedda, F.D.; Asaro, D.; Molina, F.; Cancedda, R.; Caruso, C.; Camardella, L.; Ne;
Biochem. Biophys. Res. Commun. 168, 933-938, 1990
A:Title: The amino terminal sequence of the developmentally regulated CH21 protein sh
A:Reference number: A35491; MUID:90267487; PMID:2346493
A:Accession: A35491
A:Status: preliminary
A:Molecule type: protein
A:Residues: 21-48 <CA2>
C:Superfamily: lipocalin; lipocalin homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-178/Product: quiescence-specific protein #status predicted <MAT>
F:25-173/Domain: lipocalin homology <LIP>
Query Match 26.1%; Score 6; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 EDELEV 23
|||||
Db 65 EDELEV 70
RESULT 11
T46695
hypothetical protein ORF-180 [imported] - Lactobacillus helveticus plasmid pLH1
C:Species: Lactobacillus helveticus
C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 04-Mar-2000
C:Accession: T46695
R:Thompson, K.; McConville, K.J.; McReynolds, C.; Foley, S.
submitted to the EMBL Data Library, December 1997
A:Description: Complete sequence of plasmid pLH1 from Lactobacillus helveticus ATCC15
A:Reference number: 223135
A:Accession: T46695
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-180 <THO>
A:Cross-references: EMBL:AJ222725; PIDN:CAA10962.1
A:Experimental source: ATCC 15009
C:Genetics:
A:Genome: plasmid pLH1
C:Superfamily: Lactobacillus helveticus plasmid pLH1 hypothetical protein ORF-180

Query Match 26.1%; Score 6; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWL 6
 |||||
 Db 31 ALAGWL 36

RESULT 12
 A91082
 hypothetical protein ECS3625 [imported] - Escherichia coli (strain O157:H7, substrain R1)
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C:Accession: A91082
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic islands
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: A91082
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-189 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA837048.1; PID:g13363096; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain R1MD 0509952
 C:Genetics:
 A:Gene: ECS3625

Query Match 26.1%; Score 6; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWL 6
 |||||
 Db 14 ALAGWL 19

RESULT 13
 B85927
 hypothetical protein Z4080 [imported] - Escherichia coli (strain O157:H7, substrain EDL5)
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: B85927
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: B85927
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-189 <STO>
 A:Cross-references: GB:AE005174; NID:g12517231; PIDN:AGS57878.1; GSPDB:GN00145; UWGP:Z40
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z4080

Query Match 26.1%; Score 6; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWL 6
 |||||
 Db 14 ALAGWL 19

RESULT 14
 D69070
 imidazoleglycerol-phosphate synthase - Methanobacterium thermoautotrophicum (strain Delt
 C:Species: Methanobacterium thermoautotrophicum
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C:Accession: D69070
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
 ; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: D69070
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-198 <MTH>
 A:Cross-references: GB:AE000912; GB:AE000666; NID:g2622632; PIDN:AAB85999.1; PID:g262
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH1524
 A:Start codon: TTG
 C:Superfamily: amidotransferase hish; trpG homology

Query Match 26.1%; Score 6; DB 2; Length 198;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 EGAEDE 20
 |||||
 Db 130 EGAEDE 135

RESULT 15
 A40866
 HL-60-induced differentiation immediate-early protein ETR101 - human
 C:Species: Homo sapiens (man)
 C>Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 05-Nov-1999
 C:Accession: A40866
 R:Shimizu, N.; Ohta, M.; Fujiwara, C.; Sagara, J.; Mochizuki, N.; Oda, T.; Utiyama, H.
 J. Biol. Chem. 266, 12157-12161, 1991
 A:Title: Expression of a novel immediate early gene during 12-O-tetradecanoylphorbol-
 A:Reference number: A40866; MUID:91286224; PMID:2061303
 A:Accession: A40866
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-223 <SHI>
 A:Cross-references: GB:M62831; NID:g182260; PIDN:AAA35814.1; PID:g182261

Query Match 26.1%; Score 6; DB 2; Length 223;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GQAEGA 17
 |||||
 Db 165 GQAEGA 170

Search completed: September 11, 2003, 17:57:06
 Job time : 9.73262 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:30:37 ; Search time 4.42781 Seconds
(without alignments)
244.278 Million cell updates/sec

Title: US-09-853-253-5
Perfect score: 23
Sequence: 1 ALAGWLRPEDGGQAGAEDELEV 23

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	117	1 GHRL_HUMAN	Q9ubd3 homo sapien
2	10	43.5	116	1 GHRL_BOVIN	Q9bdj6 bos taurus
3	7	30.4	328	1 MPR2_STRCO	Q91127 streptomyce
4	7	30.4	344	1 MPRR_STRLI	P43161 streptomyce
5	7	30.4	1239	1 V120_EBV	P03189 epstein-bar
6	6	26.1	117	1 GHRL_CANFA	Q9bef8 canis famli
7	6	26.1	178	1 EFAB_CHICK	P21760 gallus gall
8	6	26.1	198	1 HIS5_METTH	O27568 methanobact
9	6	26.1	267	1 COLI_PIG	P01192 s corticotr
10	6	26.1	284	1 TPW2_DROME	P09491 drosophila
11	6	26.1	288	1 PCD1_HUMAN	Q15116 homo sapien
12	6	26.1	289	1 OPSD_LIMPA	O42431 limnocottus
13	6	26.1	290	1 PARB_HELPJ	Q9zk75 helicobacte
14	6	26.1	310	1 MTSR_STRP8	Q8p280 streptococc
15	6	26.1	310	1 MTSR_STRPY	Q9a157 streptococc
16	6	26.1	313	1 MRAW_XYLEFA	Q9pf88 xylella fas
17	6	26.1	315	1 YF56_HAEIN	P45250 haemophilus
18	6	26.1	326	1 RBRB_BACSU	P36944 bacillus su
19	6	26.1	346	1 MRAW_BRUME	Q8yi74 bruceella me
20	6	26.1	360	1 CY52_MAIZE	Q10717 zea mays (m
21	6	26.1	379	1 PURK_BACSU	P12045 bacillus su
22	6	26.1	395	1 IF5_SCHPO	Q09689 schizosacch
23	6	26.1	433	1 TIG_STAAM	Q99i66 staphylococ
24	6	26.1	436	1 CUS1_YEAST	Q02554 saccharomyc
25	6	26.1	497	1 RPSD_MYCGE	P47491 mycoplasma
26	6	26.1	499	1 RPSD_MYCPN	P78022 mycoplasma
27	6	26.1	511	1 SYS_MOUSE	P26638 mus musculu
28	6	26.1	513	1 SYS_BOVIN	Q9gmb8 bos taurus
29	6	26.1	513	1 SYS_HUMAN	P49591 homo sapien
30	6	26.1	535	1 AMYB_HORVU	P16098 hordeum vul
31	6	26.1	539	1 T173_HUMAN	Q12899 homo sapien
32	6	26.1	547	1 CH60_BUCTC	Q8kix3 buchnera ap
33	6	26.1	566	1 HS60_CANAL	O74261 candida alb

ALIGNMENTS

RESULT 1

ID	GHRL_HUMAN	STANDARD;	PRT;	117 AA.
AC	Q9UBD3; Q8TAT9; Q9H3R3;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).			
DE	GHRL OR MTLRP.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RN	SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.			
RP	MEDLINE=20067959; PubMed=10604470;			
RX	Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;			
RA	"Ghrelin is a growth-hormone-releasing acylated peptide from stomach."			
RT				
RL	Nature 402:656-660(1999).			
[2]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Kojima M.;			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Stomach;			
RA	Tomasetto C., Karam S.M., Rio M.-C.;			
RT	"Identification of a novel gastric protein m46.";			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
[4]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Wajraich M.P., Ten I.S., Gertner J.M., Leibell R.L.;			
RT	"Genomic organization of the human Ghrelin gene.";			
RL	J. Endocrinol. Genet. 1:231-233(2000).			
[5]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Blood;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg K.L., Pelngold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustun T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,			

34	6	26.1	572	1 HS60_YEAST	P19882 saccharomyc
35	6	26.1	590	1 HS60_AJECA	P50142 ajellomyces
36	6	26.1	620	1 SMP_COTJA	Q92154 coturnix co
37	6	26.1	641	1 DXS_RHOCA	P26242 rhodobacter
38	6	26.1	650	1 APPI_HUMAN	P51693 homo sapien
39	6	26.1	657	1 HUTH_MOUSE	P35492 mus musculu
40	6	26.1	683	1 Z263_HUMAN	O14978 homo sapien
41	6	26.1	702	1 HELS_AERPE	Q9Vf98 aeropyrum p
42	6	26.1	728	1 UVRG_STRCO	Q92512 streptomyce
43	6	26.1	886	1 SM6B_MOUSE	O54951 mus musculu
44	6	26.1	887	1 SM6B_RAT	O70141 rattus norv
45	6	26.1	890	1 AC01_ECOLI	P25516 escherichia

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.:
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [6]
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.:
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [7]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.:
 RA "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -!- PTM: O-n-octanoylation is essential for activity.
 CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/GhrelinID327.html".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB029434; BAA89371.1; -;
 CC EMBL; AB035700; BAB19045.1; -;
 CC EMBL; AJ252278; CAB65733.1; -;
 CC EMBL; AF296558; AAG10300.1; -;
 CC EMBL; BC025791; AAH25791.1; -;
 CC PIR; A59316; A59316.
 CC MIM; 605353; -;
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0007186; P:G-protein coupled receptor protein signaling. . .; TAS.
 CC InterPro; IPR006737; motilin_assoc.
 CC InterPro; IPR006738; motilin_ghrelin.
 CC InterPro; IPR005441; Preproghrelin.
 CC Pfam; PF04643; motilin_assoc; 1.
 CC Pfam; PF04644; motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD332162; Preproghrelin; 1.
 CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 CC Alternative splicing.
 CC SIGNAL 1 23
 CC PEPTIDE 24 51 GHRELIN.
 CC PROPEP 52 117 REMOVED IN MATURE FORM.
 CC LIPID 26 26 N-OCTANOATE.
 CC VARSPPLIC 37 37 Missing (in isoform 2).
 CC CONFLICT 72 72 L -> M (IN REF. 5).
 FT

SO SEQUENCE 117 AA; 12911 MW; 39C0572BEECA2755 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy
 Db 1 ALAGWLRPEDGGGAEGAEDELEV 23
 52 ALAGWLRPEDGGGAEGAEDELEV 74
 RESULT 2
 GHRL_BOVIN STANDARD; PRT; 116 AA.
 ID GHRL_BOVIN Q9BDJ6; Q9GKY6;
 AC Q9BDJ6; Q9GKY6;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ghrelin precursor (growth hormone secretagogue) (Growth hormone
 GN releasing peptide).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kita K., Harada K., Yokota H.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 24-99 FROM N.A.
 RA Kojima M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- PTM: O-n-octanoylation is essential for activity.
 CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF350329; AAK18612.1; -;
 CC EMBL; AB035702; BAB19047.1; -;
 CC InterPro; IPR006737; motilin_assoc.
 CC InterPro; IPR006738; motilin_ghrelin.
 CC InterPro; IPR005441; Preproghrelin.
 CC Pfam; PF04643; motilin_assoc; 1.
 CC Pfam; PF04644; motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD332162; Preproghrelin; 1.
 CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
 CC Alternative splicing.
 CC SIGNAL 1 23
 CC PEPTIDE 24 50 GHRELIN (BY SIMILARITY).
 CC PROPEP 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).
 CC LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
 CC CONFLICT 34 34 K -> E (IN REF. 2).
 SQ SEQUENCE 116 AA; 12792 MW; F55536DAC5FA59B6 CRC64;
 Query Match 43.5%; Score 10; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 QAEGAEDELE 22

```
Db          63 QAEGADELE 72
|||||
RESULT 3
MPR2_STRCO          STANDARD;          PRT;          328 AA.
ID  MPR2_STRCO          STANDARD;          PRT;          328 AA.
AC  Q9L127;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Small neutral protease regulatory protein.
GN  MPRR2 OR SC07433 OR SC6D11.29.
OS  Streptomyces coelicolor.
OC  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC  Streptomycineae; Streptomycetaceae; Streptomyces.
OX  NCBI_TaxID=1902;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=A3(2) / M145;
RX  MEDLINE=21996410; PubMed=12000953;
RA  Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA  Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA  Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA  Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA  Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA  Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA  Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA  Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA  Hopwood D.A.;
RA  "Complete genome sequence of the model actinomycete Streptomyces
RT  coelicolor A3(2).";
RL  Nature 417:141-147(2002).
CC  -!- FUNCTION: TRANSCRIPTIONAL TRANS-ACTIVATOR OF THE GENE (MPRA) FOR
CC  THE SMALL NEUTRAL PROTEASE.
CC  -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC  REGULATORS.
CC  -----
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CC  -----
CC  EMBL: AL939131; CAB76352.1; -
CC  InterPro: IPR000847; HTH_LysR.
CC  Pfam: PF00126; HTH_1; 1.
CC  PRINTS: PR00039; HTHLYSR.
CC  PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
CC  DNA-binding; Protease; Transcription regulation; Complete proteome.
CC  DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
CC  SEQUENCE 328 AA; 35885 MW; 2BA97730AE4FA16B CRC64;
CC  -----
CC  Query Match 30.4%; Score 7; DB 1; Length 328;
CC  Best Local Similarity 100.0%; Pred. No. 4;
CC  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC  QY 1 ALAGWLR 7
CC  |||||
CC  Db 104 ALAGWLR 110
CC  -----
RESULT 4
MPRR_STRLI          STANDARD;          PRT;          344 AA.
ID  MPRR_STRLI          STANDARD;          PRT;          344 AA.
AC  P43161;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Small neutral protease regulatory protein.
GN  MPRR OR SNPR.
OS  Streptomyces lividans.
OC  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC  Streptomycineae; Streptomycetaceae; Streptomyces.
OX  NCBI_TaxID=1916;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=66 / 1326;
RX  MEDLINE=93099553; PubMed=14540866;
RA  Butler M.J., Davey C.C., Krygsmann P., Walczyk E., Malek L.T.;
RT  "Cloning of genetic loci involved in endoprotease activity in
RT  Streptomyces lividans 66: a novel neutral protease gene with an
RT  adjacent divergent putative regulatory gene.";
RL  Can. J. Microbiol. 38:912-920(1992).
RN  [2]
RP  SEQUENCE OF 1-305 FROM N.A.
RC  STRAIN=TK24;
RX  MEDLINE=92192468; PubMed=1547948;
RA  Lichenstein H.S., Busse L.A., Smith G.A., Narchi L.O.,
RA  McGinley M.O., Rohde M.F., Katowitz J.L., Zukowski M.M.;
RT  "Cloning and characterization of a gene encoding extracellular
RT  metalloprotease from Streptomyces lividans.";
RL  Gene 111:125-130(1992).
CC  -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE GENE (SNPA) FOR THE
CC  SMALL NEUTRAL PROTEASE.
CC  -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC  REGULATORS.
CC  -----
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CC  -----
CC  EMBL: M81703; AAA26739.1; -
CC  EMBL: M89476; AAA26804.1; ALT_INIT.
CC  InterPro: IPR000847; HTH_LysR.
CC  InterPro: IPR005119; LysR_subst.
CC  Pfam: PF00126; HTH_1; 1.
CC  Pfam: PF03466; LysR_substrate; 1.
CC  PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
CC  Transcription regulation; DNA-binding; Activator.
CC  DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
CC  CONFLICT 270 270 G -> AR (IN REF. 2).
CC  SEQUENCE 344 AA; 37415 MW; 485C82C813B52312 CRC64;
CC  -----
CC  Query Match 30.4%; Score 7; DB 1; Length 344;
CC  Best Local Similarity 100.0%; Pred. No. 4.2;
CC  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC  QY 1 ALAGWLR 7
CC  |||||
CC  Db 104 ALAGWLR 110
CC  -----
RESULT 5
V120_EBV
ID  V120_EBV          STANDARD;          PRT;          1239 AA.
AC  P03189;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last annotation update)
DE  Capsid assembly protein BOLF1.
GN  BOLF1.
OS  Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
OC  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC  Gammaherpesvirinae; Lymphocryptovirus.
OX  NCBI_TaxID=10377;
RN  [1]
RP  SEQUENCE FROM N.A.
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RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Sequin C.,
RA Tufnell P.S., Barrall B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
CC -I- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
CC EHV-1 23, EBV BOLE1, VZV 21, HVS-1 63, AND HCMV UL47.
CC -----
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CC -----
DR EMBL; V01555; CAA24841.1; -.
DR PIR; A43041; QQBE10.
DR CAPSID assembly.
KW Capsid assembly.
SQ SEQUENCE 1239 AA; 132748 MW; 6C5DBFC55F2FF729 CRC64;

Query Match 30.48; Score 7; DB 1; Length 1239;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AEGAEDE 20
Db 696 AEGAEDE 702
|||||

RESULT 6
GHRL_CANFA
ID GHRL_CANFA STANDARD; PRT; 117 AA.
AC Q9BEF8; Q9BEF7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide).
DE GHRL OR MTLRP.
GN Canis familiaris (Dog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Gastric fundus;
RA Tomasetto C., Wendling C., Rio M.-C., Poltras P.;
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
RT fundus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9BEF8-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9BEF8-2; Sequence=VSP_003244;
CC -I- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -I- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
DR EMBL; AJ298295; CAC29155.1; -.
DR EMBL; AJ298296; CAC29156.1; -.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD33216; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 36 N-OCTANOATE (BY SIMILARITY).
FT VARSPIC 37 37 Missing (in isoform 2).
FT FTID=VSP_003244.
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Query Match 26.18; Score 6; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 AEDELE 22
Db 68 AEDELE 73
|||||

RESULT 7
EFAB_CHICK
ID EFAB_CHICK STANDARD; PRT; 178 AA.
AC P21760; P21928; O9PWN9;
DT 01-MAY-1991 (Rel. 18, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Extracellular fatty acid binding protein precursor (Ex-FABP)
DE Quiescence-specific protein (p20K) (Ch21 protein).
DE EXFABP.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89261749; PubMed=2498647;
RA Bedard P.-A., Yannoni Y., Simmons D.L., Erikson R.L.;
RT "Rapid repression of quiescence-specific gene expression by epidermal
RT growth factor, insulin, and pp60v-src.";
RL Mol. Cell. Biol. 9:1371-1375(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92147639; PubMed=1737754;
RA Dozin B., Descalzi F., Briata L., Hayashi M., Gentili C.,
RA Hayashi K., Quarto R., Cancedda R.;
RT "Expression, regulation, and tissue distribution of the Ch21 protein
RT during chicken embryogenesis.";
RL J. Biol. Chem. 267:2979-2985(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Leghorn;
RA Giannoni P., Dozin B., Zambotti A., Neri M., Cancedda R.;
RT "Differentiation-dependent activation of the extracellular fatty acid
RT binding protein (EXFABP) gene in chicken embryo chondrocytes.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 25-178 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91035433; PubMed=2229062;
RA Cancedda F.D., Dozin B., Rossi F., Molina F., Cancedda R.,
RA Negri A., Ronchi S.;
RT "The Ch21 protein, developmentally regulated in chick embryo, belongs

```


RT to the superfamily of lipophilic molecule carrier proteins.";

RL J. Biol. Chem. 265:19060-19064(1990).

RN [5]

RP SEQUENCE OF 21-48.

RX MEDLINE=90267487; PubMed=2346493;

RA Cancedda F.D., Asaro D., Molina F., Cancedda R., Caruso C.,

RA Camardella L., Negri A., Ronchi S.;

RT "The amino terminal sequence of the developmentally regulated Ch21

RT protein shows homology with amino terminal sequences of low molecular

RT weight proteins binding hydrophobic molecules.";

RL Biochem. Biophys. Res. Commun. 168:933-938(1990).

RN [6]

RN SEQUENCE OF 103-178 FROM N.A.

RP STRAIN=White leghorn; TISSUE=Bone marrow;

RX MEDLINE=92195690; PubMed=1549365;

RA Nakano T., Graf T.;

RT "Identification of genes differentially expressed in two types of

RT v-myb-transformed avian myelomonocytic cells.";

RL Oncogene 7:527-534(1992).

RN [7]

RP CHARACTERIZATION.

RX MEDLINE=96355330; PubMed=8702740;

RA Cancedda F.D., Malpeli M., Gentili C., Di Marzo V., Bet P.,

RA Carlevaro M., Cermelli S., Cancedda R.;

RT "The developmentally regulated avian Ch21 lipocalin is an

RT extracellular fatty acid-binding protein.";

RL J. Biol. Chem. 271:20163-20169(1996).

RN [8]

RP CHARACTERIZATION.

RX MEDLINE=20513977; PubMed=11058755;

RA Descalzi Cancedda F., Dozin B., Zerega B., Cermelli S., Cancedda R.;

RT "Ex-PABP: a fatty acid binding lipocalin developmentally regulated in

RT chicken endochondral bone formation and myogenesis.";

RL Biochim. Biophys. Acta 1482:127-135(2000).

CC -!- FUNCTION: Preferentially binds long-chain unsaturated fatty acids

CC such as linoleic acid, oleic acid, arachidonic acid. Also binds

CC with a lower affinity long chain saturated fatty acids such as

CC stearic acid. May act as survival protein by playing a role in

CC maintaining cell viability.

CC -!- SUBUNIT: Monomer.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: PREFERENTIALLY SYNTHESIZED IN NONPROLIFERATING

CC CELLS.

CC -!- PTM: Does not seem to be glycosylated.

CC -!- MISCELLANEOUS: Developmentally regulated in chick embryo.

CC -!- SIMILARITY: Belongs to the lipocalin family.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: M25784; AAA53371.1; -.

CC EMBL: M55644; AAA48677.1; -.

CC EMBL: AF121346; AAD23569.1; -.

CC EMBL: X61199; -; NOT_ANNOTATED_CDS.

CC PIR: A30230; A30230.

CC InterPro: IPR002345; Lipocalin.

CC InterPro: IPR000566; Lipocalin_cytFABP.

CC Pfam: PF00061; Lipocalin; 1.

CC PRINTS: PR00179; LIPOCALIN.

CC PROSITE: PS00213; LIPOCALIN; 1.

CC Lipocalin; Transport; Signal.

CC SIGNAL 1 20 EXTRACELLULAR FATTY ACID BINDING PROTEIN.

CC CHAIN 21 178 BLOCKED.

CC MOD_RES 21 21 BY SIMILARITY.

CC DISULFID 80 173 L -> S (IN REF. 2).

CC CONFLICT 4 4 R -> S (IN REF. 2 AND 4).

CC CONFLICT 27 27 F -> S (IN REF. 2 AND 4).

CC CONFLICT 45 45

FT CONFLICT 62 62 F -> S (IN REF. 1).

FT CONFLICT 96 96 L -> V (IN REF. 1).

SO SEQUENCE 178 AA; 20201 MW; 0DDBC33CIA0C6B8 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 178;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EDELEV 23

DB 65 EDELEV 70

|||||

RESULT 8

HIS5_METH STANDARD; PRT; 198 AA.

ID HIS5_METH

AC 027568;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Imidazole glycerol phosphate synthase subunit hsh (EC 2.4.2.-) (IGP

DE synthase glutamine amidotransferase subunit) (IGP synthase subunit

DE hsh) (ImGP synthase subunit hsh) (IGPS subunit hsh).

GN HSH OR MTH1524.

OS Methanobacterium thermoautotrophicum.

OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;

OC Methanobacteriaceae; Methanothermobacter.

OX NCBI_TaxID=187420;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Delta H;

RA MEDLINE=98037514; PubMed=9371463;

RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,

RA Aldridge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

RA Harrington D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,

RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhekar S.,

RA McDougall S., Shiner G., Goyal A., Pietrovski S., Church G.M.,

RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

RT "Complete genome sequence of Methanobacterium thermoautotrophicum

RT deltaH: functional analysis and comparative genomics.";

RL J. Bacteriol. 179:7135-7155(1997).

CC -!- FUNCTION: IGP catalyzes the conversion of PRFAR and glutamine to

CC IGP, AICAR and glutamate. The hsh subunit provides the glutamine

CC amidotransferase activity that produces the ammonia necessary to

CC hsh for the synthesis of IGP and AICAR (By similarity).

CC -!- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulos-1-

CC ylamino)methyl]ideneamino-1-(5-phosphoribosyl)imidazole-4-

CC carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-

CC aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.

CC -!- PATHWAY: Histidine biosynthesis; fifth step.

CC -!- SUBUNIT: Heterodimer of hsh and hsf (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.

CC -----

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CC -----

CC EMBL: AE000912; AAB85999.1; -.

CC PIR: D69070; D69070.

CC HAMAP: MF_00278; -; 1.

CC InterPro: IPR000991; GATase_1.

CC Pfam: PF00117; GATase; 1.

CC PROSITE: PS00442; GATASE_TYPE_I; 1.

CC Histidine biosynthesis; Transferase; Glutamine amidotransferase;

CC Complete proteome.

CC ACT_SITE 77 77 BY SIMILARITY.

CC ACT_SITE 177 177 BY SIMILARITY.


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CC CC      GLAND.
CC CC      -!- PTM: SPECIFIC ENZYMAIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
CC CC      THE DIFFERENT ACTIVE PEPTIDES.
CC CC      -!- SIMILARITY: BELONGS TO THE POMC FAMILY.
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC CC      use by non-profit institutions as long as its content is in no way
CC CC      modified and this statement is not removed. Usage by and for commercial
CC CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
CC CC      EMBL; X03561; CAA27248.1; -
CC CC      EMBL; X00135; CAA24968.1; -
CC CC      EMBL; S73519; AAB32312.1; -
CC CC      EMBL; K01879; AAB31104.1; -
CC CC      PIR; A93496; CTPGP.
CC CC      InterPro; IPR001941; Mccortin_ACTH.
CC CC      Pfam; PF00976; ACTH_domain; 1.
CC CC      PRINTS; PR00383; MELANOCORTIN.
CC CC      Endorphin; Hormone; Cleavage on pair of basic residues; Amidation;
CC CC      Glycoprotein; Signal.
CC CC      SIGNAL 1 26
CC CC      FT PEPTIDE 27 106
CC CC      FT PEPTIDE 77 87
CC CC      FT PEPTIDE 136 174
CC CC      FT PEPTIDE 136 148
CC CC      FT PEPTIDE 134 174
CC CC      FT PEPTIDE 177 267
CC CC      FT PEPTIDE 177 234
CC CC      FT PEPTIDE 217 234
CC CC      FT PEPTIDE 237 267
CC CC      FT PEPTIDE 237 241
CC CC      FT MOD_RES 87 87
CC CC      FT MOD_RES 148 148
CC CC      FT CARBOHYD 91 91
CC CC      FT VARIANT 143 143
CC CC      FT CONFLICT 6 6
CC CC      FT CONFLICT 15 15
CC CC      FT CONFLICT 23 23
CC CC      FT CONFLICT 49 49
CC CC      FT CONFLICT 267 AA; 28894 MW; A6DB487A5032B648 CRC64;
CC CC      SQ SEQUENCE 267 AA; 28894 MW; A6DB487A5032B648 CRC64;
CC CC      Query Match 26.1%; Score 6; DB 1; Length 267;
CC CC      Best Local Similarity 100.0%; Pred.No. 36;
CC CC      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC CC      QY 16 GAEDEL 21
CC CC      Db 161 GAEDEL 166
CC CC      RESULT 10
CC CC      TPML2_DROME STANDARD; PRT: 284 AA.
CC AC P09491; P09490; Q24408; Q24427; Q24428; Q8S265; Q9VF95;
CC DT 01-MAR-1989 (Rel. 10, Created)
CC DT 01-MAR-1989 (Rel. 10, Last annotation update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Tropomyosin 2 (Tropomyosin I).
CC GN TM2 OR TM1 OR CG4843.
CC OS Drosophila melanogaster (Fruit fly).
CC OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC OC Ephydroidea; Drosophilidae; Drosophila.
CC OX NCBI_TaxID=7227;
CC RN [1]
CC RP SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
CC RC TISSUE=Embryo, Larva, and Pupae;
CC RX MEDLINE=84205661; PubMed=6202423;
CC RA Karlik C.C., Mahaffey J.W., Coutu M.D., Fyrberg E.A.;
CC RT "Organization of contractile protein genes within the 88F subdivision

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RT of the D. melanogaster third chromosome.";
RL Cell 37:469-481(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
RX MEDLINE=86085920; PubMed=3079761;
RA Basi G.S., Storti R.V.;
RT "Structure and DNA sequence of the tropomyosin I gene from Drosophila
RT melanogaster.";
RL J. Biol. Chem. 261:817-827(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brattin R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]
RP REVISIONS.
RC STRAIN=Berkeley;
RX MEDLINE=22426069; PubMed=12537572;
RA Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM EMBRYONIC).
RX STRAIN=Berkeley; TISSUE=Embryo;
RX PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";

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Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
[6]
RN SEQUENCE OF 258-284 FROM N.A. (ISOFORM EMBRYONIC).
RP MEDLINE=85215579; PubMed=4000944;
RA Boardman M., Basi G.S., Storti R.V.;
RT "Multiple polyadenylation sites in a Drosophila tropomyosin gene are
RT used to generate functional mRNAs."
RL Nucleic Acids Res. 13:1763-1776(1985).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Thoracic; Synonyms=127, t;
CC IsoId=P09491-1; Sequence=Displayed;
CC Name=Embryonic; Synonyms=129, A, B, e;
CC IsoId=P09491-2; Sequence=VSP_006616;
CC -1- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE
CC EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
CC -1- SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY.
CC -1- CAUTION: Ref.6 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: K02622; AAA28970.1; -
DR EMBL: K02623; AAA28971.1; -
DR EMBL: K02622; AAA28971.1; JOINED.
DR EMBL: K03277; AAA28973.1; -
DR EMBL: K03277; AAA28974.1; -
DR EMBL: AE003708; AAM13652.1; -
DR EMBL: AY071087; AAL48709.1; -
DR EMBL: X02220; CAA26142.1; ALT_SEQ.
DR PIR: A25624; A25624.
DR PIR: B25624; B25624.
DR FlyBase: FBgn004117; Tm2.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00261; Tropomyosin.1.
DR PRINTS: PR00194; TROPOMYOSIN.
DR PROSITE: PS00326; TROPOMYOSIN; 1.
KW Muscle protein; Coiled coil; Repeat; Alternative splicing;
KW Multigene family.
FT VARSPPLIC 259 284 RLFNEKEKYKAICDDLQDTFAELTGY -> ELGINKORYKS
FT LADMDSTFAELAGY (in isoform Embryonic).
FT /FTId=VSP_006616.
FT M -> V (IN REF. 1).
FT Q -> L (IN REF. 1).
FT I -> T (IN REF. 1).
FT R -> D (IN REF. 1).
SQ SEQUENCE 284 AA; 32981 MW; 07AD03FDD304EA5F CRC64;

Query Match 26.1%; Score 6; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EDELEV 23
Db 173 EDELEV 178
|||||

RESULT 11
PCDL_HUMAN STANDARD; PRT; 288 AA.
ID Q15116; Q00517;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Programmed cell death protein 1 precursor (Protein PD-1) (hpd-1).
GN PCD1 OR PDL.
OS Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=95154844; PubMed=7851902;
RT Shinozawa T., Taniwaki M., Ishida Y., Kawaich M., Honjo T.;
RT "Structure and chromosomal localization of the human PD-1 gene
RT (PCD1)."
RL Genomics 23:704-706(1994).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=97473511; PubMed=9332365;
RA Finger L.R., Pu J., Wasserman R., Vibhakkar R., Louie E., Hardy R.R.,
RA Burrows P.D., Billips L.D.;
RA Gene 203:253-253(1997).
CC -1- FUNCTION: POSSIBLE CELL DEATH INDUCER, IN ASSOCIATION WITH
CC OTHER FACTORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DEVELOPMENTAL STAGE: INDUCED AT PROGRAMMED CELL DEATH.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC -----
DR EMBL: L27440; AAC41700.1; -
DR EMBL: U64863; AAC51773.1; -
DR PIR: A55737; A55737.
DR HSP: P01607; IREI.
DR Genew: HGNC:8760; PDCD1.
DR MIN: 600244; -
DR GO: GO:0004871; F:signal transducer activity; TAS.
DR GO: GO:0006915; P:apoptosis; TAS.
DR GO: GO:0007275; P:development; TAS.
DR GO: GO:0006959; P:humoral immune response; TAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IgV.1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; Apoptosis.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 288 PROGRAMMED CELL DEATH PROTEIN 1.
FT DOMAIN 21 170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 191 POTENTIAL.
FT DOMAIN 192 288 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 35 145 IG-LIKE V-TYPE.
FT DISULFID 54 123 POTENTIAL.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 38 38 F -> S (IN REF. 1).
FT CONFLICT 162 162 P -> S (IN REF. 1).
SQ SEQUENCE 288 AA; 31707 MW; A5210ADS0C3046C7 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 6 LRPEDG 11
Db 277 LRPEDG 282

RESULT 12
OPSD_LIMPA STANDARD; PRT; 289 AA.
AC 042431;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
GN RHO.
OS Limnocottus pallidus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidae; Abyssocottidae; Limnocottus.
OX NCBI_TaxID=61634;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98086781; PubMed=9417898;
RA Hunt D.M., Fitzgibbon J., Slobodyanyuk S.J., Bowmaker J.K.,
RA Dulai K.S.;
RT "Molecular evolution of the cottoid fish endemic to Lake Baikal
RT deduced from nuclear DNA evidence.";
RL Mol. Phylogenet. Evol. 8:415-422(1997).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIANE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES
CC VISION IN DIM LIGHT.
CC -!- PH: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U97271; AAB61725.1; -.
DR HSSP: P02699; IBOJ.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR001760; Opsin.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PS00237; GPCRHHODPSN
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_FL1; FALSE_NEG.
DR PROSITE: PS00262; G-PROTEIN_RECEPTOR_FL2; 1.
DR PROSITE: PS00238; OPSIN; 1.
KW Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
FT NON_TER 1 1
FT DOMAIN <1 7 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 8 32 1 (POTENTIAL).
FT DOMAIN 33 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 69 2 (POTENTIAL).
FT DOMAIN 70 84 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 85 104 3 (POTENTIAL).
FT DOMAIN 105 123 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 124 147 4 (POTENTIAL).
FT DOMAIN 148 173 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 174 201 5 (POTENTIAL).
FT DOMAIN 202 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 247 6 (POTENTIAL).
FT DOMAIN 248 255 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 256 280 7 (POTENTIAL).

DOMAIN 281 >289 CYTOPLASMIC (POTENTIAL).
DISULFID 81 158 BY SIMILARITY.
BINDING 267 267 RETINAL CHROMOPHORE (BY SIMILARITY).
CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
NON_TER 289 289
SEQUENCE 289 AA; 32715 MW; 160D08E17E5E1280 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LAGWLR 7
Db 143 LAGWLR 148

RESULT 13
PARB_HELPJ
ID PARB_HELPJ STANDARD; PRT; 290 AA.
AC 092K75;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable chromosome partitioning protein parB.
GN PARB OR JHP1066.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Gullid B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: INVOLVED IN CHROMOSOME PARTITION. LOCALIZE TO BOTH POLES
CC OF THE PREDIVISIONAL CELL FOLLOWING COMPLETION OF DNA REPLICATION.
CC BINDS TO THE DNA ORIGIN OF REPLICATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARB FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE001534; AAD06646.1; -.
DR PIR: H71852; H71852.
DR InterPro: IPR004437; ParB_part.
DR InterPro: IPR003115; ParBc.
DR Pfam: PF02195; ParBc; 1.
DR SMART: SM00470; ParB; 1.
DR TIGRFAMs: TIGR00180; parB_part; 1.
KW Chromosome partition; DNA-binding; Complete proteome.
SQ SEQUENCE 290 AA; 33405 MW; 6709BA0547A55A4F CRC64;

Query Match 26.1%; Score 6; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 AEDELE 22
Db 245 AEDELE 250

RESULT 14
```

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MTSA_STRP8      STANDARD;      PRT;      310 AA.
ID   Q8P280;
DC   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Metal ABC transporter substrate-binding lipoprotein precursor.
GN   MTSA OR SPYM18_0494.
OS   Streptococcus pyogenes (serotype M18).
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus
OX   NCBI_TaxID=186103;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN-MGAS8232 / Serotype M18;
RX   MEDLINE=21927593; PubMed=11917108;
RA   Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA   Sylva G.B., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA   Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA   Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT   "Genome sequence and comparative microarray analysis of serotype M18
RT   group A Streptococcus strains associated with acute rheumatic fever
RT   outbreaks.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC   -1- FUNCTION: Part of an ATP-driven transport system for a metal; this
CC   protein has affinity for Zn(II), Fe(III) and Cu(II).
CC   -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC   -1- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC   9. Lipoprotein receptor antigen (Lral) subfamily.
-----
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-----
CC   EMBL: AE009988; AAL97215.1; -.
CC   InterPro: IPR006128; Lipoprotein_4.
CC   InterPro: IPR006127; SBP_bac_9.
CC   Pfam: PF01297; SBP_bac_9; 1.
CC   PRINTS: PR00690; ADHESNFAMILY.
CC   PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
CC   Transport; Zinc transport; Iron transport; Copper; Membrane;
CC   Lipoprotein; Signal; Complete proteome.
CC   SIGNAL 1 20 PROBABLE.
CC   CHAIN 21 310 METAL ABC TRANSPORTER SUBSTRATE-
CC   BINDING LIPOPROTEIN.
CC   LIPID 21 21 N-ACYL DIGLYCERIDE (PROBABLE).
CC   SQ SEQUENCE. 310 AA; 34330 MW; 40F613659AAD1768 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 EDGGQA 14
      |||||
Db 94 EDGGQA 99

RESULT 15
MTSA_STRP8      STANDARD;      PRT;      310 AA.
ID   Q9A157; Q9RN17; Q9RNJ0;
DC   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Metal ABC transporter substrate-binding lipoprotein precursor.
GN   MTSA OR SPY0453 OR SPYM3_0318 OR SPS1539.
OS   Streptococcus pyogenes, and
OS   Streptococcus pyogenes (serotype M3).
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

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Streptococcus.
OX   NCBI_TaxID=1314, 198466;
RN   [1]
RP   SEQUENCE FROM N.A., SEQUENCE OF 30-39, AND CHARACTERIZATION.
RC   STRAIN-SF370 / ATCC 700294 / Serotype M1, and API / Serotype M1;
RX   MEDLINE=20032372; PubMed=10564500;
RA   Janutczyk R., Fallon J., Bjoerck L.;
RT   "Identification and characterization of a Streptococcus pyogenes ABC
RT   transporter with multiple specificity for metal cations.";
RL   Mol. Microbiol. 34:596-606(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN-SF370 / ATCC 700294 / Serotype M1;
RX   MEDLINE=21192684; PubMed=11296296;
RA   Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA   Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA   Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA   Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT   "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN-MGAS315 / Serotype M3;
RX   MEDLINE=22133808; PubMed=12122206;
RA   Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA   Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA   Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA   Schlievert P.M., Musser J.M.;
RT   "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT   phage-encoded toxins, the high-virulence phenotype, and clone
RT   emergence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN-SSI-1 / Serotype M3;
RA   Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA   Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA   Hayashi H., Hamada S.;
RT   "The genome of invasive Streptococcus pyogenes: a comparative analysis
RT   of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC   -1- FUNCTION: Part of an ATP-driven transport system for a metal; this
CC   protein has affinity for Zn(II), Fe(III) and Cu(II).
CC   -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC   -1- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC   9. Lipoprotein receptor antigen (Lral) subfamily.
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CC   or send an email to license@isb-sib.ch).
-----
CC   EMBL: AF180520; AAD56936.1; -.
CC   EMBL: AF180521; AAD56939.1; -.
CC   EMBL: AE006505; AAK33468.1; -.
CC   EMBL: AE014143; AAM78925.1; ALT_INIT.
CC   EMBL: AP005145; BAC64634.1; ALT_INIT.
CC   HSPSP; P96116; ITOA.
CC   InterPro: IPR006128; Lipoprotein_4.
CC   InterPro: IPR006127; SBP_bac_9.
CC   Pfam: PF01297; SBP_bac_9; 1.
CC   PRINTS: PR00690; ADHESNFAMILY.
CC   PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
CC   Transport; Zinc transport; Iron transport; Copper; Membrane;
CC   Lipoprotein; Signal; Complete proteome.
CC   SIGNAL 1 20 PROBABLE.
CC   CHAIN 21 310 METAL ABC TRANSPORTER SUBSTRATE-
CC   BINDING LIPOPROTEIN.
CC   LIPID 21 21 N-ACYL DIGLYCERIDE (PROBABLE).
CC   VARIANT 77 77 V -> A (IN STRAIN API).

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FT CONFLICT 26 26 T -> A (IN REF. 1).
FT CONFLICT 30 30 K -> E (IN REF. 1).
FT CONFLICT 44 44 A -> G (IN REF. 1).
FT CONFLICT 49 50 AI -> VM (IN REF. 1).
SQ SEQUENCE 310 AA: 34358 MW: B0F829EF1C72CADC CRC64;

Query Match 26.1%; Score 6; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 EDGGOA 14
Db 94 EDGGOA 99

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Search completed: September 11, 2003, 17:52:41
Job time : 5.42781 secs

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OM protein - protein search, using sw model
Run on: September 11, 2003, 17:46:02 ; Search time 22.016 seconds
(without alignments)
269.586 Million cell updates/sec

Title: US-09-853-253-5
Perfect score: 23
Sequence: 1 ALAGWLRPDGGQAEDELEV 23

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	87.0	117	Q8TAT9	Q8ch53 meriones un
2	11	47.8	117	Q8CH53	Q93zv7 arabidopsis
3	8	34.8	433	Q93ZV7	Q817e4 arabidopsis
4	8	34.8	433	Q8L7E4	Q85529 arabidopsis
5	8	34.8	483	Q85529	Q91063 streptomyce
6	7	30.4	103	Q9L063	Q8vp52 streptomyce
7	7	30.4	313	Q8VP52	Q8cny4 staphylococ
8	7	30.4	433	Q8CNY4	Q8xy49 raltstonia s
9	7	30.4	887	Q8XY49	Q913f5 pseudomonas
10	7	30.4	910	Q913F5	Q9v5j0 drosophila
11	7	30.4	2376	Q9V5J0	Q966v1 drosophila
12	7	30.4	2376	Q966V1	Q9a542 caulobacter
13	6	26.1	69	Q9A542	Q8zr1 pyrobaculum
14	6	26.1	88	Q8ZZR1	P91785 onchocerca
15	6	26.1	98	P91785	Q8pbn4 xanthomonas
16	6	26.1	100	Q8PBN4	

17	6	26.1	106	10	P93359	P93359 nicotiana t
18	6	26.1	110	2	Q87801	Q87801 pseudomonas
19	6	26.1	112	5	Q26847	Q26847 trypanosoma
20	6	26.1	113	16	Q8G7N5	Q8G7N5 blifidobacte
21	6	26.1	117	12	Q85548	Q85548 bovine herp
22	6	26.1	129	4	Q43180	Q43180 homo sapien
23	6	26.1	133	13	Q8JFY6	Q8Jfy6 liktoria cae
24	6	26.1	137	4	Q8N8H9	Q8n8h9 homo sapien
25	6	26.1	138	16	Q9RD30	Q9rd30 streptomyce
26	6	26.1	142	16	Q8ZBU1	Q8zbul yersinia pe
27	6	26.1	147	5	Q25622	Q25622 onchocerca
28	6	26.1	148	5	Q8WT59	Q8wt59 onchocerca
29	6	26.1	154	5	Q8WT58	Q8wt58 onchocerca
30	6	26.1	154	5	Q8WT56	Q8wt56 litomosoid
31	6	26.1	154	5	Q8WT57	Q8wt57 onchocerca
32	6	26.1	159	3	Q05697	Q05697 saccharomyc
33	6	26.1	159	4	Q8N9A4	Q8n9a4 homo sapien
34	6	26.1	161	10	Q9LWY4	Q9lwy4 oryza sativ
35	6	26.1	165	2	Q9RNJ3	Q9rnj3 zymomonas m
36	6	26.1	165	16	Q8XXY6	Q8xyy6 raltstonia s
37	6	26.1	171	5	Q25624	Q25624 onchocerca
38	6	26.1	175	13	Q8JFY7	Q8Jfy7 liktoria cae
39	6	26.1	175	16	Q9KQ90	Q9kq90 vibrio chol
40	6	26.1	177	11	Q8CIQ8	Q8ciq8 rattus norv
41	6	26.1	178	5	Q25619	Q25619 onchocerca
42	6	26.1	178	5	Q8WZJ8	Q8wzj8 acanthochei
43	6	26.1	178	16	Q98IM5	Q98im5 rhizobium l
44	6	26.1	180	2	O50344	O50344 lactobacilli
45	6	26.1	186	5	Q9UIY0	Q9uiy0 caenorhabdi

ALIGNMENTS

RESULT 1

Q8TAT9	PRELIMINARY;	PRT;	117 AA.
AC	Q8TAT9		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Ghrilin.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Blood;		
RA	Strausberg R.;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC025791; AAH25791.1; .		
DR	InterPro; IPR006737; motilin_assoc.		
DR	InterPro; IPR006738; motilin_ghrilin.		
DR	Pfam; PF04643; motilin_assoc.1.		
DR	Pfam; PF04644; motilin_ghrilin.1.		
SQ	SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;		

Query Match 87.0%; Score 20; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.4e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ALAGWLRPDGGQAEDE	20
Db	52	ALAGWLRPDGGQAEDE	71

RESULT 2			
Q8CH53	PRELIMINARY;	PRT;	117 AA.
ID	Q8CH53		
AC	Q8CH53		
DT	01-MAR-2003 (TREMBLrel. 23, Created)		
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)		

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoaka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AAO06965.1; -;
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 47.8%; Score 11; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GOAEGAEDELE 22
Db 63 GOAEGAEDELE 73

RESULT 3
Q932V7 PRELIMINARY; PRT; 433 AA.
ID Q932V7;
AC Q932V7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative RNA-binding protein LAHI.
GN AT4G32720
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banno F., Banno J., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene AT4G32720 (GI:7270219).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY056237; AAL07086.1; -;
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR PROSITE; PS50102; RRM; 1.
DR Hypothetical protein.
KW SEQUENCE 433 AA; 48095 MW; E58EBAF51C35A8F7 CRC64;

Query Match 34.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAEDE 20
Db 287 QAEGAEDE 294

RESULT 4
Q8L7E4 PRELIMINARY; PRT; 433 AA.
ID Q8L7E4;
AC Q8L7E4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN AT4G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Hsuan Y.W., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Shinn P., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
RA Theologis A., Davis R.W.;
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banno J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY136302; AAM96968.1; -;
DR EMBL; BT000396; AAN15715.1; -;
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR PROSITE; PS50102; RRM; 1.
DR Hypothetical protein.
KW SEQUENCE 433 AA; 48126 MW; CFF611A29AA0318 CRC64;

Query Match 34.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAEDE 20
Db 287 QAEGAEDE 294

RESULT 5
O65529 PRELIMINARY; PRT; 483 AA.
ID O65529;
AC O65529;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 54.1 kDa protein.
GN F4D11.80 OR AT4G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoorge W., Hohseisel J.,
RA Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]

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RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.:
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022537; CAA18589.1; -.
DR EMBL; AL161582; CAB79989.1; -.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;

Query Match 34.8%; Score 8; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAED 20
DB 302 QAEGAED 309
|||||||

RESULT 6
Q9L063
ID Q9L063 PRELIMINARY; PRT; 103 AA.
AC Q9L063:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein SC02791.
GN SC02791 OR SCCL05_22C
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939114; CAB87228.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;

Query Match 30.4%; Score 7; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAE 16
DB 48 DGGQAE 54
|||||||

RESULT 7
Q8XY49
ID Q8XY49 PRELIMINARY; PRT; 887 AA.

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Q8VP52
ID Q8VP52 PRELIMINARY; PRT; 313 AA.
AC Q8VP52:
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE LysR-like transcriptional activator Snpr.
OS Streptomyces sp. C5.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=45212;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C5;
RA Desanti C.L., Strohl W.R.;
RT "Characterization of the Streptomyces sp. strain C5 snp locus and
RT development of an snp-derived expression vector family.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AY072041; AAL61992.1; -.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; Transcription; Transcription regulation.
SQ SEQUENCE 313 AA; 34258 MW; C907C8AF51C3FA13 CRC64;

Query Match 30.4%; Score 7; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
DB 103 ALAGWLR 109
|||||||

RESULT 8
Q8CNY4
ID Q8CNY4 PRELIMINARY; PRT; 433 AA.
AC Q8CNY4:
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Trigger factor.
GN SEI350.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RA Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016748; AAO04949.1; -.
KW Complete proteome.
SQ SEQUENCE 433 AA; 48732 MW; FF2490AD097F437D CRC64;

Query Match 30.4%; Score 7; DB 16; Length 433;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAE 16
DB 180 DGGQAE 186
|||||||

RESULT 9
Q8XY49
ID Q8XY49 PRELIMINARY; PRT; 887 AA.

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AC Q8XY49;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Probable phage-related tail transmembrane protein..
 GN RSC1914 OR R503483.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 DR EMBL: AL646067; CAD15616.1; .
 KW Complete proteome.
 SQ SEQUENCE 887 AA; 94105 MW; 9A8840E5362E740E CRC64;
 Query Match 30.4%; Score 7; DB 16; Length 887;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 QOAGAE 18
 Db 290 QOAGAE 296
 RESULT 10
 Q913F5 PRELIMINARY; PRT; 910 AA.
 AC Q913F5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Aconitase hydratase 1.
 GN ACNA OR PA1562.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Slover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RL Nature 406:959-964(2000).
 DR EMBL: AE004584; AAG04951.1; .
 DR HSSP: P20004; IACO.
 DR InterPro: IPR006249; Aconitase_1.
 DR InterPro: IPR000573; Aconitase_C.
 DR InterPro: IPR001030; Aconitase_N.
 DR Pfam: PF00330; aconitase; 1.
 DR Pfam: PF00694; Aconitase_C; 1.
 DR PRINTS: PR00415; ACONITASE.
 DR ProDom: PD000511; Aconitase_N; 1.
 DR TIGRFAMS: TIGR01341; aconitase_1; 1.
 DR PROSITE: PS00450; ACONITASE_1; 1.
 DR PROSITE: PS01244; ACONITASE_2; 1.

KW Complete proteome.
 SQ SEQUENCE 910 AA; 99147 MW; C65F23CDB6FA0E1C CRC64;
 Query Match 30.4%; Score 7; DB 16; Length 910;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLR 7
 Db 65 ALAGWLR 71
 RESULT 11
 Q9V5J0 PRELIMINARY; PRT; 2376 AA.
 AC Q9V5J0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG18408 protein.
 GN REXIN OR CG3451 OR CG18408 OR CG18409.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Spierkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Gallie R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveril J.S., Smith H.O., Venter C.J., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Brygman C., Bernan B., Carlson J.W., Celnikier S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celnikier S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003830; AAF58816.2; -
DR FlyBase: FBgn0033504; rexin.
DR InterPro: IPR001452; SH3.
DR PRINTS: PR00452; SH3DOMAIN.
DR ProDom: PD000066; SH3; 3.
DR SMART: SM00326; SH3; 3.
DR PROSITE: PS00002; SH3; 3.
SQ SEQUENCE 2376 AA; 267666 MW; A5F2D0589B8B695C CRC64;
Query Match 30.4%; Score 7; DB 5; Length 2376;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 QAEGAED 19
Db 37 QAEGAED 43
RESULT 12
Q966V1 PRELIMINARY; PRT; 2376 AA.
AC Q966V1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE REXIN L1.
GN REXIN OR RXN OR CG3451 OR CG18408 OR CG18409.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki H.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamazaki H., Willert K., Fish M., Nusse R.;
RT "Drosophila REXIN, a Novel SH3 Adaptor Protein of Axin and Arrow that
RT is Essential for Living in Late Stage Embryo.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 3 SH3 DOMAINS.
DR EMBL: AB053478; BAB62017.1; -
DR FlyBase: FBgn0033504; rexin.
DR InterPro: IPR002965; P_RICH_extensn.
DR Pfam: PF00018; SH3; 3.
DR PRINTS: PR01217; PRICHEXTENS.
DR ProDom: PD000066; SH3; 3.
DR SMART: SM00326; SH3; 3.
DR PROSITE: PS00002; SH3; 3.
KW SH3 domain.
SQ SEQUENCE 2376 AA; 267657 MW; 9C7BD6C7A705C888 CRC64;
Query Match 30.4%; Score 7; DB 5; Length 2376;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 QAEGAED 19
Db 37 QAEGAED 43
RESULT 13
Q9A542 PRELIMINARY; PRT; 69 AA.
AC Q9A542;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cold-shock domain family protein.
GN CC2623.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR EMBL: AE005930; AAK24591.1; -
DR HSP: F15277; IMJC.
DR TIGR: CC2623; -
DR InterPro: IPR002059; Cold_shock.
DR Pfam: PF00313; CSD; 1.
DR PRINTS: PR00050; COLDSHOCK.
DR ProDom: PD000621; Cold_shock; 1.
DR SMART: SM00357; Csp; 1.
KW Activator; DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 69 AA; 7450 MW; 8EA80BE9EE56853C CRC64;
Query Match 26.1%; Score 6; DB 16; Length 69;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 PEDGGQ 13
Db 20 PEDGGQ 25
RESULT 14
Q8Z2R1 PRELIMINARY; PRT; 88 AA.
ID Q8Z2R1

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AC Q8Z2R1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PAE0124.
GN PAE0124.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RL aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009752; AAL62578.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 88 AA: 9492 MW; 22091651B45CADD1 CRC64;

Query Match 26.1%; Score 6; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
DB 45 ALAGWL 50

RESULT 15
P91785
ID P91785 PRELIMINARY; PRT; 98 AA.
AC P91785;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Antigen maltose binding protein (Fragment).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94336252; PubMed=8058358;
RA Trenholme K.R., Tree T.I., Gillespie A.J., Guderian R., Maizels R.M.,
RA Bradley J.E.;
RT "Heterogeneity of IgG antibody responses to cloned Onchocerca volvulus
RT antigens in microfilariemia positive individuals from Esmeraldas
RT Province, Ecuador.";
RL Parasite Immunol. 16:201-209(1994).
DR EMBL; S71371; AAC60510.2; -.
FT NON_TER 1
FT NON_TER 98
SQ SEQUENCE 98 AA: 11165 MW; 221BEFEFE14DC76 CRC64;

Query Match 26.1%; Score 6; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LRPEDG 11
DB 51 LRPEDG 56

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Search completed: September 11, 2003, 17:55:49
 Job time : 23.016 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 : Search time 23.984 Seconds
(without alignments)
152.215 Million cell updates/sec

Title: US-09-853-253-5

Perfect score: 121

Sequence: 1 ALAGWLRPEDGGQAGAEDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121	100.0	23	AAE23840	Human zsig33-linker
2	121	100.0	23	AAE23841	Human zsig33-linker
3	121	100.0	23	AAE15885	Human zsig33-linker
4	121	100.0	23	AAE15886	Human zsig33-linker
5	121	100.0	24	AAE23839	Human zsig33-linker
6	121	100.0	24	AAE15884	Human zsig33-linker
7	121	100.0	91	AAE33410	Human exon 3-delet
8	121	100.0	116	AAE60517	Human des-Gln14-gh
9	121	100.0	117	AAW87991	Protein designated

10	121	100.0	117	21	AAV87236	Human signal pepti
11	121	100.0	117	22	AAW38890	Human polypeptide
12	121	100.0	117	22	AAE62649	Human zsig33 poly
13	121	100.0	117	22	AAE20101	zsig33 protein. H
14	121	100.0	117	22	AAE60511	Human ghrelin prep
15	121	100.0	117	23	ABW78319	Amino acid sequenc
16	121	100.0	117	23	AAE23838	Human zsig33 prote
17	121	100.0	117	23	AAE15883	Human zsig33 prote
18	121	100.0	117	24	ABW66790	Human PRO polypept
19	121	100.0	117	24	ABW67066	Human secreted/tr
20	121	100.0	117	24	ABW59871	Novel secreted and
21	121	100.0	117	24	ABU59124	Novel human secret
22	121	100.0	117	24	ABU59271	Human secreted/tr
23	121	100.0	117	24	ABU59420	Novel human secret
24	121	100.0	117	24	ABU60555	Human secreted/tr
25	121	100.0	117	24	ABU58046	Human PRO polypept
26	121	100.0	117	24	ABU58977	Human secreted/tr
27	121	100.0	117	24	AAE33409	Human preproghreli
28	121	100.0	117	24	ABU13937	Human PRO1066 poly
29	121	100.0	117	24	ABU10892	Human PRO polypept
30	121	100.0	118	21	AAV66708	Membrane-bound pro
31	121	100.0	118	22	AAU12392	Human PRO1066 poly
32	121	100.0	118	22	AAE65231	Human PRO1066 (UNQ
33	121	100.0	126	22	AAW40676	Human polypeptide
34	90	74.4	90	23	ABP08975	Human OREF protein
35	90	74.4	116	22	AAE60516	Rat des-Gln14-ghre
36	90	74.4	117	22	AAE60510	Rat ghrelin prepro
37	87	71.9	117	22	AAE60521	Porcine des-Gln14-
38	87	71.9	118	22	AAE60520	Porcine ghrelin pr
39	62.5	51.7	89	22	AAE60523	Bovine ghrelin pre
40	54	44.6	200	24	ABP58240	Xenopus laevis nuc
41	50	41.3	653	17	AAE98903	Murine APLP1. Mus
42	48	39.7	82	22	AAE73526	Human colon cancer
43	48	39.7	287	22	ABE15575	Novel human diagno
44	48	39.7	570	22	ABE20671	Novel human diagno
45	48	39.7	2836	22	ABE62719	Drosophila melanog

ALIGNMENTS

RESULT 1
AAE23840
ID AAE23840 standard; peptide; 23 AA.

AC AAE23840;

DT 10-SEP-2002 (first entry)

DE Human zsig33-linker peptide #2.

KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.

OS Homo sapiens.

PN US2002055156-A1.

PD 09-MAY-2002.

PF 10-MAY-2001; 2001US-0853253.

PR 11-MAY-2000; 2000US-203300P.

PA (JASP/) JASPERS S R.

PA (SHEP/) SHEPPARD P O.

PA (DEIS/) DEISHER T A.

PA (BISH/) BISHOP P D.

PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-443750/47.

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
XX
XX
XX Claim 1; Page 28; 34pp; English.
XX
XX The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 121; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
DB 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 2
AAE23841
ID AAE23841 standard; peptide; 23 AA.
XX
XX
AC AAE23841;
XX
XX 10-SEP-2002 (first entry)
XX
XX Human zsig33-linker peptide #3.
XX
XX Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.
XX
XX Homo sapiens.
OS
XX
XX US2002055156-A1.
PN
XX
XX 09-MAY-2002.
XX
XX 10-MAY-2001; 2001US-0853253.
PF
XX
XX 11-MAY-2000; 2000US-203300P.
PR
XX
XX (JASP/) JASPERS S R.
PA (SHEP/) SHEPPARD P O.
PA (DEIS/) DEISHER T A.
PA (BISH/) BISHOP P D.
XX
XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
PI WPI; 2002-443750/47.
XX
XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
XX
XX Claim 1; Page 28; 34pp; English.
XX
XX The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 121; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
DB 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 3
AAE15885
ID AAE15885 standard; peptide; 23 AA.
XX
XX
AC AAE15885;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human zsig33-linker peptide #2.
XX
XX Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-linker peptide.
XX
XX Homo sapiens.
OS
XX
XX WO200187933-A2.
PN
XX
XX 22-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-US15091.
PF
XX
XX 11-MAY-2000; 2000US-0569271.
PR
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
PI WPI; 2002-082982/11.
XX
XX N-PSDB; AAD25760.
XX
XX New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and
PT treating gastrointestinal and growth related diseases, comprises

PT zsig33-like peptides -
XX Claim 1b; Page 81; 89pp; English.
XX
XX The invention relates to zsig33-like peptides (ZS33LP) including
CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and
CC zsig33-epsilon peptides and nucleic acid molecules encoding such
CC zsig33-like peptides. ZS33LP peptides activate the immune system
CC in boosting immunity to infectious diseases, treating immunocompromised
CC patients such as human immunodeficiency virus (HIV) patients, in
CC improving vaccines and in treatment of bacterial, viral, protozoal and
CC fungal infections. Peptides of the invention are used to identify and
CC isolate receptors involved in growth regulation in the liver, blood
CC vessel formation and other developmental processes. They are useful for
CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
CC growth and/or differentiation of tumour cells, as additives to anti-
CC hypoglycaemic preparations containing glucose and as adsorption
CC enhancers for oral drugs which require fast nutrient action and to
CC stimulate glucose-induced insulin release. They are also useful as
CC research reagents for the expansion, differentiation, growth factor and
CC hormone secretion and/or cell-cell interactions of tissues associated
CC with gastrointestinal system, brain and central nervous system. These
CC molecules are useful for treating dysfunction associated with contractile
CC tissues or to suppress or enhance contractility in vivo and to treat
CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
CC acids and/or antibodies are useful for treating disorders associated
CC with gastrointestinal contractility, secretion of digestive enzymes,
CC hormone and acids, secretion of hormones in the pancreas and/or brain,
CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
CC and regulation of nutrient absorption. Sequences of the invention are
CC useful in gene therapy. The present sequence is human zsig33-linker
CC peptide.
XX
XX Sequence 23 AA;
SQ
Query Match 100.0%; Score 121; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQGAEGAEDELEV 23
Db 1 ALAGWLRPEDGGQGAEGAEDELEV 23
RESULT 4
AAE15886
ID AAE15886 standard; peptide; 23 AA.
XX
XX AAE15886;
XX
XX 26-MAR-2002 (first entry)
XX Human zsig33-linker peptide #3.
XX
KW Human; zsig33-like peptide; ZS33LP; Immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-linker peptide.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 23
FT /note= "C-terminal amide"
FT
XX WO200187933-A2.
PN
XX
XX 22-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-US15091.
PF
XX 11-MAY-2000; 2000US-0569271.
PR

(ZYMO) ZYMOGENETICS INC.
Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
WPI; 2002-082982/11.
N-PSDB; AAD25760.
New polypeptides, useful for modulating gastric contractility, nutrient
uptake, pancreatic secretion of hormones, digestive enzymes and
treating gastrointestinal and growth related diseases, comprises
zsig33-like peptides -
Claim 1c; Page 82; 89pp; English.
The invention relates to zsig33-like peptides (ZS33LP) including
zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and
zsig33-epsilon peptides and nucleic acid molecules encoding such
zsig33-like peptides. ZS33LP peptides activate the immune system
in boosting immunity to infectious diseases, treating immunocompromised
patients such as human immunodeficiency virus (HIV) patients, in
improving vaccines and in treatment of bacterial, viral, protozoal and
fungal infections. Peptides of the invention are used to identify and
isolate receptors involved in growth regulation in the liver, blood
vessel formation and other developmental processes. They are useful for
evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
growth and/or differentiation of tumour cells, as additives to anti-
hypoglycaemic preparations containing glucose and as adsorption
enhancers for oral drugs which require fast nutrient action and to
stimulate glucose-induced insulin release. They are also useful as
research reagents for the expansion, differentiation, growth factor and
hormone secretion and/or cell-cell interactions of tissues associated
with gastrointestinal system, brain and central nervous system. These
molecules are useful for treating dysfunction associated with contractile
tissues or to suppress or enhance contractility in vivo and to treat
gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
acids and/or antibodies are useful for treating disorders associated
with gastrointestinal contractility, secretion of digestive enzymes,
hormone and acids, secretion of hormones in the pancreas and/or brain,
gastrointestinal motility, recruitment of digestive enzymes, inflammation
and regulation of nutrient absorption. Sequences of the invention are
useful in gene therapy. The present sequence is human zsig33-linker
peptide.
Query Match 100.0%; Score 121; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQGAEGAEDELEV 23
Db 1 ALAGWLRPEDGGQGAEGAEDELEV 23
RESULT 5
AAE23839
ID AAE23839 standard; peptide; 24 AA.
XX
XX AAE23839;
AC
XX
XX 10-SEP-2002 (first entry)
XX Human zsig33-linker peptide #1.
XX
KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Region 7..18
FT


```

ID  AAE33410 standard; Protein; 91 AA.
XX  AAE33410;
AC
XX
XX  02-APR-2003 (first entry)
DT
XX
XX  Human exon 3-deleted ghrelin protein.
DE
XX
XX  Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
KW  breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
KW  cancer; human.
XX
XX  Homo sapiens.
OS
XX
XX  WO200290387-A1.
PN
XX
XX  14-NOV-2002.
PD
XX
XX  10-MAY-2002; 2002WO-AU00582.
PF
XX
XX  10-MAY-2001; 2001AU-0004919.
PR
XX  17-DEC-2001; 2001AU-0009567.
PR
XX
XX  (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
PA
XX
XX  Chopin LK, Jeffery PL, Herington AC;
PI
XX
XX  WPI: 2003-111957/10.
DR
XX  N-PSDB; AAD50726.
DR
XX
XX  Identifying a cancer cell or tissue for treating prostate, ovarian,
PT  breast cancer, or benign prostatic hyperplasia, by detecting the
PT  expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
PT  1b proteins or nucleic acids -
PT
XX
XX  Claim 14; Page 34; 50pp; English.
XX
XX  The invention relates to a method for identifying a cancer cell or
CC  tissue of the reproductive system by detecting expression of a ghrelin,
CC  an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic
CC  acids. The antibodies, exon 3-deleted form of preproghrelin and
CC  antagonists are useful for treating cancer of the reproductive system
CC  such as prostate, ovarian, breast, cervical or uterine cancer,
CC  choriocarcinoma or benign prostatic hyperplasia. The present sequence
CC  is human exon 3-deleted ghrelin protein.
XX
XX  Sequence 91 AA;
SQ
    Query Match      100.0%; Score 121; DB 24; Length 91;
    Best Local Similarity 100.0%; Pred. No. 1.7e-10;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ALAGWLRPEDGGQAGAEDELEV 23
    |||||||||||||||||||
Db  52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 8
AAB60517
ID  AAB60517 standard; Protein; 116 AA.
XX
XX  AAB60517;
AC
XX
XX  24-APR-2001 (first entry)
DT
XX
XX  Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
DE
XX
XX  Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
KW  calcium concentration elevation; infant growth disorder;
KW  growth hormone deficiency.
XX
XX  Homo sapiens.
OS
XX

ID  AAE33410 standard; Protein; 91 AA.
XX  AAE33410;
AC
XX
XX  01-FEB-2001.
PD
XX
XX  24-JUL-2000; 2000WO-JP04907.
PF
XX
XX  23-JUL-1999; 99JP-0210002.
PR
XX  29-NOV-1999; 99JP-0338841.
PR
XX  26-APR-2000; 2000JP-0126623.
PR
XX
XX  (KANG/) KANGAWA K.
PA
XX
XX  Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
PI
XX
XX  WPI: 2001-159704/16.
DR
XX  N-PSDB; AAF59647.
DR
XX
XX  New peptide compounds which induce growth hormone secretion and
PT  elevate cell calcium concentrations, useful in treatment and diagnosis
PT  of infant growth disorders -
PT
XX
XX  Claim 3; Page 186-187; 210pp; Japanese.
XX
XX  The invention relates to a novel peptide compound or its salt which
CC  induces the secretion of growth hormone and/or elevates calcium ion
CC  concentration in cells. The peptides are ghrelin homologues and are
CC  characterised in that at least one amino acid has been substituted by
CC  a modified amino acid and/or a non-amino acid compound. The invention
CC  also encompasses the unmodified peptides; the DNA encoding the peptides;
CC  vectors and host cells comprising such DNA; a method of producing the
CC  peptides comprising recombinant production, optionally followed by
CC  chemical modification; an antibody specific for a peptide of the
CC  invention; and an assay and kit for detecting the peptides. The peptides
CC  of the invention are useful for treating and/or diagnosing diseases
CC  caused by a deficiency in growth hormone expression or activity. In
CC  particular, they are useful for promoting infant growth due to growth
CC  hormone deficiency. The compounds of the invention are safe with
CC  no accompanying side effects. The present sequence represents a
CC  ghrelin-type growth hormone secretagogue (GHS) precursor protein
CC  of the invention.
XX
XX  Sequence 116 AA;
SQ
    Query Match      100.0%; Score 121; DB 22; Length 116;
    Best Local Similarity 100.0%; Pred. No. 2.2e-10;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ALAGWLRPEDGGQAGAEDELEV 23
    |||||||||||||||||||
Db  51 ALAGWLRPEDGGQAGAEDELEV 73

RESULT 9
AAW87991
ID  AAW87991 standard; Protein; 117 AA.
XX
XX  AAW87991;
AC
XX
XX  07-APR-1999 (first entry)
DT
XX
XX  Protein designated zsig33.
DE
XX
XX  Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
KW  nutrient absorption regulation; obesity; metabolic disorder.
XX
XX  Homo sapiens.
OS
XX
XX  Key
FH  Location/Qualifiers
FT  Peptide
    1..23
    /note= "signal peptide"
FT  Protein
    24..117
    /note= "mature protein"
FT
XX

```

PN W09842840-A1.
 XX PD 01-OCT-1998.
 XX PF 23-MAR-1998; 98WO-US05620.
 XX PR 24-MAR-1997; 97US-0822897.
 XX PR 24-MAR-1997; 97US-0041102.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Delsher TA, Sheppard PO;
 XX PI WPI: 1999-070071/06.
 DR N-PSDB: AAX04550.
 XX PT Human polypeptide having homology to motilin, zsig33 - useful e.g.
 PT to treat gastrointestinal motility disorders, obesity etc. and to
 PT identify antagonists to treat gastrointestinal hypermotility
 XX PT
 XX PS Claim 13; Page 55-56; 69pp; English.
 XX CC The present sequence represents a protein designated zsig33. The nucleic
 CC acids are strongly expressed in stomach tissue. The polypeptide (or
 CC allelic variants/orthologs) can be used to stimulate gastric motility,
 CC measured as increased transit time or gastric emptying of an ingested
 CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. Zsig33 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC or CNS functions. They may therefore be used e.g. to regulate satiety
 CC or treat obesity and other metabolic disorders where neurological
 CC feedback modulates nutritional absorption. They are useful to identify
 CC zsig33 agonists, antagonists and ligands and to produce antibodies.
 XX SQ
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 121; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 |||||
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 10
 AAY87236
 ID AAY87236 standard; Protein; 117 AA.
 XX AC AAY87236;
 XX DT 11-MAY-2000 (first entry)
 XX DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
 XX KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nontropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's disease; ovulatory defect;
 KW muscular dystrophy.
 XX OS Homo sapiens.
 XX PN W0200000610-A2.
 XX

PD 06-JAN-2000.
 XX PF 25-JUN-1999; 99WO-US14484.
 XX PR 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX PA (INCY-) INCYTE PHARM INC.
 XX PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX WPI: 2000-160673/14.
 DR N-PSDB: AAZ98121.
 XX PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease
 XX PS Claim 1; Page 168-169; 327pp; English.
 XX CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, nontropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPP
 CC from natural sources.
 XX SQ
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 121; DB 21; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 |||||
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 11
 AAM38890
 ID AAM38890 standard; Protein; 117 AA.
 XX AC AAM38890;
 XX DT 22-OCT-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 2035.
 XX KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX Homo sapiens.
OS WO200153312-A1.
PN 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US34263.
PF 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX (HYSE-) HYSEQ INC.
PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX WPI: 2001-442253/47.
DR N-PSDB; AAI58046.
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
PS Example 3; SEQ ID NO 2035; 10078pp; English.
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX Sequence 117 AA;
SQ
Query Match 100.0%; Score 121; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRLPEDGGQAGAEDELEV 23
DB 52 ALAGWLRLPEDGGQAGAEDELEV 74
RESULT 12
AAB62649
ID AAB62649 standard; Protein; 117 AA.
XX AAB62649;
XX 23-JUL-2001 (first entry)
DT Human zsig33 polypeptide.
DE
XX

KW zsig33; signal transduction; hormone; enzyme; neural development;
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
XX G-protein coupled receptor.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Peptide 24..37 "specifically claimed fragment that binds to
FT /note= the GHS-R"
XX
XX WO200138355-A2.
XX 31-MAY-2001.
XX 22-NOV-2000; 2000WO-US32074.
XX 22-NOV-1999; 99US-0166765.
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX WPI: 2001-355879/37.
XX N-PSDB; AAF83678.
XX Forming reversible peptide receptor complex for purifying cell and
PT peptides, stimulating signal transduction and modulating hormone
PT secretion, involves contacting a receptor with zsig33 polypeptide -
XX Claim 1; Page 93-94; 111pp; English.
XX The invention relates to a method of forming a reversible peptide-
CC receptor complex that involves providing an immobilized receptor, and
CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
CC is useful for purifying cells, purifying a peptide, stimulating signal
CC transduction in a cell expressing a receptor. It is also useful for
CC modulating secretion of hormones, neural development and/or utilization,
CC gastric contractility, nutrient uptake, secretion of digestive and
CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
CC hormone secretion in a mammal having a disease associated with abnormal
CC levels of growth hormone, such as osteoporosis, bone repair, bone
CC remodeling, low osteoblast levels, cartilage repair and remodeling,
CC skeletal dysplasia, immune suppression, obesity, growth retardation,
CC protein catabolic responses after surgery, cachexia, protein loss,
CC dwarfism, wound healing and ovulation induction, treating a mammal having
CC a metabolic disorder requiring neurological feedback, such as satiety
CC regulation, glucose absorption and metabolism and neuropathy-associated
CC gastrointestinal disorders, and stimulating glucose-induced insulin
CC release in a mammal. The present sequence represents the human zsig33
CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
XX Sequence 117 AA;
SQ
Query Match 100.0%; Score 121; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRLPEDGGQAGAEDELEV 23
DB 52 ALAGWLRLPEDGGQAGAEDELEV 74
RESULT 13
AAB20101
ID AAB20101 standard; Protein; 117 AA.
XX AC AAB20101;
XX

Search completed: September 11, 2003, 17:25:03
Job time : 24.984 secs

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OM protein - protein search, using sw model

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(without alignments)
158.243 Million cell updates/sec

Title: US-09-853-253-5

Perfect score: 121

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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/6CTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121	100.0	117	3	US-09-046-479-2
2	121	100.0	117	4	US-08-822-897C-2
3	121	100.0	117	4	US-09-608-810A-4
4	121	100.0	117	4	US-09-996-243-268
5	52	43.0	233	4	US-09-252-991A-27758
6	50	41.3	634	1	US-08-339-152A-17
7	50	41.3	653	1	US-08-339-152A-16
8	50	41.3	653	2	US-08-007-999B-3
9	50	41.3	653	2	US-08-689-276A-3
10	49	40.5	139	2	US-08-039-198B-10
11	48	39.7	518	4	US-09-252-991A-23604
12	47	38.8	283	4	US-09-252-991A-29700
13	46	38.0	341	4	US-09-252-991A-27327
14	46	38.0	428	4	US-09-252-991A-19723
15	46	38.0	517	4	US-09-252-991A-25921
16	46	38.0	1044	4	US-09-252-991A-18853
17	45.5	37.6	579	3	US-08-704-711A-1
18	45.5	37.6	579	4	US-09-521-220-1
19	45.5	37.6	582	3	US-08-704-711A-2
20	45.5	37.6	582	3	US-08-448-489-1
21	45.5	37.6	582	3	US-09-211-704A-9
22	45.5	37.6	582	4	US-09-521-220-2
23	45.5	37.6	582	4	US-09-391-104-28
24	45.5	37.6	591	2	US-08-889-402-1
25	45	37.2	174	4	US-09-252-991A-18600
26	45	37.2	494	1	US-08-464-340A-4
27	45	37.2	494	5	PCT-US94-08449A-4

28	45	37.2	1059	4	US-09-394-272-5	Sequence 5, Appli
29	44	36.4	405	4	US-09-252-991A-20326	Sequence 20326, A
30	43	35.5	118	3	US-08-482-304-12	Sequence 12, Appl
31	43	35.5	118	3	US-08-483-474-12	Sequence 12, Appl
32	43	35.5	140	3	US-08-482-304-9	Sequence 9, Appli
33	43	35.5	140	3	US-08-483-474-9	Sequence 9, Appli
34	43	35.5	162	4	US-09-252-991A-24838	Sequence 24838, A
35	43	35.5	191	4	US-09-252-991A-21437	Sequence 21437, A
36	43	35.5	212	3	US-09-154-083-4	Sequence 4, Appli
37	43	35.5	247	4	US-09-252-991A-27419	Sequence 27419, A
38	43	35.5	268	4	US-09-252-991A-27950	Sequence 27950, A
39	43	35.5	311	4	US-09-252-991A-28068	Sequence 28068, A
40	43	35.5	380	3	US-08-765-743-2	Sequence 2, Appli
41	43	35.5	380	4	US-09-341-446B-2	Sequence 2, Appli
42	43	35.5	424	4	US-09-341-446B-6	Sequence 6, Appli
43	43	35.5	424	4	US-09-341-446B-8	Sequence 8, Appli
44	43	35.5	427	4	US-09-341-446B-4	Sequence 4, Appli
45	43	35.5	450	4	US-09-252-991A-25523	Sequence 25523, A

ALIGNMENTS

RESULT 1

US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 121; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches .23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEV 23
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Db 52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 2

US-08-822-897C-2
; Sequence 2, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,897C
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-822-897C-2

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 3

US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608,810A
; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 4

US-09-996-243-268
; Sequence 268, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 5

US-09-252-991A-27758
; Sequence 27758, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27758
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27758

Query Match 43.0%; Score 52; DB 4; Length 233;
Best Local Similarity 72.7%; Pred. No. 2.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWRPDDGQA 14
|||||
Db 203 GWRPDDGSA 213

RESULT 6

US-08-339-152A-17
; Sequence 17, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-152A-17

Query Match 41.3%; Score 50; DB 1; Length 634;
Best Local Similarity 76.9%; Pred. No. 16;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGOAEGAEDELEV 23
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Db 213 GGRAEGGEDEEV 225

RESULT 7

US-08-339-152A-16
; Sequence 16, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-152A-16

Query Match 41.3%; Score 50; DB 1; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGOAEGAEDELEV 23
|||||
Db 233 GGRAEGGEDEEV 245

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RESULT 8
US-08-007-999B-3
; Sequence 3, Application US/08007999B
; Patent No. 5851787
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/007,999B
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,022
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: 0609.3520002/JAG/GKT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-007-999B-3
Query Match 41.3%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGQAEGAEDELEV 23
||:|||||
Db 233 GGRAEGGEDEEV 245

RESULT 9
US-08-689-276A-3
; Sequence 3, Application US/08689276A
; Patent No. 5891991
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,276A
; FILING DATE: 06-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,999
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,022
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3520003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-689-276A-3
Query Match 41.3%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGQAEGAEDELEV 23
||:|||||
Db 233 GGRAEGGEDEEV 245

RESULT 10
US-08-039-198B-10
; Sequence 10, Application US/08039198B
; Patent No. 5858725
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODIES
; TITLE OF INVENTION: RECOMBINANT PCR STRATEGY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/039,198B
; FILING DATE: 29-JUL-1993
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01744
; FILING DATE: 08-OCT-91
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-039-198B-10

Query Match 40.5%; Score 49; DB 2; Length 139;
Best Local Similarity 61.5%; Pred. No. 4.4;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGQAE 16
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Db 68 GWIDPEDGTRYG 80

RESULT 11

US-09-252-991A-23604
; Sequence 23604, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23604
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23604

Query Match 39.7%; Score 48; DB 4; Length 518;
Best Local Similarity 47.4%; Pred. No. 26;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 3 AGWLRPEDGGQAEDEL 21
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Db 412 AGWAQPEPGCGGGAERL 430

RESULT 12

US-09-252-991A-29700
; Sequence 29700, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29700
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29700

Query Match 38.8%; Score 47; DB 4; Length 283;
Best Local Similarity 58.8%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 AGWLRPEDGGQAE 19
| | | | |
Db 86 AAGLRQEDGADGTGAED 102

RESULT 13

US-09-252-991A-27327
; Sequence 27327, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27327
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27327

Query Match 38.0%; Score 46; DB 4; Length 341;
Best Local Similarity 52.4%; Pred. No. 33;
Matches 11; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

Qy 7 RPEDGGQAE-----DELEV 23
: || || | | :
Db 181 QPEOGGQGEHAQADRPDPLEV 201

RESULT 14

US-09-252-991A-19723
; Sequence 19723, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19723
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19723

Query Match 38.0%; Score 46; DB 4; Length 428;
Best Local Similarity 55.0%; Pred. No. 42;
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAEDELE 21
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 Db 293 LALWSLPEDPRPADWADEL 312

RESULT 15

US-09-252-991A-25921
 ; Sequence 25921, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25921
 ; LENGTH: 517
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25921

Query Match 38.0%; Score 46; DB 4; Length 517;
 Best Local Similarity 47.6%; Pred. No. 52;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAEDELE 22
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 Db 338 LAGQLDPHPGIAOGPHOQLQ 358

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:26:32 ; Search time 14.0214 Seconds
(without alignments)
239.348 Million cell updates/sec

Title: US-09-853-253-5

Perfect score: 121

Sequence: 1 ALAGWLRPDGGQAGAEDELEV 23

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Searched: 541936 segs, 145912426 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	121	100.0	23	US-09-853-253-6	Sequence 6, Appli
3	121	100.0	24	US-09-853-253-4	Sequence 4, Appli
4	121	100.0	117	US-09-794-987-2	Sequence 2, Appli
5	121	100.0	117	US-09-853-253-2	Sequence 2, Appli
6	121	100.0	117	US-09-989-722-268	Sequence 268, App
7	121	100.0	117	US-09-989-723-268	Sequence 268, App
8	121	100.0	117	US-09-989-279-268	Sequence 268, App
9	121	100.0	117	US-09-989-727-268	Sequence 268, App
10	121	100.0	117	US-09-989-731-268	Sequence 268, App
11	121	100.0	117	US-09-989-732-268	Sequence 268, App
12	121	100.0	117	US-09-991-073-268	Sequence 268, App
13	121	100.0	117	US-09-990-442-268	Sequence 268, App
14	121	100.0	117	US-09-991-163-268	Sequence 268, App
15	121	100.0	117	US-09-993-604-268	Sequence 268, App

16	121	100.0	117	10	US-09-990-456-268	Sequence 268, App
17	121	100.0	117	10	US-09-989-721-268	Sequence 268, App
18	121	100.0	117	10	US-09-992-598-268	Sequence 268, App
19	121	100.0	117	10	US-09-989-293A-268	Sequence 268, App
20	121	100.0	117	10	US-09-989-735-268	Sequence 268, App
21	121	100.0	117	10	US-09-990-444-268	Sequence 268, App
22	121	100.0	117	10	US-09-991-181-268	Sequence 268, App
23	121	100.0	117	10	US-09-989-730-268	Sequence 268, App
24	121	100.0	117	10	US-09-990-436-268	Sequence 268, App
25	121	100.0	117	10	US-09-993-687-268	Sequence 268, App
26	121	100.0	117	11	US-09-989-734-268	Sequence 268, App
27	121	100.0	117	11	US-09-997-653-268	Sequence 268, App
28	121	100.0	117	11	US-09-993-667-268	Sequence 268, App
29	121	100.0	117	11	US-09-997-428-268	Sequence 268, App
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31	121	100.0	117	11	US-09-990-438-268	Sequence 268, App
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33	121	100.0	117	11	US-09-990-711-268	Sequence 268, App
34	121	100.0	117	11	US-09-989-726-268	Sequence 268, App
35	121	100.0	117	11	US-09-998-156-268	Sequence 268, App
36	121	100.0	117	11	US-09-990-437-268	Sequence 268, App
37	121	100.0	117	11	US-09-991-157-268	Sequence 268, App
38	121	100.0	117	11	US-09-997-514-268	Sequence 268, App
39	121	100.0	117	11	US-09-997-573-268	Sequence 268, App
40	121	100.0	117	11	US-09-991-172-268	Sequence 268, App
41	121	100.0	117	11	US-09-990-726-268	Sequence 268, App
42	121	100.0	117	11	US-09-997-559-268	Sequence 268, App
43	121	100.0	117	11	US-09-997-601-268	Sequence 268, App
44	121	100.0	117	11	US-09-990-443-268	Sequence 268, App
45	121	100.0	117	11	US-09-991-854-268	Sequence 268, App

ALIGNMENTS

RESULT 1
US-09-853-253-5
; Sequence 5, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-5

Query Match 100.0%; Score 121; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAGAEDELEV 23
|||||
DB 1 ALAGWLRPDGGQAGAEDELEV 23

RESULT 2
US-09-853-253-6
; Sequence 6, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN

```

; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Query Match          100.0%; Score 121; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ALAGWLRPEDGGGAEGAEDELEV 23
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Db       52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 5
US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-2

Query Match          100.0%; Score 121; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ALAGWLRPEDGGGAEGAEDELEV 23
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Db 52 ALAGWLRPBDGGCAEGAEDLEV 74

RESULT 6

US-09-989-722-268

Sequence 268, Application US/09989722

Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC63

CURRENT APPLICATION NUMBER: US/09/989,722

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

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PRIOR FILING DATE: 1997-11-24

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PRIOR FILING DATE: 1998-02-25

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 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.2e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPDGGGAEGAEDEV 23
 Db 52 ALAGWLRPDGGGAEGAEDEV 74
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RESULT 7
 US-09-989-723-268
 ; Sequence 268, Application US/09989723
 ; Patent No. US20020072092A1

; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1G62
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: US/09/989,723
 ; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/090431
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; PRIOR APPLICATION NUMBER: 60/090435
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; PRIOR APPLICATION NUMBER: 60/091978
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
DB 52 ALAGWLRPEDGGQAGAEDELEV 74
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RESULT 8
US-09-989-279-268
; Sequence 268, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerbitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGADELEV 23
Db 52 ALAGWLRPEDGGGAEGADELEV 74

RESULT 9

US-09-989-727-268
Sequence 268, Application US/09989727
Patent No. US2002007497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09; Mismatches 0; Indels 0; Gaps 0; Matches 23; Conservative 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
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 Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 10

US-09-989-731-268
 ; Sequence 268, Application US/09989731
 ; Patent No. US20020103125A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 121; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPDGGGAEGAEDELEV 23
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RESULT 11

; Sequence 268, Application US/09989732
 ; Patent No. US20020123463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Bolstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
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 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730F1C57

; CURRENT APPLICATION NUMBER: US/09/989,732
 ; CURRENT FILING DATE: 2001-11-19
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Query Match 100.0%; Score 121; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09; Mismatches 0; Indels 0; Caps 0;

Matches 23; Conservative 0;

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Db 52 ALAGWLRPEDGGQAGAEDELEV 74
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RESULT 12

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US-09-991-073-268
; Sequence 268, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 52 ALAGWLRPDGGQAEGADELEV 74

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; Sequence 268, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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 ; PRIOR FILING DATE: 1998-07-09

 Query Match 100.0%; Score 121; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 4.2e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 52 ALAGMLRPEDGGQAGAEDELEV 74

 RESULT 14
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 ; Sequence 268, Application US/09991163
 ; Patent No. US20020132253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C17
 ; CURRENT APPLICATION NUMBER: US/09/991,163
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
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;	PRIOR FILING DATE:	1998-07-02	
;	PRIOR APPLICATION NUMBER:	60/091544	
;	PRIOR FILING DATE:	1998-07-01	
;	PRIOR APPLICATION NUMBER:	60/091519	
;	PRIOR FILING DATE:	1998-07-02	
;	PRIOR APPLICATION NUMBER:	60/091626	
;	PRIOR FILING DATE:	1998-07-02	
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;	PRIOR FILING DATE:	1998-07-02	
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;	PRIOR FILING DATE:	1998-07-07	
;	PRIOR APPLICATION NUMBER:	60/091982	

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  1 ALAGWLRPEDGGQGAEGAEDELEV 23
Db  52 ALAGWLRPEDGGQGAEGAEDELEV 74

RESULT 15
US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Aclods Encoding the Same
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
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; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
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;	PRIOR FILING DATE:	1998-06-19	
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;	PRIOR APPLICATION NUMBER:	60/091360	
;	PRIOR FILING DATE:	1998-07-01	
;	PRIOR APPLICATION NUMBER:	60/091478	
;	PRIOR FILING DATE:	1998-07-02	
;	PRIOR APPLICATION NUMBER:	60/091544	
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;	PRIOR APPLICATION NUMBER:	60/091519	
;	PRIOR FILING DATE:	1998-07-02	
;	PRIOR APPLICATION NUMBER:	60/091626	
;	PRIOR FILING DATE:	1998-07-02	
;	PRIOR APPLICATION NUMBER:	60/091633	
;	PRIOR FILING DATE:	1998-07-02	
;	PRIOR APPLICATION NUMBER:	60/091978	
;	PRIOR FILING DATE:	1998-07-07	
;	PRIOR APPLICATION NUMBER:	60/091982	
;	PRIOR FILING DATE:	1998-07-07	
;	PRIOR APPLICATION NUMBER:	60/092182	
;	PRIOR FILING DATE:	1998-07-09	

QY 1 ALAGWLRPEDGGQAEGADELEV 23
Dbb 52 ALAGWLRPEDGGQAEGADELEV 74

Search completed: September 11, 2003, 17:48:32
Job time : 15.0214 secs

Query Match	100.0%;	Score 121;	DB 10;	Length 117;
Best Local Similarity	100.0%;	Pred. No. 4.2e-09;		
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 8.60963 Seconds
(without alignments)
256.908 Million cell updates/sec

Title: US-09-853-253-5

Perfect score: 121

Sequence: 1 ALAGWLRPEDGGQAGAEDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121	100.0	117	1 A59316	ghrelin precursor
2	90	74.4	117	1 B59316	ghrelin precursor
3	54	44.6	200	2 A26169	nucleoplasm - Af
4	52	43.0	232	2 G83609	probable transcrip
5	51.5	42.6	249	2 T21920	hypothetical prote
6	51	42.1	91	2 B69811	conserved hypothet
7	51	42.1	604	2 A82760	chloride channel P
8	51	42.1	604	2 C97541	hypothetical prote
9	50	41.3	131	2 B75433	hypothetical prote
10	50	41.3	653	2 A46362	amyloid precursor-
11	49.5	40.9	484	2 C75609	amino acid ABC tra
12	49	40.5	274	2 A26050	exfoliative toxin
13	48	39.7	114	2 T49338	hypothetical prote
14	48	39.7	1199	2 S20969	Na+/Ca2+,K+-exchan
15	47	38.8	355	2 T09738	protein kinase PK1
16	47	38.8	380	2 A52529	kappa opioid recep
17	47	38.8	1273	2 C96767	unknown protein F2
18	46.5	38.4	80	2 T26398	hypothetical prote
19	46	38.0	259	2 A87377	hypothetical prote
20	46	38.0	287	2 C82965	hypothetical prote
21	46	38.0	528	2 H97088	protein containing
22	46	38.0	528	2 C84110	xylan beta-1,4-xy
23	46	38.0	871	2 B71039	hypothetical prote
24	45.5	37.6	582	2 I38028	matrix metalloprot
25	45.5	37.6	582	2 I48673	matrix metalloprot
26	45.5	37.6	582	2 I84471	matrix metalloprot
27	45	37.2	69	2 C87574	cold-shock domain
28	45	37.2	184	2 T43321	ribosomal protein
29	45	37.2	191	2 S62409	40s ribosomal prot

30	45	37.2	242	2 S67270	CCAAT-binding fact
31	45	37.2	296	2 T15550	hypothetical prote
32	45	37.2	297	2 G71446	hypothetical prote
33	45	37.2	494	2 JC5919	potassium channel
34	45	37.2	544	2 B75379	ATP synthase - Del
35	45	37.2	600	2 T17436	ATP-binding protei
36	45	37.2	600	2 AF0233	inner membrane ABC
37	45	37.2	1059	2 T12195	sucrose-phosphate
38	44.5	36.8	777	2 T08659	ral guanine nucleo
39	44.5	36.8	1233	1 P3ARD3	major core protein
40	44	36.4	102	2 T44994	probable tryptopha
41	44	36.4	273	2 JC4634	vertebrate NK-2 ho
42	44	36.4	358	2 AC2960	hypothetical prote
43	44	36.4	413	2 C98323	algS protein (AB01
44	44	36.4	449	1 A41520	chromogranin A pre
45	44	36.4	479	2 A75353	mock protein - Del

ALIGNMENTS

RESULT 1

A59316
ghrelin precursor - human
N:Alternate names: preproghrelin
C:Species: Homo sapiens (man)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C:Accession: A59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: A59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-117 <KOJ>
A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BAA89371.1; PID:g6691572
A:Experimental source: tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gr
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 121; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
DB 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 2

B59316
ghrelin precursor - rat
N:Alternate names: preproghrelin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C:Accession: B59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: B59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA; protein
A:Residues: 1-117 <KOJ>
A:Cross-references: GB:AB029433; NID:g6691569; PIDN:BAA89370.1; PID:g6691570
A:Experimental source: strain SD; tissue stomach endocrine cells

chloride channel protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AE2760
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, G.; Gilllet, W.; Grant, C.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AE2760
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AAI42499.1; PID:g17739917; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: clc
 A:Map position: circular chromosome

Query Match 42.1%; Score 51; DB 2; Length 604;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAGWLRPDDGGQAG 16
 I: ||||| ||| I
 Db 288 AIPGWLRLPLGGVAVG 303

RESULT 8
 C97541
 chloride channel, clc (AE005067) [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C:Accession: C97541
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: C97541
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK87284.1; PID:g15156576; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C2753
 A:Map position: circular chromosome

Query Match 42.1%; Score 51; DB 2; Length 604;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAGWLRPDDGGQAG 16
 I: ||||| ||| I
 Db 288 AIPGWLRLPLGGVAVG 303

RESULT 9
 B75433
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
 C:Accession: B75433
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: B75433

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-131 <WHI>
 A:Cross-references: GB:AE001963; GB:AE000513; NID:g6458869; PIDN:AAF10714.1; PID:g6458869
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1139
 A:Map position: 1
 C:Superfamily: Deinococcus radiodurans hypothetical protein DR1139

Query Match 41.3%; Score 50; DB 2; Length 131;
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 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 ALAGWLRPDDGGQAG 19
 I: ||| ||| ||| I
 Db 101 ALLANFPFPPGGAQVGGAAE 119

RESULT 10
 A46362
 amyloid precursor-like protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
 C:Accession: A46362
 R:Wasco, W.; Bupp, K.; Magendanz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
 Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
 A:Title: Identification of a mouse brain cDNA that encodes a protein related to the A-beta peptide
 A:Reference number: A46362; MUID:93066322; PMID:1279693
 A:Accession: A46362
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-653 <WAS>
 A:Experimental source: brain
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBI:118683, NCBI:118684)
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinases
 C:Keywords: transmembrane protein

Query Match 41.3%; Score 50; DB 2; Length 653;
 Best Local Similarity 76.9%; Pred. No. 29;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGQAGGAEDELEV 23
 I: ||| ||| ||| I
 Db 233 GGRAEGGEDEEV 245

RESULT 11
 C75609
 amino acid ABC transporter, permease protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: C75609
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: C75609
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <WHI>
 A:Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12224.1; PID:g6460468
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DRA0136
 A:Map position: 2

Query Match 40.9%; Score 49.5; DB 2; Length 484;
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QY 2 LAGWLRPEDGGQAGAEDELE 19
 ||||| | | : || | | :
 Db 468 LAGWLTFR-GLRAEGEE 484

RESULT 12

A26050
 exfoliative toxin B precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 18-Nov-2002
 C:Accession: A26050
 R:Jackson, M.P.; Iandolo, J.J.
 J. Bacteriol. 167, 726-728, 1986
 A:Title: Sequence of the exfoliative toxin B gene of Staphylococcus aureus.
 A:Reference number: A26050; MUID:86277939; PMID:3733674
 A:Accession: A26050
 A:Molecule type: DNA
 A:Residues: 1-274 <JAC>
 C:Superfamily: staphylococcal serine proteinase
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-274/Product: exfoliative toxin B #status predicted <NAT>

Query Match 40.5%; Score 49; DB 2; Length 274;
 Best Local Similarity 44.4%; Pred. No. 17;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 WLRPEDGGQAGAEDELE 22
 ||: |||| | ||: |
 Db 86 WLKIQDGGDTTGGEEQPE 103

RESULT 13

T49338
 hypothetical protein B13N20.230 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
 C:Accession: T49338
 R:Schulte, U.; Algn, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, May 2000
 A:Reference number: Z25022
 A:Accession: T49338
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-114 <SCH>
 A:Cross-references: EMBL:AL355925; GSPDB:GNO0116; NCSP:B13N20.230
 A:Experimental source: BAC clone B13N20; strain OR74A
 C:Genetics:
 A:Gene: NCSP:B13N20.230
 A:Map position: 6
 C:Superfamily: Neurospora crassa hypothetical protein B13N20.230

Query Match 39.7%; Score 48; DB 2; Length 114;
 Best Local Similarity 66.7%; Pred. No. 9.9;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 EDGGQAGAEDELEV 23
 |||| | | ||||
 Db 44 EDGFDDEKEDQLEV 58

RESULT 14

S20969
 Na+/Ca2+,K+-exchanging protein - bovine
 N:Alternate names: Na+/Ca2+,K+ antiporter; Na/Ca,K-exchanger
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S20969
 R:Reilaender, H.; Achilles, A.; Friedel, U.; Maul, G.; Lottspeich, F.; Cook, N.J.
 EMBO J. 11, 1689-1695, 1992
 A:Title: Primary structure and functional expression of the Na/Ca,K-exchanger from bovin
 A:Reference number: S20969; MUID:92258377; PMID:1582405
 A:Accession: S20969

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1199 <REI>
 A:Cross-references: GB:X66481; NID:g505578; PIDN:CAA47108.1; PID:g505579

Query Match 39.7%; Score 48; DB 2; Length 1199;
 Best Local Similarity 45.0%; Pred. No. 1e+02;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 GWLRPEDGGQAGAEDELEV 23
 | : | : || | || | :
 Db 816 GEIQAGEGGEVEGEDEGEI 835

RESULT 15

T09738
 protein kinase PK1 (EC 2.7.1.1) - Craterostigma plantagineum
 C:Species: Craterostigma plantagineum
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
 C:Accession: T09738
 R:Heino, P.; Nylander, M.; Palva, T.; Bartels, D.
 submitted to the EMBL Data Library, April 1998
 A:Description: Isolation of a cDNA corresponding to a protein kinase differentially e
 A:Reference number: Z16839
 A:Accession: T09738
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-355 <HEI>
 A:Cross-references: EMBL:AJ005373
 C:Genetics:
 A:Gene: pk1
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase; protein kinase
 F:2-260/Domain: protein kinase homology <KIN>

Query Match 38.8%; Score 47; DB 2; Length 355;
 Best Local Similarity 37.0%; Pred. No. 43;
 Matches 10; Conservative 4; Mismatches 5; Indels 8; Gaps 1;

QY 4 GW-----LRPEDGGQAGAEDELE 22
 || : | : || | || |
 Db 313 GWCTEEDENVEEVEEGEGEDEV 339

Search completed: September 11, 2003, 17:26:24
 Job time : 9.60963 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 3.32086 Seconds
(without alignments)
325.703 Million cell updates/sec

Title: US-09-853-253-5
Perfect score: 121
Sequence: 1 ALAGWLRPEDGGQAEAGAELEEV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match %	Length	ID	Description
1	121	100.0	117	GHRL_HUMAN	Q9ub33 homo sapien
2	90	74.4	117	GHRL_RAT	Q9qyh7 rattus norv
3	87	71.9	118	GHRL_PIG	Q9gky5 sus scrofa
4	86	71.1	117	GHRL_MOUSE	Q9eqx0 mus musculu
5	72	59.5	116	GHRL_BOVIN	Q9bd16 bos taurus
6	68	56.2	117	GHRL_CANFA	Q9bef8 canis fami
7	54	44.6	200	NUPX_XENLA	P05221 xenopus lae
8	51	42.1	91	ACRP_BACSU	Q03031 bacillus su
9	50	41.3	653	APPI_MOUSE	Q03157 mus musculu
10	48	39.7	300	NKX1_BISBI	Q46383 bison bison
11	48	39.7	668	SYM_METKA	Q8tx28 methanopyru
12	48	39.7	1216	NKX1_BOVIN	Q28139 bos taurus
13	47	38.8	380	OPRK_CAVPO	P41144 cavia porce
14	47	38.8	1168	DDX8_ARATH	Q38953 arabidopsis
15	45.5	37.6	580	MM14_PIG	Q9xt90 sus scrofa
16	45.5	37.6	582	MM14_HUMAN	P50281 homo sapien
17	45.5	37.6	582	MM14_MOUSE	P53690 mus musculu
18	45.5	37.6	582	MM14_RAT	Q10739 rattus norv
19	45.5	37.6	591	PAX1_HUMAN	P49023 homo sapien
20	45	37.2	190	RS9A_SCHPO	Q09757 schizosacch
21	45	37.2	242	HAP5_YEAST	Q02516 saccharomyc
22	45	37.2	494	KCF1_HUMAN	Q9h3m0 homo sapien
23	45	37.2	544	PYRG_DEIRA	Q9ru23 deinococcus
24	45	37.2	992	SNX1_HUMAN	Q92543 homo sapien
25	45	37.2	1059	SPS_VICFA	Q34876 vicla faba
26	44.5	36.8	777	RLG2_HUMAN	O15211 homo sapien
27	44.5	36.8	1233	VLJ_REQVD	P15024 reovirus (t
28	44	36.4	115	INS_VERMO	Q9w7r2 verasper mo
29	44	36.4	168	TC2P_BRAOL	Q944w6 brassica ol
30	44	36.4	273	NK22_MOUSE	P42586 mus musculu
31	44	36.4	449	CMGA_BOVIN	P05059 bos taurus
32	44	36.4	4447	PKSK_BACSU	P40803 bacillus su
33	43.5	36.0	525	SYK_DEIRA	Q9rxel deinococcus

34	43.5	36.0	582	1	MM14_RABIT	Q95220 oryctolagus
35	43	35.5	365	1	SVAP_MOUSE	Q9d5v6 mus musculu
36	43	35.5	380	1	OPRK_HUMAN	P41145 homo sapien
37	43	35.5	579	1	SYQ_XANAC	Q8pnz5 xanthomonas
38	43	35.5	852	1	SRCH_RABIT	P16230 oryctolagus
39	43	35.5	862	1	SYV_THETH	P96142 thermus the
40	43	35.5	864	1	KLTK_HUMAN	P29376 homo sapien
41	43	35.5	894	1	WPKA_BACSU	P54423 bacillus su
42	43	35.5	1876	1	GLS1_YEAST	P38631 saccharomyc
43	42.5	35.1	116	1	INS_LOPPI	P01341 lophius pls
44	42.5	35.1	195	1	IGFB_HUMAN	P05019 homo sapien
45	42.5	35.1	214	1	GRP2_NICSY	P27484 nicotiana s

ALIGNMENTS

RESULT 1
GHRL_HUMAN
ID GHRL_HUMAN STANDARD; PRT: 117 AA.
AC Q9UBU3: Q8TAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
DE releasing peptide)
GN GHRL OR MLRP
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach."
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Stomach;
RA Tomasetto C., Karam S.M., Rio M.-C.;
RT "Identification of a novel gastric protein m46."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wajhrach M.P., Ten I.S., Gertner J.M., Leibell R.L.;
RT "Genomic organization of the human Ghrelin gene."
RL J. Endocrinol. Genet. 1:231-233(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.M., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustun T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6].
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [7].
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -1- PTM: O-n-octanoylation is essential for activity.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/GhrelinID327.html".
 CC -----
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 CC -----
 DR EMBL; AB029434; BAB89371.1; -
 DR EMBL; AB035700; BAB19045.1; -
 DR EMBL; AJ252278; CAB65733.1; -
 DR EMBL; AF296558; AAG10300.1; -
 DR EMBL; BC025791; AAH25791.1; -
 DR PIR; A59316; A59316.
 DR MIM; 605353; -
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; TAS.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc; 1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23
 FT PEPTIDE 24 51 GHRELIN.
 FT PROPEP 52 117 REMOVED IN MATURE FORM.
 FT LIPID 26 26 N-OCTANOATE.
 FT VARSPIC 37 37 Missing (in isoform 2).
 FT /FTID=VSP_003245.
 FT CONFLICT 72 72 L -> M (IN REF. 5).

SQ SEQUENCE 117 AA; 12911 MW; 39C0572BECA2755 CRC64;
 Query Match 100.0%; Score 121; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
 Db 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 2
 GHRL_RAT
 ID GHRL_RAT STANDARD; PRT; 117 AA.
 AC Q9QYH7; Q9ET69;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide).
 GN GHRL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,
 RP AND ACYLATION OF SER-26.
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
 RX MEDLINE=20067959; PubMed=10604470;
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
 RT "Ghrelin is a growth-hormone-releasing acylated peptide from
 RT stomach.";
 RL Nature 402:656-660(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS
 RP SPECTROMETRY, AND ACYLATION OF SER-26.
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
 RX MEDLINE=20357315; PubMed=10801861;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Purification and characterization of rat des-Gln14-ghrelin, a second
 RT endogenous ligand for the growth hormone secretagogue receptor.";
 RL J. Biol. Chem. 275:21995-22000(2000).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=21092536; PubMed=11162448;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
 RT in gastrointestinal tissue.";
 RL Biochem. Biophys. Res. Commun. 279:909-913(2000).
 RN [4]
 RP STRUCTURE-ACTIVITY RELATIONSHIP.
 RX MEDLINE=21433488; PubMed=11549267;
 RA Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
 RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
 RT "Structure-activity relationship of ghrelin: pharmacological study of
 RT ghrelin peptides.";
 RL Biochem. Biophys. Res. Commun. 287:142-146(2001).
 RN [5]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;


```

CC Name=1; Synonyms=Ghrelin;
CC ISOID=Q9GPH7-1; Sequence-Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC ISOID=Q9GPH7-2; Sequence=VSP_003248;
CC TISSUE SPECIFICITY: Broadly expressed with higher expression in
CC the stomach. Very low levels are detected in the hypothalamus,
CC heart, lung, pancreas, intestine and adipose tissue.
CC -!- PTM: O-n-octanoylation is essential for activity. The replacement
CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.
CC -!- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;
CC RANGE=24-51.
CC -!- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;
CC RANGE=24-36, 38-51.
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC
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CC -----
DR EMBL; AB029433; BAA89370.1; -.
DR EMBL; AB035699; BAB11956.1; -.
DR PIR; B59316; B59316.
DR InterPro: IPR006737; motilin_assoc.
DR InterPro: IPR006738; motilin_ghrelin.
DR InterPro: IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD32162; preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23
FT PEPTIDE 24 51 GHRELIN.
FT PROPEP 52 117 REMOVED IN MATURE FORM.
FT LIPID 26 26 N-OCTANOATE.
FT VARSPLIC 37 37 Missing (in isoform 2).
FT SEQUENCE 117 AA; 13176 MW; 8857546FES1A7691 CRC64;
Query Match 74.4%; Score 90; DB 1; Length 117;
Best Local Similarity 73.9%; Pred. No. 4.1e-06;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQAGAEDELEV 23
Db 52 ALEGWLRPEDRGQAGAEDELEI 74
II III III III III III
RESULT 3
GHRL_PIG STANDARD; PRT; 118 AA.
AC Q9GKY5; Q9BDG8; Q9GKY4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide).
DE GHRL.
GN Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Stomach;
RA Rousselle J., Lacroix D., Dubreuil P.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC ISOID=Q9GKY5-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC ISOID=Q9GKY5-2; Sequence=VSP_003247;
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC
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CC -----
DR EMBL; AB035703; BAB19048.1; -.
DR EMBL; AB035704; BAB19049.1; -.
DR EMBL; AF308930; AAK19243.1; -.
DR EMBL; AY028942; AAK30002.1; -.
DR InterPro: IPR006737; motilin_assoc.
DR InterPro: IPR006738; motilin_ghrelin.
DR InterPro: IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD32162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 24 BY SIMILARITY.
FT PEPTIDE 25 52 GHRELIN.
FT PROPEP 53 118 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 27 27 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC 38 38 Missing (in isoform 2).
FT SEQUENCE 118 AA; 12795 MW; 856D3E1D6DAB1A76 CRC64;
Query Match 71.9%; Score 87; DB 1; Length 118;
Best Local Similarity 65.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQAGAEDELEV 23
Db 53 ALEGWLGPEDSGEVEGTEKLEI 75
II III III III III III
RESULT 4
GHRL_MOUSE STANDARD; PRT; 117 AA.
AC Q9EQX0; Q9WU21;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide) (M46 protein).
DE GHRL OR MTLRP.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.

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RC RX TISSUE=Stomach;
RA RX MEDLINE=20389976; PubMed=10930375;
RA RX Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA RX Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide
RT hormone: the motilin-related peptide.";
RL Gastroenterology 119:395-405(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Kojima M.;
RA "Mouse mRNA for preproghrelin.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RN [5]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=09EQX0-1; Sequence=Displayed;
CC IsoId=09EQX0-2; Sequence=Vsp_003246;
CC -1- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
CC with higher levels in the stomach, medium levels in the duodenum,
CC jejunum, ileum and colon. Low expression in the testis and brain.
CC Not detected in the salivary gland, pancreas, liver and lung.
CC -1- PPM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC EMBL; AJ243503; CAB46500.1; -
DR EMBL; AB035701; BAB19046.1; -
DR EMBL; AB060078; BAB69857.1; -
DR EMBL; AK008658; BAB25814.1; -
DR EMBL; AK008860; BAB25934.1; -
DR MGD; MGI:1930008; Ghrl.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005576; C:extracellular; IDA.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23
FT PEPTIDE 24 51
FT PROPEP 52 117
FT LIPID 26 26
FT VANSPLIC 37 37
FT SQ SEQUENCE 117 AA; 13207 MW; EACB49D2E3CA7203 CRC64;
Query Match 71.18; Score 86; DB 1; Length 117;
Best Local Similarity 69.68; Pred. No. 1.5e-05;
Matches 16; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Oy 1 ALACWLRPEDGGQAGAEDELEV 23
Db 52 ALGGLHPEDRGQAEELEEI 74
RESULT 5
GHRL_BOVIN STANDARD; PRT; 116 AA.
ID GHRL_BOVIN
AC O9BDJ6: O9GKY6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide).
GN GHRL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Kita K., Harada K., Yokota H.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-99 FROM N.A.
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- PPM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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DR EMBL; Y00204; CAA68363.1; -.
DR PIR; A26169; A26169.
DR PDB; 1EE5; 26-SEP-01.
DR PDB; 1EJY; 24-APR-00.
DR PDB; 1K5J; 21-NOV-01.
DR InterPro; IPR004301; Nucleoplasm.
DR Pfam; PF03066; Nucleoplasm.
KW Nuclear protein; Phosphorylation; 3D-structure.
FT DOMAIN 138 145 POLY-GLU (PROBABLE HISTONE BINDING SITE).
FT CONFLICT 11 15 L -> V (IN REF. 2).
FT CONFLICT 27 27 E -> N (IN REF. 2).
FT CONFLICT 31 31 E -> A (IN REF. 2).
FT CONFLICT 34 34 V -> I (IN REF. 2).
FT CONFLICT 61 61 N -> H (IN REF. 2).
FT CONFLICT 72 72 A -> K (IN REF. 2).
FT CONFLICT 75 75 S -> P (IN REF. 2).
FT CONFLICT 80 80 T -> S (IN REF. 2).
FT CONFLICT 111 111 L -> V (IN REF. 2).
FT CONFLICT 134 137 MISSING (IN REF. 2).
FT CONFLICT 147 147 Q -> P (IN REF. 2).
SQ SEQUENCE 200 AA; 22023 MW; A91DD110F2965812 CRC64;

Query Match 44.6%; Score 54; DB 1; Length 200;
Best Local Similarity 55.6%; Pred. No. 1;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 WLRPEDGGQAGAEDELE 22
D 126 WABEEDGEGAEGEDEEE 143

RESULT 8
ACYP_BACSU STANDARD; PRT; 91 AA.
AC O35031;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative acylphosphatase (EC 3.6.1.7) (Acylphosphate
DE phosphohydrolase).
GN YFLL.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AC327;
RX MEDLINE=97417488; PubMed=9272861;
RA Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;
RT "Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region
RT of the Bacillus subtilis genome reveal genes for a new two-component
RT system, three spore germination proteins, an iron uptake system and a
RT general stress response protein.";
RL Gene 194:191-199(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Brusch C., Brans A., Braun M., Brignell S.C., Bron S.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Huillo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

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RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujić P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche D., Rose M., Sadale F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -1- CATALYTIC ACTIVITY: An acyl phosphate + H(2)O -> a fatty acid anion
CC + phosphate.
CC -1- SIMILARITY: BELONGS TO THE ACYLPHOSPHATASE FAMILY.
CC -----
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CC -----
DR EMBL; D86417; BAA22305.1; -.
DR EMBL; Z99108; CAB12593.1; -.
DR PIR; B69811; B69811.
DR HSP; P00818; IAPS.
DR Subtilist; BG12947; yfll.
DR InterPro; IPR001792; Acylphosphatase.
DR Pfam; PF00708; Acylphosphatase; 1.
DR PRINTS; PR00112; ACYLPHPTASE.
DR ProDom; PD001884; Acylphosphatase; 1.
DR PROSITE; PS00150; ACYLPHOSPHATASE_1; 1.
DR PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.
KW Hypothetical protein; Hydrolase; Complete proteome.
SQ SEQUENCE 91 AA; 10318 MW; 50795631BF310F4 CRC64;

Query Match 42.1%; Score 51; DB 1; Length 91;
Best Local Similarity 44.0%; Pred. No. 1.2;
Matches 11; Conservative 5; Mismatches 5; Indels 4; Gaps 1;

Qy 2 LAGWLRPEDGGQ---AEGAEDELE 22
D 30 LAGWVRNRDDGRVEIIAEGPENALQ 54

RESULT 9
ACYP_MOUSE STANDARD; PRT; 653 AA.
AC Q03137; Q8VC38;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
GN APLP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93056322; PubMed=1279693;
RA Wasco W., Bupp K., Magendanz M., Guseella J.F., Tanzi R.E.,
RA Solomon F.;
RT "Identification of a mouse brain cDNA that encodes a protein related
RT to the Alzheimer disease-associated amyloid beta protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RX COLLAGEN-BINDING.
RP MEDLINE=96139497; PubMed=8576160;
RA Behr D., Hesse L., Masters C.L., Muthaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RL mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [4]
RX INTERACTION WITH DAB1.
RP MEDLINE=99389880; PubMed=10460257;
RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
RL protein 1.";
RL J. Neurosci. 19:7507-7515(1999).
RN [5]
RX INTERACTION WITH MAPK8IP1.
RP MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "c-Jun N-terminal kinase (JNK)-interacting protein-1b/isllet-brain-1
RL scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [6]
RX GAMMA-SECRETASE PROCESSING, INTERACTION WITH APPB1, AND MUTAGENESIS OF
RP TYR-641.
RX MEDLINE=22313598; PubMed=12228233;
RA Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.;
RT "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
RL secretase regulates transcription.";
RL J. Biol. Chem. 277:44195-44201(2002).
RX -1- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC gamma-secretase processed fragment, ALDI, activates transcription
CC activation through APPB1 (Fe65) binding. Couples to JIP signal
CC transduction through C-terminal binding. May interact with
CC cellular G-protein signaling pathways. Can regulate neurite
CC outgrowth through binding to components of the extracellular
CC matrix such as heparin and collagen I.
CC -1- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC neuronal apoptosis (By similarity).
CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APPB and APA family members,
CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC serine phosphorylation.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC processed in the Golgi complex.
CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-

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CC terminal to the NPXY motif are often required for complete
CC interaction. The NPXY site is also involved in clatherin-mediated
CC endocytosis.
CC -1- PTM: Proteolytically cleaved by caspases during neuronal
CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
CC similarity).
CC -1- PTM: N-glycosylated.
CC -1- PTM: O-glycosylated.
CC -1- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC Zinc-binding increases heparin binding. No Cu(II) reducing
CC activity with copper-binding.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L04538; AAA37247.1; -.
CC EMBL; BC021877; AAH21877.1; -.
CC PIR; A46362; A46362.
CC HSSP; P05067; 1MWP.
CC MGD; MGI:88046; Aplp1.
CC InterPro; IPR001868; A4_APP.
CC Pfam; PF02177; A4_EXTRA; 1.
CC PRINTS; PR00203; AMYLOIDA4.
CC SMART; SM00006; A4_EXTRA; 1.
CC PROSITE; PS00319; A4_EXTRA; 1.
CC PROSITE; PS00320; A4_EXTRA; 1.
CC Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
CC Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
CC Glycoprotein.
CC SIGNAL 1 37 POTENTIAL.
CC CHAIN 38 653 AMYLOID-LIKE PROTEIN 1.
CC CHAIN 624 653 C30 (BY SIMILARITY).
CC DOMAIN 38 583 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 584 606 POTENTIAL.
CC DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 157 177 COPPER-BINDING.
CC DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
CC DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
CC DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
CC DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
CC DOMAIN 263 271 POLY-GLU.
CC DOMAIN 535 538 POLY-SER.
CC DOMAIN 601 606 POLY-LEU.
CC SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY
CC SIMILARITY).
CC SITE 607 618 BASOLATERAL SORTING SIGNAL (BY
CC SIMILARITY).
CC SITE 623 624 CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
CC SITE 641 644 ENDOCYTOSIS SIGNAL.
CC SITE 643 646 NPXY MOTIF.
CC CARBOHYD 464 464 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 554 554 N-LINKED (GLCNAC...) (POTENTIAL).
CC MUTAGEN 641 641 Y->G: REDUCED BINDING OF APPB1.
CC CONFLICT 17 17 P -> PP (IN REF. 2).
CC SEQUENCE 653 AA; 72750 MW; 56516DC3EA40E4B0 CRC64;
CC -----
CC Query Match 41.3%; Score 50; DB 1; Length 653;
CC Best Local Similarity 76.9%; Pred. No. 12;
CC Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CC -----
CC QY 11 GGOAEGAEDDEEV 23
CC II:III III II
CC DB 233 GGRAEGGEDEEV 245
CC -----
CC RESULT 10
CC NKX1_BISBI

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ID NKX1_BISBI STANDARD; PRT; 300 AA.
AC O46383;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 (Na(+)/K(+)/Ca(2+)-
DE exchange protein 1) (Retinal rod Na-Ca+K exchanger) (Fragment).
GN SLC24A1 OR NCKX1.
OS Bison bison (American bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bison.
OC NCBI_TaxID=9901;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98138491; PubMed=9478004;
RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison
RT with a revised bovine sequence.";
RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
CC -1- FUNCTION: Critical component of the visual transduction cascade,
CC controlling the calcium concentration of outer segments during
CC light and darkness. Light causes a rapid lowering of cytosolic
CC free calcium in the outer segment of both retinal rod and cone
CC photoreceptors and the light-induced lowering of calcium is caused
CC by extrusion via this protein which plays a key role in the
CC process of light adaptation. Transports one Ca(2+) and one K(+) in
CC exchange for four Na(+) (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC -----
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CC -----
DR EMBL; AF025480; AAC13320.1; -.
DR KMWision; Transport; Antiprot; Sympot; Calcium transport;
DR Potassium transport; Sodium transport; Transmembrane.
FT NON_TER 1
FT TRANSMEM 259 275 POTENTIAL.
FT DOMAIN 218 242 POLY-GLU.
FT NON_TER 300 300
SQ SEQUENCE 300 AA; 31671 MW; 2BE592DA5AB9781E CRC64;

Query Match 39.78; Score 48; DB 1; Length 300;
Best Local Similarity 45.08; Pred. No. 11;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 4 GWRPDEGGQAGAEDELEV 23
I::: :||: ||| ||:
DB 84 GEIQAGEGGEVDEGEI 103

RESULT 11
SYM_METKA
ID SYM_METKA STANDARD; PRT; 668 AA.
AC Q8TX28;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
DE (MetRS).
DE METG OR MK0850.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OC NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Nalcate D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozayvkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -1- FUNCTION: Is required not only for elongation of protein synthesis
CC but also for the initiation of all mRNA translation through
CC initiator tRNA(fMet) aminoacylation (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) -> AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC MetG subfamily 1.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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CC -----
DR EMBL; AE010375; AM02063.1; -.
DR HAMAP; MF_00098; fused; 1.
DR InterPro; IPR004495; MetG_Cterm.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002304; tRNA-synt_met.
DR InterPro; IPR002347; tRNA_bind.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR Pfam; PF01588; tRNA_bind; 1.
DR Pfam; PIRSF001528; MetRS_dimerising; 1.
DR TIGRFAMS; TIGR00398; metG; 1.
DR TIGRFAMS; TIGR00399; metG_Cterm; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
DR PROSITE; PS00886; TRBD; 1.
DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
DR RNA-binding; tRNA-binding; Metal-binding; Zinc; Complete proteome.
FT SITE 11 21 "HIGH" REGION.
FT SITE 332 336 "KMSKS" REGION.
FT SITE 567 668 tRNA-BINDING.
FT DOMAIN 146 146 ZINC (BY SIMILARITY).
FT METAL 149 149 ZINC (BY SIMILARITY).
FT METAL 159 159 ZINC (BY SIMILARITY).
FT METAL 162 162 ZINC (BY SIMILARITY).
SQ SEQUENCE 668 AA; 77386 MW; FBC5734FF5FEF015 CRC64;

Query Match 39.78; Score 48; DB 1; Length 668;
Best Local Similarity 53.78; Pred. No. 24;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 6 LRPEDGGQAGAEDE 20
I::: :||: ||| ||:
DB 547 LLPESGEGSEGGQDDE 561

RESULT 12
NKX1_BOVIN
ID NKX1_BOVIN STANDARD; PRT; 1216 AA.
AC Q28139; O46384;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-
DE exchange protein 1) (Retinal rod Na-Ca+K exchanger).
DE SLC24A1 OR NCKX1.
GN

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OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RX SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 66-88; 232-249;
 RP 647-660 AND 1119-1136.
 RC TISSUE=Retina;
 RX MEDLINE=92258377; PubMed=1582405;
 RA Reilaender H., Achilles A., Friedel U., Maul G., Lottspeich F.,
 RA Cook N.J.;
 RT "Primary structure and functional expression of the Na/Ca,K-exchanger
 RT from bovine rod photoreceptors.";
 RL EMBO J. 11:1689-1695(1992).
 RN [2]
 RP SEQUENCE OF 725-1216 FROM N.A. (ISOFORM 1).
 RC TISSUE=Retina;
 RX MEDLINE=98138491; PubMed=9478004;
 RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.M.;
 RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger:
 RT comparison with a revised bovine sequence.";
 RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
 CC -1- FUNCTION: Critical component of the visual transduction cascade,
 CC controlling the calcium concentration of outer segments during
 CC light and darkness. Light causes a rapid lowering of cytosolic
 CC free calcium in the outer segment of both retinal rod and cone
 CC photoreceptors and the light-induced lowering of calcium is caused
 CC by extrusion via this protein which plays a key role in the
 CC process of light adaptation. Transports one Ca(2+) and one K(+) in
 CC exchange for four Na(+) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC Name=2;
 CC IsoId=Q28139-1; Sequence-Displayed;
 CC IsoId=Q28139-2; Sequence=VSP_006159;
 CC Note-No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Retina.
 CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
 CC
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 CC -----
 CC EMBL: X66481; CAA47108.1; -;
 CC EMBL: AF025664; AAB88884.1; -;
 CC PIR: S20969; S20969.
 CC InterPro: IPR004817; K_NaCaexchang.
 CC InterPro: IPR004481; K_NaCaexchang.
 CC InterPro: IPR004837; NaCa_Exmemb.
 CC Pfam: PF01699; NaCa_Ex; 2.
 CC TIGRfams: TIGR00927; 2A1904; 1.
 CC TIGRfams: TIGR00367; TIGR00367; 1.
 CC Vision: Transport; Antiport; Symport; Calcium transport;
 CC Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
 CC Phosphorylation; Signal; Repeat; Alternative splicing.
 CC SIGNAL 1 38 POTENTIAL
 CC CHAIN 39 1216 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
 CC DOMAIN 39 446 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 447 467 POTENTIAL.
 CC DOMAIN 468 491 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 492 512 POTENTIAL.
 CC DOMAIN 513 518 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 519 539 POTENTIAL.
 CC DOMAIN 540 557 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 558 578 POTENTIAL.
 CC DOMAIN 579 579 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 580 600 POTENTIAL.
 FT DOMAIN 601 1024 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1025 1045 POTENTIAL.
 FT DOMAIN 1046 1052 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1053 1073 POTENTIAL.
 FT DOMAIN 1074 1088 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1089 1109 POTENTIAL.
 FT DOMAIN 1110 1127 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1128 1148 POTENTIAL.
 FT DOMAIN 1149 1157 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1158 1178 POTENTIAL.
 FT DOMAIN 1179 1185 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1186 1206 POTENTIAL.
 FT DOMAIN 1207 1216 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 796 928 8 X 17 AA TANDEM REPEATS OF D-E-D-E-G-E-
 FT I-Q-A-G-E-[GA]-G-E-V-[EK]-G.
 FT 1 (APPROXIMATE).
 FT REPEAT 796 811
 FT REPEAT 812 828
 FT REPEAT 829 845
 FT REPEAT 846 862
 FT REPEAT 863 879
 FT REPEAT 880 896
 FT REPEAT 897 913
 FT REPEAT 914 928 8 (APPROXIMATE).
 FT REPEAT 488 528 ALPHA-1.
 FT REPEAT 1096 1127 ALPHA-2.
 FT DOMAIN 984 1009 POLY-GLU.
 FT MOD_RES 652 652 PHOSPHORYLATION (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 868 884 Missing (in isoform 2).
 FT /FTId=VSP_006159.
 FT CONFLICT 84 84 MISSING (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 234 234 MISSING (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 244 245 MISSING (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 857 857 A -> G (IN REF. 2).
 SQ SEQUENCE 1216 AA; 131614 MW; 39F149A74D1D0523 CRC64;
 Query Match 39.7%; Score 48; DB 1; Length 1216;
 Best Local Similarity 45.0%; Pred. No. 44;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 4 GWLPRDGGGAEGADELEV 23
 Db 816 GEIQAGEGGEVGEDEGEI 835
 ID OPRK_CAVPO STANDARD; PRT; 380 AA.
 AC P41144;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Kappa-type opioid receptor (KOR-1).
 GN OPRK1.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley; TISSUE=Brain;
 RX MEDLINE=94224825; PubMed=8170987;
 RA Xie G.X., Meng F., Mansour A., Thompson R.C., Hoversten M.T.,
 RA Goldstein A., Watson S.J., Akil H.;
 RT "Primary structure and functional expression of a guinea pig kappa
 RT opioid (dynorphin) receptor";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3779-3783(1994).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
 CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: U04092; AAA67171.1; -.
 CC PIR: A55259; A55259.
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCRHHODPSN.
 CC PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL1; 1.
 CC PROSITE: PS00262; G_PROTEIN_RECEPTOR_FL2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC phosphorylation; Lipoprotein; Palmitate.
 CC DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 59 85 1 (POTENTIAL).
 CC DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 96 95 2 (POTENTIAL).
 CC DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 133 154 3 (POTENTIAL).
 CC DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 174 196 4 (POTENTIAL).
 CC DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 223 247 5 (POTENTIAL).
 CC DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 276 299 6 (POTENTIAL).
 CC DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 312 333 7 (POTENTIAL).
 CC DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
 CC DISULFID 131 210 BY SIMILARITY.
 CC LIPID 345 345 PALMITATE (POTENTIAL).
 CC CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 380 AA; 42736 MW; 4FF053834DBBA623 CRC64;

Query Match 38.8%; Score 47; DB 1; Length 380;
 Best Local Similarity 38.1%; Pred. No. 19;
 Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
 QY 2 LAGWLRPEDGGQAGAEDELE 22
 D 30 LPGAEPDGNAGPQDEQLE 50

RESULT 14
 DDX8_ARATH
 ID DDX8_ARATH STANDARD; PRT; 1168 AA.
 AC Q38953; Q9LRV0;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative pre-mRNA splicing factor ATP-dependent RNA helicase.
 GN AT3G26560 OR MEF16.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 NCBI_TaxID=3702;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=37086699; PubMed=8932388;
 RA Quigley F., Dao P., Cottet A., Mache R.;
 RT "Sequence analysis of an 81 kb contig from Arabidopsis thaliana
 RL chromosome III.";
 RL Nucleic Acids Res. 24:4313-4318(1996).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty Pl and TAC
 RL clones.";
 RL DNA Res. 7:131-135(2000).
 CC -1- FUNCTION: COULD ACT LATE IN THE SPLICING OF PRE-MRNA AND MEDIANTE
 CC THE RELEASE OF THE SPLICED MRNA FROM SPLICEOSOMES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. DEAH
 CC SUBFAMILY. DDX8/PRP22 ORTHOLOG.
 CC -1- SIMILARITY: Contains 1 S1 motif domain.
 CC -1- CAUTION: Ref.1 sequences differ from that shown due to a
 CC frameshift in position 57.
 CC -----
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 CC -----
 CC EMBL: X98130; CAA66825.1; ALT_FRAME.
 CC EMBL: X97970; CAA66613.1; ALT_FRAME.
 CC EMBL: AB028611; BAB01838.1; -.
 CC HSP: P05055; ISRO.
 CC InterPro: IPR001410; DEAD.
 CC InterPro: IPR002464; DEAH_box.
 CC InterPro: IPR001650; Helicase_C.
 CC InterPro: IPR003029; S1.
 CC Pfam: PF00271; helicase_C; 1.
 CC Pfam: PF00575; S1; 1.
 CC SMART: SM00487; DEXDC; 1.
 CC SMART: SM00490; HELIC; 1.
 CC SMART: SM00316; S1; 1.
 CC PROSITE: PS00690; DEAH_ATP_HELICASE; 1.
 CC PROSITE: PS00126; S1; 1.
 CC Hypothetical protein; mRNA processing; mRNA splicing; Helicase;
 KW ATP-binding; Nuclear protein.
 KW DOMAIN 214 283 S1 MOTIF.
 FT NP_BIND 518 545 ATP (POTENTIAL).
 FT SITE 635 638 DEAH_BOX.
 FT DOMAIN 777 780 POLY-PRO.
 SQ SEQUENCE 1168 AA; 134156 MW; B3632DE47A7690C CRC64;
 Query Match 38.8%; Score 47; DB 1; Length 1168;
 Best Local Similarity 57.9%; Pred. No. 59;
 Matches 11; Conservative 2; Mismatches 2; Indels 4; Gaps 1;
 QY 9 EDGG----QAEGAEDELEV 23
 D 372 EDGGMLYQEGAELEELEI 390
 RESULT 15
 MM14_PIG
 ID MM14_PIG STANDARD; PRT; 580 AA.
 AC Q9XT90;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update).
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Matrix metalloproteinase-14 precursor (EC 3.4.24.-) (MMP-14)
 DE (Membrane-type matrix metalloproteinase 1) (MT-MMP 1) (MTMMP1)
 DE (Membrane-type-1 matrix metalloproteinase) (MT1-MMP) (MT1MMP).
 GN MMP14.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE-9905929; PubMed-9881602;
RA Caron C., Xue J., Bartlett J.D.;
RT "Expression and localization of membrane type 1 matrix
RT metalloproteinase in tooth tissues.";
RL Matrix Biol. 17:501-511(1998).
CC -!- FUNCTION: SEEMS TO SPECIFICALLY ACTIVATE OF PRO-
CC THUS TRIGGER INVASION BY TUMOR CELLS BY ACTIVATING PRO-
CC A ON THE TUMOR CELL SURFACE (BY SIMILARITY). MAY PLAY A ROLE IN
CC THE BIOMINERALIZATION OF ENAMEL AND DENTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN DEVELOPING TOOTH TISSUES
CC AND MAY PLAY A ROLE IN THE BIOMINERALIZATION OF ENAMEL AND DENTIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC -----
DR EMBL; AF067419; AAD38324.1; -.
DR HSSP; P08254; 1HFS.
DR MEROPS; M10.014; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR006026; Zn_Mtpeptdse.
DR InterPro; IPR006025; Zn_Mtpeptdse.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolase; Metalloprotease; Zinc; Zymogen; Calcium; Signal;
KW Transmembrane.
FT SIGNAL 1 28 POTENTIAL.
FT PROPEP 29 109 ACTIVATION PEPTIDE.
FT CHAIN 110 580 MATRIX METALLOPROTEINASE-14.
FT DOMAIN 110 539 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 540 560 POTENTIAL.
FT DOMAIN 561 580 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 314 509 HEMOPEXIN-LIKE.
FT SITE 91 91 CYSTEINE SWITCH (POTENTIAL).
FT METAL 237 237 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 238 238 BY SIMILARITY.
FT METAL 241 241 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 247 247 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 317 506 BY SIMILARITY.
SQ SEQUENCE 580 AA; 65934 MW; B7B2C569A96CAC CRC64;

Query Match 37.6%; Score 45.5; DB 1; Length 580;
Best Local Similarity 45.8%; Pred. No. 48;
Matches 11; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 ALAGWLRPEDGGQA-EGAEDELEV 23
|||:|||||
Db 499 ALRDWMCPSGGRPDEGTEETEY 522

Search completed: September 11, 2003, 17:21:44
Job time : 3.32086 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 21.893 seconds
(without alignments)
271.100 Million cell updates/sec

Title: US-09-853-253-5

Perfect score: 121

Sequence: 1 ALAGWLRPDGGQAEDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	119	98.3	117	4 Q8TAT9	Q8tat9 homo sapien
2	92	76.0	117	11 Q8CH53	Q8ch53 meriones un
3	59	48.8	1208	5 Q815T3	Q815t3 plasmodium
4	59	48.8	1264	5 Q9U445	Q9u445 plasmodium
5	55	45.5	183	10 Q8LNL6	Q8lnl6 oryza sativ
6	53	43.8	202	15 Q90P58	Q90p58 human immun
7	53	43.8	1228	5 Q27724	Q27724 plasmodium
8	52	43.0	201	15 Q90P50	Q90p50 human immun
9	52	43.0	232	16 Q916L1	Q916l1 pseudomonas
10	52	43.0	249	12 Q82036	Q82036 hirame rhab
11	52	43.0	392	12 Q9QL89	Q9ql89 hirame rhab
12	52	43.0	977	6 Q95169	Q95169 capra hircu
13	51.5	42.6	436	5 Q9N638	Q9n638 caenorhabdi
14	51	42.1	158	16 Q8XW90	Q8xw90 raistonia s
15	51	42.1	201	15 Q90NL5	Q90nl5 human immun
16	51	42.1	604	16 Q8UFA5	Q8ufa5 agrobacteri

17	51	42.1	609	2 Q9RH77	Q9rh77 bradyrhizob
18	50	41.3	131	16 Q9RV90	Q9rv90 deinococcus
19	50	41.3	202	15 Q90P76	Q90p76 human immun
20	50	41.3	202	15 Q90P77	Q90p77 human immun
21	50	41.3	472	10 Q8LRD5	Q8lrd5 oryza sativ
22	50	41.3	582	6 Q9XSP0	Q9xsp0 capra hircu
23	50	41.3	582	6 Q9GLE4	Q9gle4 bos taurus
24	49.5	40.9	484	16 Q9RZ17	Q9rz17 deinococcus
25	49	40.5	201	15 Q90P55	Q90p55 human immun
26	49	40.5	201	15 Q90NK8	Q90nk8 human immun
27	49	40.5	286	12 Q8QRU5	Q8qr5 chimpanzee
28	48.5	40.1	110	10 Q93VB3	Q93vb3 oryza sativ
29	48.5	40.1	172	2 Q9RBY2	Q9rby2 pseudomonas
30	48.5	40.1	172	2 Q9R2S2	Q9r2s2 pseudomonas
31	48.5	40.1	269	2 Q9ETM8	Q9etm8 pseudomonas
32	48	39.7	106	16 Q8ELH4	Q8elh4 oceanobacil
33	48	39.7	115	10 Q8LI79	Q8li79 oryza sativ
34	48	39.7	120	15 Q78494	Q78494 human immun
35	48	39.7	201	15 Q90P53	Q90p53 human immun
36	48	39.7	201	15 Q90NL3	Q90nl3 human immun
37	48	39.7	201	15 Q90NL6	Q90nl6 human immun
38	48	39.7	201	15 Q90NL0	Q90nl0 human immun
39	48	39.7	201	15 Q90NLI	Q90nl1 human immun
40	48	39.7	201	15 Q90NMI	Q90nm1 human immun
41	48	39.7	201	15 Q90NM2	Q90nm2 human immun
42	48	39.7	201	15 Q90NL9	Q90nl9 human immun
43	48	39.7	202	15 Q90P31	Q90p31 human immun
44	48	39.7	202	15 Q90P37	Q90p37 human immun
45	48	39.7	211	10 Q943L4	Q943l4 oryza sativ

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY; PRT; 117 AA.
AC Q8TAT9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025791; AAH25791.1; -
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
SQ SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;

Query Match 98.3%; Score 119; DB 4; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.6e-09;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAEDELEV 23
|||||
DB 52 ALAGWLRPDGGQAEDELEV 74

RESULT 2
Q8CH53 PRELIMINARY; PRT; 117 AA.
ID Q8CH53
AC Q8CH53;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Mariones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA SUZUKI H., Ota T., Masosaka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF42491; AAC06965.1; -.
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 76.0%; Score 92; DB 11; Length 117;
Best Local Similarity 73.9%; Pred. No. 1.3e-05;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAGAEDELE 23
DB 52 ALEGWLRPDGGQAGAEDELEI 74

RESULT 3
Q815T3
ID Q815T3 PRELIMINARY; PRT; 1208 AA.
AC Q815T3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase, putative.
GN PFL0590C
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Partea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McRadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014846; AAN36207.1; -.
SQ SEQUENCE 1208 AA; 133873 MW; 25AA7752E707E621 CRC64;

Query Match 48.8%; Score 59; DB 5; Length 1208;
Best Local Similarity 52.6%; Pred. No. 8.2;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 GWRPDDGGQAGAEDELE 22
DB 1072 GWCRPKDKTSDGYNDELE 1090

RESULT 4
Q9U445
ID Q9U445 PRELIMINARY; PRT; 1264 AA.
AC Q9U445;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase4.

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GN ATPASE4.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA KRISHNA S., Woodrow C., Webb R., Penny J., Takeyasu K., Kimura M.,
RA East J.M.;
RT "Expression and Functional Characterization of a Plasmodium falciparum
RT Ca2+-ATPase (PfATP4) Belonging to a Subclass Unique to Apicomplexan
RT Organisms.";
RL J. Biol. Chem. 276:10782-10787(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
CC ATPASES).
DR EMBL; AF203980; AAF17245.1; -.
DR HSP; P04191; IEUL.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00122; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 5.
DR PROSITE; PS00154; ATPASE_E1_E2; 1.
KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SQ SEQUENCE 1264 AA; 140261 MW; 638142BB1B433640 CRC64;

Query Match 48.8%; Score 59; DB 5; Length 1264;
Best Local Similarity 52.6%; Pred. No. 8.6;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 GWRPDDGGQAGAEDELE 22
DB 1128 GWCRPKDKTSDGYNDELE 1146

RESULT 5
Q8LNL6
ID Q8LNL6 PRELIMINARY; PRT; 183 AA.
AC Q8LNL6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0071120.2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartodiaceae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA McCombie W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,
RA Kuit K., Nascimento L., Zutavern T., Balija V., Bell M., Baker J.,
RA Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,
RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone
RT OSJNBA0071120, from chromosome 10, complete sequence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC074355; AAM74240.1; -.
DR Gramene; Q8LNL6; -.
KW Hypothetical protein.
SQ SEQUENCE 183 AA; 20492 MW; DE73BD8607292D7B CRC64;

Query Match 45.5%; Score 55; DB 10; Length 183;
Best Local Similarity 47.6%; Pred. No. 4.2;
Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

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QY 3 AGWLRPEDGGQAGAEDELEV 23
 |||: ||| | | : ||
 Db 53 AGWIETEDGSDSESDSEV 73

RESULT 6

Q90P58 PRELIMINARY; PRT; 202 AA.
 AC Q90P58;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nickle D.C.;
 RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF370911; AAK66310.1; -;
 DR InterPro; IPR000777; GP120.
 KW Pfam; PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 202
 SQ SEQUENCE 202 AA; 22572 MW; 4CB8ACAFBFB14314 CRC64;

Query Match 43.8%; Score 53; DB 15; Length 202;
 Best Local Similarity 45.5%; Pred. No. 9.1;
 Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDELEV 23
 : | | | | | : | | | |
 Db 180 ITGLLTRDGGGGGTDETEV 201

RESULT 7

Q27724 PRELIMINARY; PRT; 1228 AA.
 AC Q27724;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE P-type ATPase.
 GN PFATPASE4.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=96408665; PubMed=8813672;
 RA Dyer M., Jackson M., McWhinney C., Zhao G., Mikkelsen R.;
 RT "Analysis of a cation-transporting ATPase of Plasmodium falciparum.";
 RL Mol. Biochem. Parasitol. 78:1-12(1996).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES).
 CC EMBL; U39298; AAC47167.1; -;
 DR HSSP; P04191; 1EUL.
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR006068; Cation_ATPase_C.
 DR InterPro; IPR004014; Cation_ATPase_N.
 DR InterPro; IPR005834; Hydrolase.
 DR InterPro; IPR000695; H_ATPase.
 DR Pfam; PF00689; Cation_ATPase_C; 1.
 DR Pfam; PF00690; Cation_ATPase_N; 1.
 DR Pfam; PF00122; E1-E2_ATPase; 1.
 DR Pfam; PF00702; Hydrolase; 1.

DR PRINTS; PRO0119; CATAPASE.
 DR PRINTS; PRO0120; HATPASE.
 DR TIGRFAMS; TIGR01494; ATPase_p-type; 5.
 DR PROSITE; PS00154; ATPASE_E1-E2; 1.
 KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
 SQ SEQUENCE 1228 AA; 135989 MW; 32C3CFD324964CBE CRC64;

Query Match 43.8%; Score 53; DB 5; Length 1228;
 Best Local Similarity 50.0%; Pred. No. 61;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 WLRPEDGGQAGAEDELEV 22
 | | | | : | | | | |
 Db 1131 WCRPKDNKTSDDYNDLE 1148

RESULT 8

Q90P50 PRELIMINARY; PRT; 201 AA.
 AC Q90P50;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nickle D.C.;
 RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF370919; AAK66318.1; -;
 DR InterPro; IPR000777; GP120.
 KW Pfam; PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 201
 SQ SEQUENCE 201 AA; 22550 MW; 6CAF6C4609BA517 CRC64;

Query Match 43.0%; Score 52; DB 15; Length 201;
 Best Local Similarity 45.5%; Pred. No. 13;
 Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDELEV 23
 : | | | | | : | | | |
 Db 179 ITGLLTRDGGGGGTDETEV 200

RESULT 9

Q916L1 PRELIMINARY; PRT; 232 AA.
 AC Q916L1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Probable transcriptional regulator.
 GN PA0279.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Miziouchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen." ;
RL Nature 405:959-964(2000).
CC 1- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AE004466; AAC03668.1; -.
DR InterPro; IPR001845; HTH_ArsR.
DR Pfam; PF01022; HTH_5; 1.
DR PRINTS; PR00778; HTHARSR.
DR SMART; SM00418; HTHARSR; 1.
KW DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 232 AA; 24440 MW; E3C29187694CF936 CRC64;

Query Match 43.0%; Score 52; DB 16; Length 232;
Best Local Similarity 72.7%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWRPQDGSRA 212
Db 202 GWRPQDGSRA 212
||||:|||||

RESULT 10

ID Q82036 PRELIMINARY; PRT; 249 AA.
AC Q82036;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Hirame rhabdovirus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=38142;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8401-H;
RA Nishizawa T.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; D45422; BAA08261.1; -.
DR InterPro; IPR004902; Rhabdo_ncap_2.
DR Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ SEQUENCE 249 AA; 26936 MW; 62FF2BFA5D47DB89 CRC64;

Query Match 43.0%; Score 52; DB 12; Length 249;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 EDGGQAEAGDE 20
Db 235 EDGGEDEGEDE 246
||||:|||||

RESULT 11

Q9QL89 PRELIMINARY; PRT; 392 AA.
AC Q9QL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Hirame rhabdovirus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=38142;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA 9703;
RA Oh H.K., Choi T.J.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104985; AAF14116.1; -.
SQ SEQUENCE 392 AA; 42465 MW; C5A282238FC7A638 CRC64;

DR InterPro; IPR004902; Rhabdo_ncap_2.
DR Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ SEQUENCE 392 AA; 42465 MW; C5A282238FC7A638 CRC64;

Query Match 43.0%; Score 52; DB 12; Length 392;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 EDGGQAEAGDE 20
Db 378 EDGGEDEGEDE 389
||||:|||||

RESULT 12

Q95169 PRELIMINARY; PRT; 977 AA.
ID Q95169;
AC Q95169;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Skeletal muscle voltage-gated chloride channel gClc-1 (Fragment).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Beck C.L., Fahlke C., George A.L.;
RT "Molecular basis for decreased muscle chloride conductance in the
RT myotonic goat." ;
RL Proc. Natl. Acad. Sci. U.S.A. 93:11248-11252(1996).
DR EMBL; U60275; AAC48666.1; -.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR001807; Cl-channel_volt.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
FT NON_TER 1
SQ SEQUENCE 977 AA; 107894 MW; 1E462B3CB307A148 CRC64;

Query Match 43.0%; Score 52; DB 6; Length 977;
Best Local Similarity 62.5%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWRPQDGSRA 19
Db 895 GWSLPEDGAGATGAGD 910
||||:|||||

RESULT 13

Q9N638 PRELIMINARY; PRT; 436 AA.
ID Q9N638;
AC Q9N638;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F37D6.6 protein.
GN F37D6.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J.;
RA Wilkinson J.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;

RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RL investigating biology."
 RL Science 282:2012-2018(1998).
 RN [3]

RP SEQUENCE FROM N.A.

RA McMurray A.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z79600; CAB70221.1; -.
 DR EMBL: Z75540; CAB70221.1; JOINED.
 DR EMBL: Z75540; CAB70215.1; -.
 DR EMBL: Z79600; CAB70215.1; JOINED.
 DR WormPep; F37D6.6; CE24960.
 DR InterPro: IPR001132; DwarfIn.
 DR InterPro: IPR003619; DwarfIn_A.
 DR Pfam: PF03166; MH2; 1.
 DR SMART: SM00523; DWA; 1.
 DR SMART: SM00524; DWA; 1.
 SQ SEQUENCE 436 AA; 49496 MW; E0C71263BC580EEE CRC64;

Query Match 42.6%; Score 51.5; DB 5; Length 436;
 Best Local Similarity 52.9%; Pred. No. 34;
 Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 5 WLRPE-DGQAGAEDE 20
 I:III :II :I:II:
 Db 169 WIRPETNGDDGSEDK 185

RESULT 14

Q8XW90
 ID Q8XW90 PRELIMINARY; PRT; 158 AA.
 AC Q8XW90;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein RSC2585.
 GN RSC2585 OR RS00797.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
 Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,
 Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
 RL Nature 415:497-502(2002).
 DR EMBL: AL646070; CAD16292.1; -.
 DR InterPro: IPR002145; HTH_CopG.
 DR Pfam: PF01402; HTH 4; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 158 AA; 17814 MW; C9BA42BF9C10E1BC CRC64;

Query Match 42.1%; Score 51; DB 16; Length 158;
 Best Local Similarity 58.8%; Pred. No. 14;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGA 17
 III I I : I I I
 Db 36 ALASWLSPDAGDQREAA 52

RESULT 15

Q90NL5
 ID Q90NL5 PRELIMINARY; PRT; 201 AA.
 AC Q90NL5;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human Immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nickle D.C.;
 RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF371104; AAK66503.1; -.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR AIDS; Coat protein; Glycoprotein.
 KW NON_TER 1
 FT NON_TER 201
 SQ SEQUENCE 201 AA; 22470 MW; E1993A2A412EC118 CRC64;

Query Match 42.1%; Score 51; DB 15; Length 201;
 Best Local Similarity 40.9%; Pred. No. 18;
 Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDELEV 23
 : I I I I I I I : I I I
 Db 179 ITGLLLTRDGGGGNGTDTNETEI 200

Search completed: September 11, 2003, 17:30:28
 Job time : 22.893 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:27:22 : Search time 24.2299 Seconds
(without alignments)
150.669 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 23

Sequence: 1 ALAGWLRPEDGGQAEAEDELEV 23

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	23	AAE23840	Human zsig33-linker
2	23	100.0	23	AAE23841	Human zsig33-linker
3	23	100.0	23	AAE15885	Human zsig33-linker
4	23	100.0	23	AAE15886	Human zsig33-linker
5	23	100.0	24	AAE23839	Human zsig33-linker
6	23	100.0	24	AAE15884	Human zsig33-linker
7	23	100.0	91	AAE33410	Human exon 3-delet
8	23	100.0	116	AAE60517	Human des-Gln14-gh
9	23	100.0	117	AAW87991	Protein designated

10	23	100.0	117	21	AAW87236	Human signal pepti
11	23	100.0	117	22	AAW38890	Human polypeptide
12	23	100.0	117	22	AAW62649	Human zsig33 polyp
13	23	100.0	117	22	AAW20101	zsig33 protein. H
14	23	100.0	117	22	AAW60511	Human ghrelin prep
15	23	100.0	117	23	ABW78319	Amino acid sequenc
16	23	100.0	117	23	AAE23838	Human zsig33 prote
17	23	100.0	117	23	AAE15883	Human zsig33 prote
18	23	100.0	117	24	ABU65790	Human PRO polypept
19	23	100.0	117	24	ABU67066	Human secreted/tra
20	23	100.0	117	24	ABU59871	Novel secreted and
21	23	100.0	117	24	ABU59124	Novel human secret
22	23	100.0	117	24	ABU59271	Human secreted/tra
23	23	100.0	117	24	ABU59420	Novel human secret
24	23	100.0	117	24	ABU60555	Human secreted/tra
25	23	100.0	117	24	ABU58046	Human PRO polypept
26	23	100.0	117	24	ABU58977	Human secreted/tra
27	23	100.0	117	24	AAE33409	Human preproghreli
28	23	100.0	117	24	ABU13937	Human PRO1066 poly
29	23	100.0	117	24	ABU10892	Human PRO polypept
30	23	100.0	118	21	AAW66708	Membrane-bound pro
31	23	100.0	118	22	AAU12392	Human PRO1066 poly
32	23	100.0	118	22	AAW65231	Human PRO1066 (UNQ
33	23	100.0	126	22	AAW40676	Human polypeptide
34	10	43.5	89	22	AAW60523	Bovine ghrelin pre
35	8	34.8	334	21	AAW29677	Arabidopsis thalia
36	8	34.8	428	21	AAW29676	Arabidopsis thalia
37	8	34.8	483	21	AAW29675	Arabidopsis thalia
38	7	30.4	311	19	AAW36129	Snpr activator pro
39	7	30.4	311	21	AAW30494	Amino acid sequenc
40	7	30.4	442	23	ABP38188	Staphylococcus epi
41	7	30.4	1931	22	ABW65948	Drosophila melanog
42	6	26.1	14	22	AAW65893	Human peptide #168
43	6	26.1	26	24	AAE33406	PD-1_Ctall2 peptid
44	6	26.1	26	24	ABU18534	PD-1-related pepti
45	6	26.1	39	20	AAW50239	Neutrophil-activat

ALIGNMENTS

RESULT 1
AAE23840
ID AAE23840 standard; peptide; 23 AA.
XX
AC AAE23840;

XX
XX
DT 10-SEP-2002 (first entry)
DE Human zsig33-linker peptide #2.
XX

KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.

XX Homo sapiens.

XX US2002055156-A1.

XX 09-MAY-2002.

XX 10-MAY-2001; 2001US-0853253.

XX 11-MAY-2000; 2000US-203300P.

XX (JASP/) JASPERS S R.

XX (SHEP/) SHEPPARD P O.

XX (DEIS/) DEISHER T A.

XX (BISH/) BISHOP P D.

XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-443750/47.

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
XX
XX
PS Claim 1; Page 28; 34pp; English.
XX
CC The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 23; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
DB 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 2

AAE23841
ID AAE23841 standard; peptide; 23 AA.

XX AAE23841;

DT 10-SEP-2002 (first entry)

XX Human zsig33-linker peptide #3.

XX Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.

XX Homo sapiens.

XX US2002055156-A1.

PN 09-MAY-2002.

XX 10-MAY-2001; 2001US-0853253.

XX 11-MAY-2000; 2000US-203300P.

XX (JASP/) JASPERS S R.
PA (SHEP/) SHEPPARD P O.
PA (DEIS/) DEISHER T A.
PA (BISH/) BISHOP P D.

XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-443750/47.

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
XX
XX
PS Claim 1; Page 28; 34pp; English.

XX The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.

XX Sequence 23 AA;

Query Match 100.0%; Score 23; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
DB 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 3

AAE15885
ID AAE15885 standard; peptide; 23 AA.

XX AAE15885;

DT 26-MAR-2002 (first entry)

XX Human zsig33-linker peptide #2.

XX Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-linker peptide.

XX Homo sapiens.

XX WO200187933-A2.

PN 22-NOV-2001.

XX 10-MAY-2001; 2001WO-US15091.

XX 11-MAY-2000; 2000US-0569271.

XX (ZYMO) ZYMOGENETICS INC.

XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-082982/11.

DR N-PSDB; AAD25760.

XX New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and
PT treating gastrointestinal and growth related diseases, comprises

PT zsig33-like peptides -
 PS Claim 1b; Page 81; 89pp; English.
 CC The invention relates to zsig33-like peptides (ZS33LP) including
 CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and
 CC zsig33-epsilon peptides and nucleic acid molecules encoding such
 CC zsig33-like peptides. ZS33LP peptides activate the immune system
 CC in boosting immunity to infectious diseases, treating immunocompromised
 CC patients such as human immunodeficiency virus (HIV) patients, in
 CC improving vaccines and in treatment of bacterial, viral, protozoal and
 CC fungal infections. Peptides of the invention are used to identify and
 CC isolate receptors involved in growth regulation in the liver, blood
 CC vessel formation and other developmental processes. They are useful for
 CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
 CC growth and/or differentiation of tumour cells, as additives to anti-
 CC hypoglycaemic preparations containing glucose and as adsorption
 CC enhancers for oral drugs which require fast nutrient action and to
 CC stimulate glucose-induced insulin release. They are also useful as
 CC research reagents for the expansion, differentiation, growth factor and
 CC hormone secretion and/or cell-cell interactions of tissues associated
 CC with gastrointestinal system, brain and central nervous system. These
 CC molecules are useful for treating dysfunction associated with contractile
 CC tissues or to suppress or enhance contractility in vivo and to treat
 CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
 CC acids and/or antibodies are useful for treating disorders associated
 CC with gastrointestinal contractility, secretion of digestive enzymes,
 CC hormone and acids, secretion of hormones in the pancreas and/or brain,
 CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
 CC and regulation of nutrient absorption. Sequences of the invention are
 CC useful in gene therapy. The present sequence is human zsig33-linker
 CC peptide.
 SQ Sequence 23 AA;
 Query Match 100.0%; Score 23; DB 23; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.9e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 |||||||
 DB 1 ALAGWLRPEDGGQAGAEDELEV 23
 |||||||
 RESULT 4
 AAE15886
 ID AAE15886 standard; peptide; 23 AA.
 AC AAE15886;
 XX
 DT 26-MAR-2002 (first entry)
 DE Human zsig33-linker peptide #3.
 XX
 KW Human; zsig33-like peptide; ZS33LP; Immunity; developmental process;
 KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
 KW adsorption enhancer; gastrointestinal disease; growth related disease;
 KW inflammation; gene therapy; growth regulation; blood vessel formation;
 KW HIV; zsig33-linker peptide.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 23
 FT /note= "C-terminal amide"
 FT
 XX WO200187933-A2.
 PN
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-US15091.
 XX
 PR 11-MAY-2000; 2000US-0569271.

XX (ZYMO) ZYMOGENETICS INC.
 XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 PI WPI; 2002-082982/11.
 XX N-PSDB; AAD25760.
 PT New polypeptides, useful for modulating gastric contractility, nutrient
 PT uptake, pancreatic secretion of hormones, digestive enzymes and
 PT treating gastrointestinal and growth related diseases, comprises
 PT zsig33-like peptides -
 XX
 PS Claim 1c; Page 82; 89pp; English.
 XX The invention relates to zsig33-like peptides (ZS33LP) including
 CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and
 CC zsig33-epsilon peptides and nucleic acid molecules encoding such
 CC zsig33-like peptides. ZS33LP peptides activate the immune system
 CC in boosting immunity to infectious diseases, treating immunocompromised
 CC patients such as human immunodeficiency virus (HIV) patients, in
 CC improving vaccines and in treatment of bacterial, viral, protozoal and
 CC fungal infections. Peptides of the invention are used to identify and
 CC isolate receptors involved in growth regulation in the liver, blood
 CC vessel formation and other developmental processes. They are useful for
 CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
 CC growth and/or differentiation of tumour cells, as additives to anti-
 CC hypoglycaemic preparations containing glucose and as adsorption
 CC enhancers for oral drugs which require fast nutrient action and to
 CC stimulate glucose-induced insulin release. They are also useful as
 CC research reagents for the expansion, differentiation, growth factor and
 CC hormone secretion and/or cell-cell interactions of tissues associated
 CC with gastrointestinal system, brain and central nervous system. These
 CC molecules are useful for treating dysfunction associated with contractile
 CC tissues or to suppress or enhance contractility in vivo and to treat
 CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
 CC acids and/or antibodies are useful for treating disorders associated
 CC with gastrointestinal contractility, secretion of digestive enzymes,
 CC hormone and acids, secretion of hormones in the pancreas and/or brain,
 CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
 CC and regulation of nutrient absorption. Sequences of the invention are
 CC useful in gene therapy. The present sequence is human zsig33-linker
 CC peptide.
 XX
 SQ Sequence 23 AA;
 Query Match 100.0%; Score 23; DB 23; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.9e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
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 DB 1 ALAGWLRPEDGGQAGAEDELEV 23
 |||||||
 RESULT 5
 AAE23839
 ID AAE23839 standard; peptide; 24 AA.
 XX
 AC AAE23839;
 XX
 DT 10-SEP-2002 (first entry)
 DE Human zsig33-linker peptide #1.
 XX
 KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
 KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
 KW protein therapy; gastrointestinal; endocrine; anabolic.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Region 7..18

FT XX /note= "Hydrophilic region"
 PN US2002055156-A1.
 XX 09-MAY-2002.
 PD 10-MAY-2001; 2001US-0853253.
 XX 11-MAY-2000; 2000US-203300P.
 XX (JASP/) JASPERS S R.
 PA (SHEP/) SHEPPARD P O.
 PA (DEIS/) DEISHER T A.
 PA (BISH/) BISHOP P D.
 XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 XX WPI: 2002-443750/47.
 DR N-PSDB: AAD38239.
 XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
 PT contractility, nutrient uptake, growth hormones and/or secretion of
 PT digestive/pancreatic enzymes and hormones
 XX Claim 1; Page 28; 34pp; English.
 XX The invention relates to zsig33-like peptides and their corresponding
 CC nucleic acids and methods for modulating gastric contractility, nutrient
 CC uptake, growth hormones, secretion of digestive enzymes and hormones.
 CC The sequences of the invention are used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate ZSIG33 expression.
 CC The nucleic acids of the invention and their complements are used as
 CC DNA probes in diagnostic assays to detect and quantitate the presence
 CC of similar nucleic acids in samples, and therefore which patients may be
 CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
 CC in the production of antibodies against ZSIG33 and in assays to identify
 CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
 CC and antagonists are used to down regulate expression and activity. The
 CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
 CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
 CC assay (ELISA)). The peptides and nucleic acids of the invention are used
 CC to modulate gastric contractility, nutrient uptake, growth hormones, the
 CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
 CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
 CC and zsig33-like peptide is used in protein therapy. The present sequence
 CC is human zsig33-like peptide, zsig33-linker peptide.
 XX SQ Sequence 24 AA;
 Query Match 100.0%; Score 23; DB 23; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.1e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGGAEGAEDELEV 23
 DB 1 ALAGWLRPEDGGGGAEGAEDELEV 23
 RESULT 6
 AAE15884
 ID AAE15884 standard; peptide; 24 AA.
 AC AAE15884;
 XX 26-MAR-2002 (first entry)
 DT Human zsig33-linker peptide #1.
 DE Human zsig33-like peptide; ZS33LP; immunity; developmental process;
 XX infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
 KW adsorption enhancer; gastrointestinal disease; growth related disease;
 KW inflammation; gene therapy; growth regulation; blood vessel formation;
 KW HIV; zsig33-linker peptide.

XX Homo sapiens.
 OS Key Location/Qualifiers
 XX Region 6..22 /note= "Hydrophilic antigenic site"
 FT Region 7..18 /note= "Hydrophilic region"
 FT Region 7..18 /note= "Hydrophilic region"
 XX WO200187933-A2.
 PN 22-NOV-2001.
 XX 10-MAY-2001; 2001WO-US15091.
 XX 11-MAY-2000; 2000US-0569271.
 XX (ZYMO) ZYMOGENETICS INC.
 PA Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 XX WPI: 2002-082982/11.
 DR N-PSDB: AAD25760.
 XX New polypeptides, useful for modulating gastric contractility, nutrient
 PT uptake, pancreatic secretion of hormones, digestive enzymes and
 PT treating gastrointestinal and growth related diseases, comprises
 PT zsig33-like peptides -
 XX Claim 1a; Page 81; 89pp; English.
 XX The invention relates to zsig33-like peptides (ZS33LP) including
 CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and
 CC zsig33-epsilon peptides and nucleic acid molecules encoding such
 CC zsig33-like peptides. ZS33LP peptides activate the immune system
 CC in boosting immunity to infectious diseases, treating immunocompromised
 CC patients such as human immunodeficiency virus (HIV) patients, in
 CC improving vaccines and in treatment of bacterial, viral, protozoal and
 CC fungal infections. Peptides of the invention are used to identify and
 CC isolate receptors involved in growth regulation in the liver, blood
 CC vessel formation and other developmental processes. They are useful for
 CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
 CC growth and/or differentiation of tumour cells, as additives to anti-
 CC hypoglycaemic preparations containing glucose and as adsorption
 CC enhancers for oral drugs which require fast nutrient action and to
 CC stimulate glucose-induced insulin release. They are also useful as
 CC research reagents for the expansion, differentiation, growth factor and
 CC hormone secretion and/or cell-cell interactions of tissues associated
 CC with gastrointestinal system, brain and central nervous system. These
 CC molecules are useful for treating dysfunction associated with contractile
 CC tissues or to suppress or enhance contractility in vivo and to treat
 CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
 CC acids and/or antibodies are useful for treating disorders associated
 CC with gastrointestinal contractility, secretion of digestive enzymes,
 CC hormone and acids, secretion of hormones in the pancreas and/or brain,
 CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
 CC and regulation of nutrient absorption. Sequences of the invention are
 CC useful in gene therapy. The present sequence is human zsig33-linker
 CC peptide.
 XX SQ Sequence 24 AA;
 Query Match 100.0%; Score 23; DB 23; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.1e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGGAEGAEDELEV 23
 DB 1 ALAGWLRPEDGGGGAEGAEDELEV 23
 RESULT 7
 AAE33410

ID AAE33410 standard; Protein; 91 AA.
 AC AAE33410;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human exon 3-deleted ghrelin protein.
 XX
 KW Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
 KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
 KW cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200290387-A1.
 XX
 PD 14-NOV-2002.
 XX
 XX 10-MAY-2002; 2002WO-AU00582.
 XX
 PR 10-MAY-2001; 2001AU-0004919.
 PR 17-DEC-2001; 2001AU-0009567.
 XX
 PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 PI Chopin LK, Jeffery PL, Herington AC;
 XX
 DR WPI; 2003-111957/10.
 DR N-PSDB; AAD50726.
 XX
 PT Identifying a cancer cell or tissue for treating prostate, ovarian,
 PT breast cancer, or benign prostatic hyperplasia, by detecting the
 PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
 PT 1b proteins or nucleic acids -
 XX
 PS Claim 14; Page 34; 50pp; English.
 XX
 CC The invention relates to a method for identifying a cancer cell or
 CC tissue of the reproductive system by detecting expression of a ghrelin,
 CC an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic
 CC acids. The antibodies, exon 3-deleted form of preproghrelin and
 CC antagonists are useful for treating cancer of the reproductive system
 CC such as prostate, ovarian, breast, cervical or uterine cancer,
 CC choriocarcinoma or benign prostatic hyperplasia. The present sequence
 CC is human exon 3-deleted ghrelin protein.
 XX
 SQ Sequence 91 AA;
 Query Match 100.0%; Score 23; DB 24; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 8
 AAB60517
 ID AAB60517 standard; Protein; 116 AA.
 XX
 AC AAB60517;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
 XX
 KW Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX

PN WO200107475-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-JP04907.
 XX
 PR 23-JUL-1999; 99JP-0210002.
 PR 29-NOV-1999; 99JP-0338841.
 PR 26-APR-2000; 2000JP-0126623.
 XX
 PA (KANG/) KANGAWA K.
 XX
 PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 XX
 DR WPI; 2001-159704/16.
 DR N-PSDB; AAF59647.
 XX
 PT New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 XX
 PS Claim 3; Page 186-187; 210pp; Japanese.
 XX
 CC The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 SQ Sequence 116 AA;
 Query Match 100.0%; Score 23; DB 22; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 51 ALAGWLRPEDGGQAGAEDELEV 73
 RESULT 9
 AAW87991
 ID AAW87991 standard; Protein; 117 AA.
 XX
 AC AAW87991;
 XX
 DT 07-APR-1999 (first entry)
 XX
 DE Protein designated zsig33.
 XX
 KW Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
 KW nutrient absorption regulation; obesity; metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 PI Key Location/Qualifiers
 FT Peptide 1..23 "signal peptide"
 FT Protein 24..117
 FT "note="mature protein"
 XX

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PN WO9842840-A1.
XX 01-OCT-1998.
XX 23-MAR-1998; 98WO-US05620.
XX 24-MAR-1997; 97US-0822897.
PR 24-MAR-1997; 97US-0041102.
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Deisher TA, Sheppard PO;
XX WPI; 1999-070071/06.
DR N-PSDB; AAX04550.
XX
XX Human polypeptide having homology to motilin, zsig33 - useful e.g.
XX to treat gastrointestinal motility disorders, obesity etc. and to
XX identify antagonists to treat gastrointestinal hypermotility
XX
XX Claim 13; Page 55-56; 69pp; English.
XX
XX The present sequence represents a protein designated zsig33. The nucleic
XX acids are strongly expressed in stomach tissue. The polypeptide (or
XX allelic variants/orologs) can be used to stimulate gastric motility,
XX measured as increased transit time or gastric emptying of an ingested
XX substance in mammals. The products are used to treat disorders associated
XX with gastrointestinal cell contractility, secretion of digestive
XX enzymes/acids, gastrointestinal motility, recruitment of digestive
XX enzymes, gastrointestinal inflammation, reflux disease and nutrient
XX absorption regulation. zsig33 polypeptides may also be important
XX neurologically, since the family of gut-brain peptides to which the
XX homologous protein motilin belongs has been associated with neurological
XX and CNS functions. They may therefore be used e.g. to regulate satiety
XX or treat obesity and other metabolic disorders where neurological
XX feedback modulates nutritional absorption. They are useful to identify
XX zsig33 agonists, antagonists and ligands and to produce antibodies.
XX
XX Sequence 117 AA:
XX
XX Query Match 100.0%; Score 23; DB 20; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-14;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ALAGWLRPEDGGQGAEGAEDEV 23
XX |||||
XX 52 ALAGWLRPEDGGQGAEGAEDEV 74
XX
XX RESULT 10
XX AAY87236
XX ID AAY87236 standard; Protein: 117 AA.
XX
XX XX
XX AC AAY87236;
XX
XX DT 11-MAY-2000 (first entry)
XX
XX DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
XX
XX KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
XX inflammation; cardiovascular disease; anticancer; anti-inflammatory;
XX antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
XX antiasthmatic; gene therapy; cell proliferation; neurological disorder;
XX reproductive disorder; developmental disorder; arteriosclerosis;
XX cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
XX asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
XX Parkinson's disease; Huntington's diseases; ovulatory defect;
XX muscular dystrophy.
XX
XX OS Homo sapiens.
XX
XX PN WO200000610-A2.
XX

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PD 06-JAN-2000.
XX 25-JUN-1999; 99WO-US14484.
XX 26-JUN-1998; 98US-0090762.
PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX (INCY-) INCYTE PHARM INC.
XX
XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
XX Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
XX Bandman O;
XX WPI; 2000-160673/14.
XX N-PSDB; AAZ98121.
XX
XX New human signal peptide-containing proteins useful in treatment,
XX prevention and diagnosis of e.g. cancer, inflammation and
XX cardiovascular disease
XX
XX Claim 1; Page 168-169; 327pp; English.
XX
XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
XX human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
XX anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
XX neuroprotective, cardiovascular and antiasthmatic activities, and can
XX be used in gene therapy. HSPPs can be used to treat or prevent disorders
XX associated with decreased activity or function of HSPP. Antagonists of
XX HSPP are used to treat or prevent disorders associated with increased
XX activity or function of HSPP. Such diseases include cell proliferation
XX (including cancer), inflammation, cardiovascular, neurological,
XX reproductive or developmental disorders (e.g. arteriosclerosis,
XX cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
XX aschma, Crohn's disease, microbial or other infections, congestive or
XX ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
XX diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
XX nucleic acids can be used for the recombinant production of HSPP, for
XX detecting HSPP in standard hybridisation and amplification assays (for
XX diagnosis and monitoring), in gene therapy as antisense,
XX triplex-forming or ribozyme therapeutics, for detecting related sequences
XX or genetic variations, and for chromosomal mapping. HSPP are also used to
XX raise specific antibodies (Ab) and to screen for agonists and
XX antagonists (potential therapeutic agents). Ab are used to diagnose, or
XX monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
XX antagonists, in competitive drug screens, and for purification of HSPP
XX from natural sources.
XX
XX SQ Sequence 117 AA;
XX
XX Query Match 100.0%; Score 23; DB 21; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-14;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ALAGWLRPEDGGQGAEGAEDEV 23
XX |||||
XX 52 ALAGWLRPEDGGQGAEGAEDEV 74
XX
XX Db
XX
XX RESULT 11
XX AAM38890
XX ID AAM38890 standard; Protein: 117 AA.
XX
XX AC AAM38890;
XX
XX XX 22-OCT-2001 (first entry)
XX
XX DE Human polypeptide SEQ ID NO 2035.
XX
XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

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KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX Homo sapiens.
XX WO200153312-A1.
XX 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US34263.
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX WPI: 2001-442253/47.
XX N-PSDB; AA158046.
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX Example 3; SEQ ID NO 2035; 10078pp; English.
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AA138642-AA142213) with nootropic,
XX immunosuppressant and cytoskeletal activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
XX Sequence 117 AA;
XX
XX Query Match 100.0%; Score 23; DB 22; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-14;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ALAGWLRPEDGGGAEGAEDELEV 23
XX Db 52 ALAGWLRPEDGGGAEGAEDELEV 74
XX
XX RESULT 12
XX AAB62649
XX ID AAB62649 standard; Protein; 117 AA.
XX AC AAB62649;
XX XX
XX 23-JUL-2001 (first entry)
XX DT
XX Human zsig33 polypeptide.
XX DE
XX

KW zsig33; signal transduction; hormone; enzyme; neural development;
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
KW glucose; osteopathic; anorectic; vulnerable; immunomodulator; GHS-R;
KW G-protein coupled receptor.
XX Homo sapiens.
XX OS
XX Location/Qualifiers
XX Key
XX Peptide 24..37
XX /note= "specifically claimed fragment that binds to
XX the GHS-R"
XX
XX WO200138355-A2.
XX 31-MAY-2001.
XX 22-NOV-2000; 2000WO-US32074.
XX 22-NOV-1999; 99US-0166765.
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO, Jaspers SR, Delisher TA, Bishop PD;
XX WPI: 2001-355879/37.
XX N-PSDB; AA583678.
XX Forming reversible peptide receptor complex for purifying cell and
XX peptides, stimulating signal transduction and modulating hormone
XX secretion, involves contacting a receptor with zsig33 polypeptide -
XX Claim 1; Page 93-94; 111pp; English.
XX The invention relates to a method of forming a reversible peptide-
XX receptor complex that involves providing an immobilized receptor, and
XX contacting the receptor with a zsig33 peptide (comprising residues 24-37
XX of AAB62649), where the receptor binds to the zsig33 peptide. The method
XX is useful for purifying cells, purifying a peptide, stimulating signal
XX transduction in a cell expressing a receptor. It is also useful for
XX modulating secretion of hormones, neural development and/or utilization,
XX gastric contractility, nutrient uptake, secretion of digestive and
XX pancreatic enzymes and hormones, secretion of insulin-like growth factor
XX -I, secretion of non-zsig33 proteins. It is useful for modulating growth
XX hormone secretion in a mammal having a disease associated with abnormal
XX levels of growth hormone, such as osteoporosis, bone repair, bone
XX remodeling, low osteoblast levels, cartilage repair and remodeling,
XX skeletal dysplasia, immune suppression, obesity, growth retardation,
XX protein catabolic responses after surgery, cachexia, protein loss,
XX dwarfism, wound healing and ovulation induction, treating a mammal having
XX a metabolic disorder requiring neurological feedback, such as satiety
XX regulation, glucose absorption and metabolism and neuropathy-associated
XX gastrointestinal disorders, and stimulating glucose-induced insulin
XX release in a mammal. The present sequence represents the human zsig33
XX polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
XX Sequence 117 AA;
XX
XX Query Match 100.0%; Score 23; DB 22; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-14;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ALAGWLRPEDGGGAEGAEDELEV 23
XX Db 52 ALAGWLRPEDGGGAEGAEDELEV 74
XX
XX RESULT 13
XX AAB20101
XX ID AAB20101 standard; Protein; 117 AA.
XX XX
XX AAB20101;
XX XX

DT 23-APR-2001 (first entry)
 XX zsig33 protein.
 DE
 XX SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
 KW nutritional absorption modulator; growth hormone secretagogue;
 KW therapy; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT Protein /label= Signal_peptide
 FT Protein 24..117
 FT Peptide /label= Mature_protein
 FT Peptide 24..34
 FT /label= SGIP_peptide
 FT /note= "this peptide is claimed in Claim 1"
 XX
 PN WO200100830-A1.
 XX
 XX 04-JAN-2001.
 PD
 XX 30-JUN-2000; 2000WO-US18306.
 PF
 XX 30-JUN-1999; 99US-0345157.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 PI WPI; 2001-123010/13.
 XX N-PSDB; AAF30033.
 DR
 XX Novel variants of SGIP peptides for modulating contractility in
 PT duodenum or jejunum tissue, pancreatic secretion of hormones and
 PT digestive enzymes, inducing growth hormone secretion or modulating
 PT gastric emptying -
 XX
 XX Disclosure; 54; 61pp; English.
 PS
 XX The present sequence is that of zsig33, a secreted protein with
 CC homology to motilin (see AAB20102). zsig33 is expressed at high
 CC levels in the stomach, and at lower levels in the small intestine
 CC and pancreas. A novel peptide fragment of zsig33, termed SGIP (see
 CC AAB20100), is claimed. SGIP is a ligand for growth hormone
 CC secretagogue receptor, and is therefore useful for modulating
 CC secretion of growth hormone and insulin like growth factor 1.
 CC SGIP, and variant SGIP peptides, are used in claimed methods for
 CC stimulating contractility in duodenum or jejunum tissue,
 CC modulating pancreatic secretion of hormones and digestive enzymes,
 CC inducing growth hormone secretion, and modulating gastric emptying.
 XX
 XX Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 23; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAEAEDELEV 23
 DB 52 ALAGWLRPEDGGQAEAEDELEV 74
 RESULT 14
 AAB60511
 ID AAB60511 standard; Protein; 117 AA.
 XX
 AC AAB60511;
 XX
 XX 24-APR-2001 (first entry)
 DT
 DE Human ghrelin preproprotein, SEQ ID NO:5.

XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX
 PN WO200107475-A1.
 XX
 PD 01-FEB-2001.
 XX
 XX 24-JUL-2000; 2000WO-JP04907.
 PF
 XX 23-JUL-1999; 99JP-0210002.
 PR 29-NOV-1999; 99JP-0338841.
 PR 26-APR-2000; 2000JP-0126623.
 XX
 XX (KANG/) KANGAWA K.
 PA
 XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 PI WPI; 2001-159704/16.
 XX N-PSDB; AAF59645.
 DR
 XX New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 XX
 PS Claim 3; Page 182; 210pp; Japanese.
 XX
 XX The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 XX Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 23; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAEAEDELEV 23
 DB 52 ALAGWLRPEDGGQAEAEDELEV 74
 RESULT 15
 ABB78319
 ID ABB78319 standard; Protein; 117 AA.
 XX
 AC ABB78319;
 XX
 XX 05-DEC-2002 (first entry)
 DT
 XX Amino acid sequence of a human zsig33.
 DE
 XX Short gastrointestinal peptide; SGIP; zsig33; motilin.
 KW
 XX Homo sapiens.
 OS
 XX

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:48:42 ; Search time 7.87166 Seconds
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Title: US-09-853-253-6

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SUMMARIES

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2	23	100.0	117	4	US-08-822-897C-2
3	23	100.0	117	4	US-09-608-810A-4
4	23	100.0	117	4	US-09-996-243-268
5	7	30.4	442	4	US-09-134-001C-3033
6	7	30.4	552	4	US-09-252-991A-27032
7	7	30.4	599	4	US-09-252-991A-20368
8	7	30.4	981	4	US-09-252-991A-16798
9	6	26.1	39	1	US-08-428-488-13
10	6	26.1	97	2	US-08-403-852D-31
11	6	26.1	97	3	US-08-510-646B-32
12	6	26.1	97	3	US-09-231-818-31
13	6	26.1	129	3	US-09-135-994-12
14	6	26.1	129	4	US-09-684-843A-12
15	6	26.1	183	4	US-09-198-452A-612
16	6	26.1	199	4	US-09-252-991A-32089
17	6	26.1	202	4	US-09-252-991A-26333
18	6	26.1	259	4	US-09-252-991A-17300
19	6	26.1	288	1	US-08-396-650-1
20	6	26.1	288	1	US-08-768-626-1
21	6	26.1	292	4	US-09-252-991A-18951
22	6	26.1	292	4	US-09-252-991A-30162
23	6	26.1	305	4	US-09-328-352-6794
24	6	26.1	326	4	US-09-252-991A-33000
25	6	26.1	329	4	US-09-843-297-2
26	6	26.1	359	4	US-09-266-965-120
27	6	26.1	366	4	US-09-252-991A-29569

28	6	26.1	378	4	US-09-325-932A-158	Sequence 158, App
29	6	26.1	399	4	US-09-252-991A-25687	Sequence 25687, A
30	6	26.1	402	3	US-09-464-483-4	Sequence 4, Appl1
31	6	26.1	402	3	US-09-414-664-4	Sequence 4, Appl1
32	6	26.1	489	4	US-09-252-991A-22896	Sequence 22896, A
33	6	26.1	502	4	US-09-207-388-19	Sequence 19, Appl
34	6	26.1	510	4	US-09-252-991A-17695	Sequence 2, Appl1
35	6	26.1	529	3	US-09-464-483-2	Sequence 17695, A
36	6	26.1	529	3	US-09-414-664-2	Sequence 2, Appl1
37	6	26.1	531	1	US-08-531-601-1	Sequence 1, Appl1
38	6	26.1	531	2	US-08-859-032-1	Sequence 1, Appl1
39	6	26.1	535	1	US-08-737-597-10	Sequence 10, Appl
40	6	26.1	548	4	US-09-207-388-23	Sequence 23, Appl
41	6	26.1	550	4	US-09-207-388-20	Sequence 20, Appl
42	6	26.1	568	4	US-09-207-388-22	Sequence 22, Appl
43	6	26.1	568	4	US-09-207-388-24	Sequence 24, Appl
44	6	26.1	570	4	US-09-207-388-21	Sequence 21, Appl
45	6	26.1	588	4	US-09-252-991A-31356	Sequence 31356, A

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-09-046-479-2

Query Match 100.0%; Score 23; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5	PRIOR APPLICATION NUMBER: 60/0899655
6	PRIOR FILING DATE: 1998-06-17
7	PRIOR APPLICATION NUMBER: 60/089801
8	PRIOR FILING DATE: 1998-06-18
9	PRIOR APPLICATION NUMBER: 60/089907
10	PRIOR FILING DATE: 1998-06-18
11	PRIOR APPLICATION NUMBER: 60/089908
12	PRIOR FILING DATE: 1998-06-18
13	PRIOR APPLICATION NUMBER: 60/089947
14	PRIOR FILING DATE: 1998-06-19
15	PRIOR APPLICATION NUMBER: 60/089948
16	PRIOR FILING DATE: 1998-06-19
17	PRIOR APPLICATION NUMBER: 60/089952
18	PRIOR FILING DATE: 1998-06-19
19	PRIOR APPLICATION NUMBER: 60/090246
20	PRIOR FILING DATE: 1998-06-22
21	PRIOR APPLICATION NUMBER: 60/090252
22	PRIOR FILING DATE: 1998-06-22
23	PRIOR APPLICATION NUMBER: 60/090254
24	PRIOR FILING DATE: 1998-06-22
25	PRIOR APPLICATION NUMBER: 60/090349
26	PRIOR FILING DATE: 1998-06-23
27	PRIOR APPLICATION NUMBER: 60/090355
28	PRIOR FILING DATE: 1998-06-23
29	PRIOR APPLICATION NUMBER: 60/090429
30	PRIOR FILING DATE: 1998-06-24
31	PRIOR APPLICATION NUMBER: 60/090431
32	PRIOR FILING DATE: 1998-06-24
33	PRIOR APPLICATION NUMBER: 60/090435
34	PRIOR FILING DATE: 1998-06-24
35	PRIOR APPLICATION NUMBER: 60/090444
36	PRIOR FILING DATE: 1998-06-24
37	PRIOR APPLICATION NUMBER: 60/090445
38	PRIOR FILING DATE: 1998-06-24
39	PRIOR APPLICATION NUMBER: 60/090472
40	PRIOR FILING DATE: 1998-06-24
41	PRIOR APPLICATION NUMBER: 60/090535
42	PRIOR FILING DATE: 1998-06-24
43	PRIOR APPLICATION NUMBER: 60/090540
44	PRIOR FILING DATE: 1998-06-24
45	PRIOR APPLICATION NUMBER: 60/090542
46	PRIOR FILING DATE: 1998-06-24
47	PRIOR APPLICATION NUMBER: 60/090557
48	PRIOR FILING DATE: 1998-06-24
49	PRIOR APPLICATION NUMBER: 60/090676
50	PRIOR FILING DATE: 1998-06-25
51	PRIOR APPLICATION NUMBER: 60/090678
52	PRIOR FILING DATE: 1998-06-25
53	PRIOR APPLICATION NUMBER: 60/090690
54	PRIOR FILING DATE: 1998-06-25
55	PRIOR APPLICATION NUMBER: 60/090694
56	PRIOR FILING DATE: 1998-06-25
57	PRIOR APPLICATION NUMBER: 60/090695
58	PRIOR FILING DATE: 1998-06-25
59	PRIOR APPLICATION NUMBER: 60/090696
60	PRIOR FILING DATE: 1998-06-25
61	PRIOR APPLICATION NUMBER: 60/090699
62	PRIOR FILING DATE: 1998-07-01
63	PRIOR APPLICATION NUMBER: 60/091478
64	PRIOR FILING DATE: 1998-07-02
65	PRIOR APPLICATION NUMBER: 60/091544
66	PRIOR FILING DATE: 1998-07-01
67	PRIOR APPLICATION NUMBER: 60/091519
68	PRIOR FILING DATE: 1998-07-02
69	PRIOR APPLICATION NUMBER: 60/091626
70	PRIOR FILING DATE: 1998-07-02
71	PRIOR APPLICATION NUMBER: 60/091633
72	PRIOR FILING DATE: 1998-07-02
73	PRIOR APPLICATION NUMBER: 60/091978

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPDGGQAGAEDELEV 23
Db 52 ALAGWLRPDGGQAGAEDELEV 74
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RESULT 5

US-09-134-001C-3033
; Sequence 3033, Application US/09134001C
; Patent No. 6380370

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3033

LENGTH: 442

TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3033

Query Match 30.4%; Score 7; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DGGQAG 16
Db 189 DGGQAG 195
|||||

RESULT 6

US-09-252-991A-27032
; Sequence 27032, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27032

LENGTH: 552

TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27032

Query Match 30.4%; Score 7; DB 4; Length 552;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DGGQAG 16

Db 22 DGGQAG 28
|||||

RESULT 7

US-09-252-991A-20368
; Sequence 20368, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20368

LENGTH: 599

TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20368

Query Match 30.4%; Score 7; DB 4; Length 599;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGQAEA 17
Db 383 GGQAEA 389
|||||

RESULT 8

US-09-252-991A-16798
; Sequence 16798, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 16798

LENGTH: 981

TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-16798

Query Match 30.4%; Score 7; DB 4; Length 981;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7
Db 136 ALAGWLR 142
|||||

RESULT 9

US-08-428-488-13
; Sequence 13, Application US/08428488
; Patent No. 5624894

GENERAL INFORMATION:

; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE

;; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
;; NUMBER OF SEQUENCES: 107
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/428,488
;; FILING DATE: 27-APR-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Baumeister, Mary Katherine
;; REGISTRATION NUMBER: 26,254
;; REFERENCE/DOCKET NUMBER: 028724-087
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 39 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /note= "Position 1 - H-Ser."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 39
;; OTHER INFORMATION: /note= "Position 39.- Phe-OH."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 30
;; OTHER INFORMATION: /note= "Position 30 - Glu-NH2."
;; US-08-428-488-13

Query Match 26.1%; Score 6; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GAEDEL 21
Db 26 GAEDEL 31

RESULT 10
US-08-403-852D-31
; Sequence 31, Application US/08403852D
; Patent No. 5891695
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/403,852D
;; FILING DATE: 10-MAY-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR 93/00923
;; FILING DATE: 25-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 92/11441
;; FILING DATE: 25-SEP-1992
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03806.0054-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 97 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-403-852D-31

Query Match 26.1%; Score 6; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAE 18
Db 2 QAEGAE 7

RESULT 11
US-08-510-646B-32
; Sequence 32, Application US/08510646B
; Patent No. 6077699
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/510.646B
 ; FILING DATE: 03-AUG-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/403.852
 ; FILING DATE: 10-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/FR 93/00923
 ; FILING DATE: 25-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 92/11441
 ; FILING DATE: 25-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyers, Kenneth J.
 ; REGISTRATION NUMBER: 25,146
 ; REFERENCE/DOCKET NUMBER: 03806.0054-01000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4000
 ; TELEFAX: (202) 408-4400
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 97 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-510-646B-32

Query Match 26.1%; Score 6; DB 3; Length 97;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAE 18
 DB 2 QAEGAE 7

RESULT 12

; US-09-231-818-31
 ; Sequence 31, Application US/09231818
 ; Patent No. 6171846

GENERAL INFORMATION:

; APPLICANT: Blanc, Veronique
 ; APPLICANT: Blanche, Francis
 ; APPLICANT: Crouzet, Joel
 ; APPLICANT: Jacques, Nathalie
 ; APPLICANT: Lacroix, Patricia
 ; APPLICANT: Thibaut, Denis
 ; APPLICANT: Zagorec, Monique
 ; APPLICANT: Debussche, Laurent
 ; APPLICANT: De Crecy-Lagard, Valerie
 ; TITLE OF INVENTION: Polypeptides Involved In The
 ; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
 ; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/231.818
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/403.852
 ; FILING DATE: 10-MAY-1995
 ; APPLICATION NUMBER: PCT/FR 93/00923
 ; FILING DATE: 25-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 92/11441
 ; FILING DATE: 25-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyers, Kenneth J.
 ; REGISTRATION NUMBER: 25,146
 ; REFERENCE/DOCKET NUMBER: 03806.0054-00000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4000
 ; TELEFAX: (202) 408-4400
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 97 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-231-818-31

Query Match 26.1%; Score 6; DB 3; Length 97;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAE 18
 DB 2 QAEGAE 7

RESULT 13

; US-09-135-994-12
 ; Sequence 12, Application US/09135994A
 ; Patent No. 6280938

GENERAL INFORMATION:

; APPLICANT: Ranut et al.
 ; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
 ; FILE REFERENCE: University of Minnesota
 ; CURRENT APPLICATION NUMBER: US/09/135,994A
 ; CURRENT FILING DATE: 1998-08-18
 ; EARLIER APPLICATION NUMBER: 60/056,170
 ; EARLIER FILING DATE: 1997-08-19
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 129
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-135-994-12

Query Match 26.1%; Score 6; DB 3; Length 129;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RPEDGG 12
 DB 57 RPEDGG 62

RESULT 14

; US-09-684-843A-12
 ; Sequence 12, Application US/09684843A
 ; Patent No. 6514755

GENERAL INFORMATION:

; APPLICANT: Ranut et al.
 ; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
 ; FILE REFERENCE: Regents of the University of Minnesota
 ; CURRENT APPLICATION NUMBER: US/09/684,843A
 ; CURRENT FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/056,170
 ; PRIOR FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 09/135,994

; PRIOR FILING DATE: 1998-08-18
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 129
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-684-843A-12

Query Match 26.1%; Score 6; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RPEDGG 12
 Db 57 RPEDGG 62

RESULT 15
 US-09-198-452A-612
 ; Sequence 612, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffais, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 612
 ; LENGTH: 183
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 US-09-198-452A-612

Query Match 26.1%; Score 6; DB 4; Length 183;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AEGAEED 19
 Db 155 AEGAEED 160

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:55:57 ; Search time 14.1444 Seconds
(without alignments)
237.266 Million cell updates/sec

Title: US-09-853-253-6
Perfect score: 23
Sequence: 1 ALAGWLPRDGGGAEGAEDELEV 23

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Gapop 60.0 , Gapext 60.0

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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	23	100.0	23	9	US-09-853-253-6
3	23	100.0	24	9	US-09-853-253-4
4	23	100.0	117	9	US-09-794-987-2
5	23	100.0	117	9	US-09-853-253-2
6	23	100.0	117	9	US-09-989-722-268
7	23	100.0	117	9	US-09-989-723-268
8	23	100.0	117	9	US-09-989-279-268
9	23	100.0	117	9	US-09-989-727-268
10	23	100.0	117	10	US-09-989-731-268
11	23	100.0	117	10	US-09-989-732-268
12	23	100.0	117	10	US-09-991-073-268
13	23	100.0	117	10	US-09-990-442-268
14	23	100.0	117	10	US-09-991-163-268
15	23	100.0	117	10	US-09-993-604-268

16	23	100.0	117	10	US-09-990-456-268	Sequence 268, App
17	23	100.0	117	10	US-09-989-721-268	Sequence 268, App
18	23	100.0	117	10	US-09-992-598-268	Sequence 268, App
19	23	100.0	117	10	US-09-989-735-268	Sequence 268, App
20	23	100.0	117	10	US-09-990-444-268	Sequence 268, App
21	23	100.0	117	10	US-09-991-181-268	Sequence 268, App
22	23	100.0	117	10	US-09-989-730-268	Sequence 268, App
23	23	100.0	117	10	US-09-990-436-268	Sequence 268, App
24	23	100.0	117	10	US-09-993-687-268	Sequence 268, App
25	23	100.0	117	11	US-09-989-734-268	Sequence 268, App
26	23	100.0	117	11	US-09-997-653-268	Sequence 268, App
27	23	100.0	117	11	US-09-993-667-268	Sequence 268, App
28	23	100.0	117	11	US-09-997-428-268	Sequence 268, App
29	23	100.0	117	11	US-09-997-666-268	Sequence 268, App
30	23	100.0	117	11	US-09-990-438-268	Sequence 268, App
31	23	100.0	117	11	US-09-990-514-268	Sequence 268, App
32	23	100.0	117	11	US-09-990-711-268	Sequence 268, App
33	23	100.0	117	11	US-09-989-726-268	Sequence 268, App
34	23	100.0	117	11	US-09-989-156-268	Sequence 268, App
35	23	100.0	117	11	US-09-990-437-268	Sequence 268, App
36	23	100.0	117	11	US-09-991-157-268	Sequence 268, App
37	23	100.0	117	11	US-09-997-573-268	Sequence 268, App
38	23	100.0	117	11	US-09-991-172-268	Sequence 268, App
39	23	100.0	117	11	US-09-990-726-268	Sequence 268, App
40	23	100.0	117	11	US-09-997-559-268	Sequence 268, App
41	23	100.0	117	11	US-09-990-601-268	Sequence 268, App
42	23	100.0	117	11	US-09-990-443-268	Sequence 268, App
43	23	100.0	117	11	US-09-991-854-268	Sequence 268, App
44	23	100.0	117	11		
45	23	100.0	117	11		

ALIGNMENTS

RESULT 1
US-09-853-253-5
; Sequence 5, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-5

Query Match 100.0%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 9e+16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLPRDGGGAEGAEDELEV 23
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Db 1 ALAGWLPRDGGGAEGAEDELEV 23
|||||

RESULT 2
US-09-853-253-6
; Sequence 6, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN

APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
SUITE: 100
CITY: Seattle, WA 98101-3200
COUNTRY: USA
TELEPHONE: 206 461 8000
FAX: 206 461 8001
E-MAIL: paul@zymogenetics.com

Qy 1 ALAGWLRPEDGGQAEAEDELEV 23
|||||

Db 52 ALAGMLRPEDGGQGAEGADEV 74

RESULT 6

US-09-989-722-268
Sequence 268, Application US/09989722
Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIORITY APPLICATION NUMBER: 60/049787
PRIORITY FILING DATE: 1997-06-16
PRIORITY APPLICATION NUMBER: 60/062250
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/065186
PRIORITY FILING DATE: 1997-11-12
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PRIORITY FILING DATE: 1997-11-13
PRIORITY APPLICATION NUMBER: 60/066770
PRIORITY FILING DATE: 1997-11-24
PRIORITY APPLICATION NUMBER: 60/075945
PRIORITY FILING DATE: 1998-02-25
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPDGGGAEGAEDEV 23
Db 52 ALAGWLRPDGGGAEGAEDEV 74
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RESULT 7
US-09-989-723-268
; Sequence 268 Application US/09989723
; Patent No. US20020072092A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsens, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
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; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
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; PRIOR FILING DATE: 1998-06-19
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; PRIOR APPLICATION NUMBER: 60/090429
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; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEV 23
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DB 52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 8

US-09-989-279-268
; Sequence 268, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 23; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.5e-15;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 52 ALAGWLRPEDGGQAGAELEV 74

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RESULT 9

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US-09-989-727-268
; Sequence 268, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gierltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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 ; Sequence 268, Application US/09989731
 ; Patent No. US20020103125A1
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 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
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 ; APPLICANT: Pan, James
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 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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FILE REFERENCE: P2730PIC70
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Query Match 100.0%; Score 23; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.5e-15; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ALAGWLRPEDGGQAGAEDELEV 23
Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 11

US-09-989-732-268
; Sequence 268, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
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; APPLICANT: Tumas, Daniel
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C57

;; CURRENT APPLICATION NUMBER: US/09/989,732
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/045787
;; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/092182
;
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDEV 23
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DB 52 ALAGWLRPEDGGGAEGAEDEV 74
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RESULT 12
US-09-991-073-268
; Sequence 268, Application US/09991073
; Patent No. US2002012756A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-01
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 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.5e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQGAEGAEDEV 23
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 Db 52 ALAGWLRPEDGGQGAEGAEDEV 74

RESULT 13

US-09-990-442-268
 ; Sequence 268, Application US/09990442
 ; Patent No. US20020132252A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC8
 ; CURRENT APPLICATION NUMBER: US/09/990,442
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Sco
Best Local Similarity 100.0%; Pre
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Db 52 ALAGWLRPEDGGQAEGADELEV

RESULT 14
US-09-991-163-268
; Sequence 368, Application US/0999116
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Benstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Tr
; TITLE OF INVENTION: Aids Encoding
; FILE REFERENCE: P2730Pc17
; CURRENT APPLICATION NUMBER: US/09/99-991-163-268
; CURRENT FILING DATE: 2001-11-14
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; PRIOR APPLICATION NUMBER: 60/087106

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RESULT 14
US-09-991-163-268
Sequence 268, Application US/0999116
Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Borstlein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gidwalski, Paul J.
APPLICANT: Gromaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wattanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Tr
FILE REFERENCE: P2730PIC17
CURRENT APPLICATION NUMBER: US/09/991-163-268
CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-07-09

Query Match      100.08; Score 23; DB 10; Length 117;
Best Local Similarity 100.08; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      52 ALAGWLRPEDGGQGAEGAEDELEV 74

RESULT 15
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; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
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24 PRIOR APPLICATION NUMBER: 60/090445
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26 PRIOR APPLICATION NUMBER: 60/090472
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62 PRIOR APPLICATION NUMBER: 60/091633
63 PRIOR FILING DATE: 1998-07-02
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66 PRIOR APPLICATION NUMBER: 60/091982
67 PRIOR FILING DATE: 1998-07-07
68 PRIOR APPLICATION NUMBER: 60/092182
69 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 23; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGADELEV 23
|||||
Db 52 ALAGWLRPEDGGGAEGADELEV 74

Search completed: September 11, 2003, 18:16:19
Job time : 15.1444 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:37 ; Search time 8.73262 Seconds
(without alignments)
253.289 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 23

Sequence: 1 ALAGWLRPEDGGQAEDELEV 23

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	117	1 A59316	ghrelin precursor
2	7	34.8	483	2 T04453	hypothetical prote
3	7	30.4	302	2 JH0572	hypothetical prote
4	7	30.4	344	2 A48990	transcription regu
5	7	30.4	910	2 B83451	aconitate hydratase
6	7	30.4	1239	1 Q0BE10	BOLFI protein - hu
7	6	26.1	69	2 C87574	cold-shock domain
8	6	26.1	142	2 AB0401	probable membrane
9	6	26.1	175	2 E82118	conserved hypothet
10	6	26.1	178	2 A30230	quiescence-specifi
11	6	26.1	180	2 T46695	hypothetical prote
12	6	26.1	189	2 A91082	hypothetical prote
13	6	26.1	189	2 B85927	hypothetical prote
14	6	26.1	198	2 D69070	imidazoleglycerol-
15	6	26.1	223	2 A40866	HL-60-induced diff
16	6	26.1	237	2 T30002	hypothetical prote
17	6	26.1	265	2 A95298	hypothetical prote
18	6	26.1	267	1 CTPGP	corticotropin / li
19	6	26.1	284	2 B25624	tropomyosin I, tho
20	6	26.1	284	2 A25624	tropomyosin I, emb
21	6	26.1	288	2 A55737	Pb-1 protein - hum
22	6	26.1	289	2 T48894	lipoprotein mtsA,
23	6	26.1	289	2 H83433	hypothetical prote
24	6	26.1	290	2 H71852	hypothetical prote
25	6	26.1	299	2 T35144	glutamate transpor
26	6	26.1	302	2 T48871	catechol 1,2-dioxy
27	6	26.1	308	2 F72508	probable hydrogena
28	6	26.1	313	2 E82762	conserved hypothet
29	6	26.1	315	2 F64129	probable phosphogl

30 26.1 326 1 E69690 transcription repr
31 26.1 343 2 AH1823 30S ribosomal prot
32 26.1 343 2 T35063 probable prolipopr
33 26.1 345 2 A83526 hypothetical prote
34 26.1 346 2 AE3323 sam-dependent meth
35 26.1 350 2 S71923 cysteine proteinase
36 26.1 360 2 S59598 cysteine proteinase
37 26.1 376 2 AD2697 hypothetical prote
38 26.1 377 2 G97314 alcohol dehydrogen
39 26.1 377 2 T47471 cysteine proteinase
40 26.1 379 1 DCBSPK phosphoribosylamin
41 26.1 379 2 D82801 molybdopterin bios
42 26.1 383 2 F83321 hypothetical prote
43 26.1 384 2 H64505 hypothetical prote
44 26.1 385 2 T26404 hypothetical prote
45 26.1 391 2 AF3633 hypothetical membr

ALIGNMENTS

RESULT 1

A59316
ghrelin precursor - human
N: Alternate names: preproghrelin
C: Species: Homo sapiens (man)
C: Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C: Accession: A59316
R: Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A: Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A: Reference number: A59316; MUID:20067959; PMID:10604470
A: Accession: A59316
A: Status: not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 1-117 <KOJ>
A: Cross-references: GB:AB029434; NID:G6691571; PIDN:BA089371.1; PID:G6691572
A: Experimental source: tissue stomach endocrine cells
A: Note: submitted to GenBank, June 1999
C: Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (9.
C: Superfamily: motilin
C: Keywords: hormone; lipoprotein; stomach
F: 1-23/Domain: signal sequence #status predicted <SIG>
F: 24-51/Product: ghrelin #status predicted <MAT>
F: 52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F: 26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 23; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 4, 1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAEDELEV 23

DB 52 ALAGWLRPEDGGQAEDELEV 74

RESULT 2

T04453
hypothetical protein F4D11.80 - Arabidopsis thaliana
C: Species: Arabidopsis thaliana (mouse-ear cress)
C: Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C: Accession: T04453
R: Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Hoheisel, J.; Mewes, F.
submitted to the Protein Sequence Database, April 1998
A: Reference number: Z15360
A: Accession: T04453
A: Molecule type: DNA
A: Residues: 1-483 <BEV>
A: Cross-references: EMBL:AL022537
A: Experimental source: cultivar Columbia; BAC clone F4D11
C: Genetics:
A: Map position: 4
A: Introns: 17/3; 44/1; 94/1; 141/3; 206/2; 247/2; 345/3; 395/1; 434/2

A>Note: F4D11.80

Query Match 34.8%; Score 8; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAED 20
| | | | |
Db 302 QAEGAED 309

RESULT 3

JH0572

hypochemical protein - Streptomyces lividans (fragment)

C:Species: Streptomyces lividans
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-1999
C:Accession: JH0572
R:Lichenstein, H.S.; Busse, L.A.; Smith, G.A.; Narhi, L.O.; McGinley, M.O.; Rohde, M.F.;
Gene 111, 125-130, 1992
A:Title: Cloning and characterization of a gene encoding extracellular metalloprotease f
A:Reference number: JH0571; MUID:92192468; PMID:1547948
A:Accession: JH0572
A:Molecule type: DNA
A:Residues: 1-302 <LIC>
A:Cross-references: GB:M09476; NID:g153411; PIDN:AAA26804.1; PID:g153412
A:Experimental source: strain TK24
A>Note: the authors translated the codon GTA for residue 260 as Asp
C:Superfamily: Pseudomonas putida regulatory protein catR

Query Match 30.4%; Score 7; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7
| | | | |
Db 100 ALAGWLR 106

RESULT 4

A48990

transcription regulator LysR family homolog SnPr - Streptomyces lividans

C:Species: Streptomyces lividans
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C:Accession: A48990
R:Butler, M.J.; Davey, C.C.; Krygsman, P.; Walczyk, E.; Malek, L.T.
Can. J. Microbiol. 38, 912-920, 1992
A:Title: Cloning of genetic loci involved in endoprotease activity in Streptomyces livid
A:Reference number: A48990; MUID:93099553; PMID:11464066
A:Contents: 66
A:Accession: A48990
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-344 <BUT>
A>Note: sequence extracted from NCBI backbone (NCBIN:121210, NCBI:P:121213)
C:Superfamily: Pseudomonas putida regulatory protein catR

Query Match 30.4%; Score 7; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7
| | | | |
Db 104 ALAGWLR 110

RESULT 5

B83451

aconitate hydratase 1 PA1562 [Imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83451
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: B83451
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-910 <STO>
A:Cross-references: GB:AE004584; GB:AE004091; NID:g9947516; PIDN:AA04951.1; GSPDB:GN
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: acnA; PA1562
C:Superfamily: iron-responsive element-binding protein

Query Match 30.4%; Score 7; DB 2; Length 910;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7
| | | | |
Db 65 ALAGWLR 71

RESULT 6

QB0E10

BOLFI protein - human herpesvirus 4 (strain B95-8)

C:Species: human herpesvirus 4, Epstein-Barr virus
C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
C:Accession: A43041; A03752; S32995
R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi
A:Reference number: A93065; MUID:85035713; PMID:6092825
A:Accession: A43041
A:Molecule type: DNA
A:Residues: 1-1239 <BAN>
A:Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24841.1; PID:g1334855
R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.
Nature 310, 207-211, 1984
A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A:Reference number: A03794; MUID:84270667; PMID:6087149
A:Contents: annotation; protein coding region
C:Superfamily: human herpesvirus 4 BOLFI protein

Query Match 30.4%; Score 7; DB 1; Length 1239;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AEGAED 20
| | | | |
Db 696 AEGAED 702

RESULT 7

C87574

cold-shock domain family protein [Imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C:Accession: C87574
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87574
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-69 <STO>

A:Cross-references: GB:AE005673; NID:g13424199; PIDN:AAK24591.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2623

C:Superfamily: major cold shock protein; cold shock domain homology

Query Match 26.1%; Score 6; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PEDGGQ 13
|||||
DB 20 PEDGGQ 25

RESULT 8

AB0401

probable membrane protein YPO3302 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C:Accession: AB0401

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AB0401

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-142 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92534.1; PID:gl5981232; GSPDB:GN00175

C:Genetics:

A:Gene: YPO3302

C:Superfamily: hypothetical protein HT0489

Query Match 26.1%; Score 6; DB 2; Length 142;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAGWLR 7
|||||
DB 104 LAGWLR 109

RESULT 9

E82118

conserved hypothetical protein VC2111 [imported] - Vibrio cholerae (strain N16961 serog

C:Species: Vibrio cholerae

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: E82118

R:Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: AB2035; MUID:20406833; PMID:10923201

A:Accession: E82118

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-175 <HE>

A:Cross-references: GB:AE004284; GB:AE003852; NID:g9656649; PIDN:AAF95256.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC2111

A:Map position: 1

Query Match 26.1%; Score 6; DB 2; Length 175;

Best Local Similarity 100.0%; Pred. No. 67;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GOAEGA 17
|||||
DB 54 GOAEGA 59

RESULT 10

A30230

quiescence-specific protein precursor - chicken

N:Alternate names: Ch21 protein

C:Species: Gallus gallus (chicken)

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 15-Nov-1996

C:Accession: A30230; A42581; A36595; A35491

R:Bedard, P.A.; Yannoni, Y.; Simmons, D.L.; Erikson, R.L.

Mol. Cell. Biol. 9, 1371-1375, 1989

A:Title: Rapid repression of quiescence-specific gene expression by epidermal growth

A:Reference number: A30230; MUID:89261749; PMID:2498647

A:Accession: A30230

A:Molecule type: mRNA

A:Residues: 1-178 <BED>

R:Dozin, B.; Descalzi, F.; Briata, L.; Hayashi, M.; Gentili, C.; Hayashi, K.; Quarto

J. Biol. Chem. 267, 2979-2985, 1992

A:Title: Expression, regulation, and tissue distribution of the Ch21 protein during c

A:Reference number: A42581; MUID:92147639; PMID:1737754

A:Accession: A42581

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-95, 'L', 97-178 <DO>

A:Experimental source: tibia hypertrophic cartilage

A>Note: sequence extracted from NCBI backbone (NCBI:80796, NCBIP:80797)

R:Cancedda, F.D.; Dozin, B.; Rossi, F.; Molina, F.; Cancedda, R.; Negri, A.; Ronchi,

J. Biol. Chem. 265, 19060-19064, 1990

A:Title: The Ch21 protein, developmentally regulated in chick embryo, belongs to the

A:Reference number: A36595; MUID:91035433; PMID:2229062

A:Accession: A36595

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 21-95, 'L', 97-178 <CAN>

A:Cross-references: GB:M37611

R:Cancedda, F.D.; Asaro, D.; Molina, F.; Cancedda, R.; Caruso, C.; Camardella, L.; Ne

Biochem. Biophys. Res. Commun. 168, 933-938, 1990

A:Title: The amino terminal sequence of the developmentally regulated CH21 protein sh

A:Reference number: A35491; MUID:90267487; PMID:2346493

A:Accession: A35491

A>Status: preliminary

A:Molecule type: protein

A:Residues: 21-48 <CA2>

C:Superfamily: lipocalin; lipocalin homology

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-178/Product: quiescence-specific protein #status predicted <MAT>

F:25-173/Domain: lipocalin homology <LIP>

Query Match 26.1%; Score 6; DB 2; Length 178;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EDELEV 23
|||||
DB 65 EDELEV 70

RESULT 11

T46695

hypothetical protein ORF-180 [imported] - Lactobacillus helveticus plasmid pLH1

C:Species: Lactobacillus helveticus

C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 04-Mar-2000

C:Accession: T46695

R:Thompson, K.; McConville, K.J.; McReynolds, C.; Foley, S.

submitted to the EMBL Data Library, December 1997

A:Description: Complete sequence of plasmid pLH1 from Lactobacillus helveticus ATCC15

A:Reference number: 223135

A:Accession: T46695

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-180 <THO>

A:Cross-references: EMBL:AJ222725; PIDN:CAAL0962.1

A:Experimental source: ATCC 15009

C:Genetics:

A:Genome: plasmid pLH1

C:Superfamily: Lactobacillus helveticus plasmid pLH1 hypothetical protein ORF-180

Query Match 26.1%; Score 6; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
 |||||
 DB 31 ALAGWL 36

RESULT 12
 A91082
 hypothetical protein Ecs3625 [imported] - Escherichia coli (strain O157:H7, substrain R1
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C;Accession: A91082
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: A91082
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-189 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BA037048.1; PID:g13363096; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrain R1MD 0509952
 C;Genetics:
 A;Gene: Ecs3625

Query Match 26.1%; Score 6; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
 |||||
 DB 14 ALAGWL 19

RESULT 13
 B85927
 hypothetical protein Z4080 [imported] - Escherichia coli (strain O157:H7, substrain EDL5
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C;Accession: B85927
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: B85927
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-189 <STO>
 A;Cross-references: GB:AE005174; NID:g12517231; PIDN:AAG57878.1; GSPDB:GN00145; UWGP:Z40
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: Z4080

Query Match 26.1%; Score 6; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
 |||||
 DB 14 ALAGWL 19

RESULT 14
 D69070
 imidazoleglycerol-phosphate synthase - Methanobacterium thermoautotrophicum (strain Delt
 C;Species: Methanobacterium thermoautotrophicum
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C;Accession: D69070
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
 ; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
 A;Reference number: A69000; MUID:98037514; PMID:9371463
 A;Accession: D69070
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-198 <MTH>
 A;Cross-references: GB:AE000912; GB:AE000666; NID:g2622632; PIDN:AAB85999.1; PID:g262
 A;Experimental source: strain Delta H
 C;Genetics:
 A;Gene: MTH1524
 A;Start codon: TTG
 C;Superfamily: amidotransferase hisH; trpG homology

Query Match 26.1%; Score 6; DB 2; Length 198;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EGAEDE 20
 |||||
 DB 130 EGAEDE 135

RESULT 15
 A40866
 HL-60-induced differentiation immediate-early protein ETR101 - human
 C;Species: Homo sapiens (man)
 C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 05-Nov-1999
 C;Accession: A40866
 R;Shimizu N.; Ohta, M.; Fujiwara, C.; Sagara, J.; Mochizuki, N.; Oda, T.; Utiyama, H
 J. Biol. Chem. 266, 12157-12161, 1991
 A;Title: Expression of a novel immediate early gene during 12-O-tetradecanoylphorbol-
 A;Reference number: A40866; MUID:91286224; PMID:2061303
 A;Accession: A40866
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-223 <SHI>
 A;Cross-references: GB:M62831; NID:g182260; PIDN:AAA35814.1; PID:g182261

Query Match 26.1%; Score 6; DB 2; Length 223;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GQAEGA 17
 |||||
 DB 165 GQAEGA 170

Search completed: September 11, 2003, 17:57:06
 Job time : 8.73262 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:30:37 : Search time 4.42781 Seconds
(without alignments)
244.278 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 23

Sequence: 1 ALAGWLRPEDGGQAGCADELEV 23

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	23	100.0	117	GHRL_HUMAN	Q9ubj3 homo sapien
2	10	43.5	116	GHRL_BOVIN	Q9bdj6 bos taurus
3	7	30.4	328	MPR2_STRCO	Q91127 streptomyc
4	7	30.4	344	MPR2_STRLI	P43161 streptomyc
5	7	30.4	1239	V120_EBV	P03189 epstein-bar
6	6	26.1	117	GHRL_CANFA	Q9bef8 canis fami
7	6	26.1	178	EFAB_CHICK	P21760 gallus gall
8	6	26.1	198	HIS5_METTH	O27568 methanobact
9	6	26.1	267	COLI_PIG	P01192 s corticotr
10	6	26.1	284	TPM2_DROME	P09491 drosophila
11	6	26.1	288	PCD1_HUMAN	Q15116 homo sapien
12	6	26.1	289	OPSD_LIMPA	O42431 limnocottus
13	6	26.1	290	PARB_HELPD	Q92k75 helicobacte
14	6	26.1	310	MTSA_STRP8	Q8p280 streptococ
15	6	26.1	310	MTSA_STRPY	Q9a157 streptococ
16	6	26.1	313	MRWV_XYLEFA	Q9pf88 xylella fas
17	6	26.1	315	YF56_HAEIN	P45250 haemophilus
18	6	26.1	326	BSR_BACSU	P36944 bacillus su
19	6	26.1	346	MRWV_BRUME	Q8y174 brucella me
20	6	26.1	360	CYS2_MAIZE	Q10717 zea mays (m
21	6	26.1	379	PURK_BACSU	P12045 bacillus su
22	6	26.1	395	IF5_SCHPO	Q09689 schizosacch
23	6	26.1	433	TIG_STAAM	Q99t16 staphylococ
24	6	26.1	436	CUS1_YEAST	Q02554 saccharomyc
25	6	26.1	497	RPSD_MYCGE	P47491 mycoplasma
26	6	26.1	499	RPSD_MYCPN	P78022 mycoplasma
27	6	26.1	511	SYS_MOUSE	P26638 mus musculu
28	6	26.1	513	SYS_BOVIN	Q9gmb8 bos taurus
29	6	26.1	513	SYS_HUMAN	P49591 homo sapien
30	6	26.1	535	AMYB_HORVU	P16098 hordeum vul
31	6	26.1	539	Z173_HUMAN	Q12899 homo sapien
32	6	26.1	547	CH60_BUCTC	Q8kix3 buchnera ap
33	6	26.1	566	HS60_CANAL	O74261 candida alb

RESULT 1

ID	GHRL_HUMAN	STANDARD;	PRT;	117 AA.
AC	Q9UBJ3: Q8TAT9, Q9H3R3;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Chrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).			
DE	GHRL OR MTLRP			
GN	Homo sapiens (human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
XP	SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.			
XP	MEDLINE=20067959; PubMed=10604470;			
RA	Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;			
RT	"Chrelin is a growth-hormone-releasing acylated peptide from stomach."			
RL	Nature 402:656-660(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Kojima M.;			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=stomach;			
RA	Tomasetto C., Karam S.M., Rio M.-C.;			
RT	"Identification of a novel gastric protein m46.";			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Wajraich M.P., Ten I.S., Gertner J.M., Leibell R.L.;			
RT	"Genomic organization of the human Ghrelin gene.";			
RL	J. Endocrinol. Genet. 1:231-233(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Blood;			
RA	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			

34	6	26.1	572	1	HS60_YEAST	P19882 saccharomyc
35	6	26.1	590	1	HS60_AJECA	P50142 ajellomyces
36	6	26.1	620	1	SMP_COTJA	Q92154 coturnix co
37	6	26.1	641	1	DXS_RHOCA	P26242 rhodobacter
38	6	26.1	650	1	APP1_HUMAN	P51693 homo sapien
39	6	26.1	657	1	HUPH_MOUSE	P35492 mus musculu
40	6	26.1	683	1	Z263_HUMAN	O14978 homo sapien
41	6	26.1	702	1	HELS_AERPE	Q9yfg8 aeropyrum p
42	6	26.1	728	1	UVRC_STRCO	Q92512 streptomyc
43	6	26.1	886	1	SM6B_MOUSE	O54951 mus musculu
44	6	26.1	887	1	SM6B_RAT	O70141 rattus norv
45	6	26.1	890	1	AC01_ECOLI	P25516 escherichia

ALIGNMENTS

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [6]
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RL hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RP [7]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RL hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -1- PTM: O-n-octanoylation is essential for activity.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/GhrelinID327.html".
 CC -----
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 CC -----
 DR EMBL; AB029434; BAA89371.1; -;
 DR EMBL; AB035700; BAB19045.1; -;
 DR EMBL; AJ252278; CAB65733.1; -;
 DR EMBL; AF296558; AAG10300.1; -;
 DR EMBL; BC025791; AAH25791.1; -;
 DR PIR; A59316; A59316.
 DR MIM; 605353; -;
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005825; C:soluble fraction; TAS.
 DR GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
 DR GO; GO:0007267; F:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_ghrelin.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23
 FT PEPTIDE 24 51 GHRELIN.
 FT PROPEP 52 117 REMOVED IN MATURE FORM.
 FT LIPID 26 26 N-OCTANOATE.
 FT VARSPLIC 37 37 Missing (in isoform 2).
 FT FTId=VSP_003245.
 FT CONFLICT 72 72 L -> M (IN REF. 5).

SQ SEQUENCE 117 AA; 12911 MW; 39C0572BBEACA2755 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
 Db 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 2
 GHRL_BOVIN STANDARD; PRT; 116 AA.
 ID GHRL_BOVIN
 AC Q9BDJ6; O9GKY6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (growth hormone
 DE releasing peptide).
 GN GHRL.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kita K., Harada K., Yokota H.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 24-99 FROM N.A.
 RA Kojima M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF350329; AAK18612.1; -;
 DR EMBL; AB035702; BAB19047.1; -;
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR Pfam; PF005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc; 1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
 KW SIGNAL 1 23 BY SIMILARITY.
 FT PEPTIDE 24 50 GHRELIN (BY SIMILARITY).
 FT PROPEP 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).
 FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
 FT CONFLICT 34 34 K -> E (IN REF. 2).
 SQ SEQUENCE 116 AA; 12792 MW; F55536DAC5FA59B6 CRC64;
 Query Match 43.5%; Score 10; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 QAEGAEDELE 22

Db 63 OAEGAEDELE 72
|||||

RESULT 3

MPR2_STRCO STANDARD; PRT; 328 AA.
AC O9L127;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Small neutral protease regulatory protein.
GN MPRR OR MPRR2 OR SCO7433 OR SC6D11.29.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wlezorek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- FUNCTION: TRANSCRIPTIONAL TRANS-ACTIVATOR OF THE GENE (MPRA) FOR
THE SMALL NEUTRAL PROTEASE.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
CC -----
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or send an email to license@lsb-sib.ch).
CC -----
CC EMBL: AL939131; CAB76352.1; -
DR InterPro: IPR000847; HTH_LysR.
DR Pfam: PF00126; HTH_1; 1.
DR PRINTS: PR00039; HTHLYSR
DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; Protease; Transcription regulation; Complete proteome.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 328 AA; 35885 MW; 2BA97730AE4FA16B CRC64;

Query Match 30.4%; Score 7; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
|||||

Db 104 ALAGWLR 110

RESULT 4

MPRR_STRLI STANDARD; PRT; 344 AA.
AC P43161;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Small neutral protease regulatory protein.
GN MPRR OR SNPR.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=66 / 1326;
RX MEDLINE=93099553; PubMed=1464066;
RA Butler M.J., Davey C.C., Krygsmann P., Walczyk E., Malek L.T.;
"Cloning of genetic loci involved in endoprotease activity in
Streptomyces lividans 66: a novel neutral protease gene with an
adjacent divergent putative regulatory gene.";
RL Can. J. Microbiol. 38:912-920(1992).
RN [2]
RP SEQUENCE OF 1-305 FROM N.A.
RC STRAIN=TK24;
RX MEDLINE=92192468; PubMed=1547948;
RA Lichenstein H.S., Busse L.A., Smith G.A., Narhi L.O.,
McGinley M.O., Rohde M.F., Katowitz J.L., Zukowski M.M.;
"Cloning and characterization of a gene encoding extracellular
metalloprotease from Streptomyces lividans.";
RL Gene 111:125-130(1992).
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE GENE (SNPA) FOR THE
SMALL NEUTRAL PROTEASE.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
CC -----
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or send an email to license@lsb-sib.ch).
CC -----
CC EMBL: M81703; AAA26739.1; -
DR EMBL: M89476; AAA26804.1; ALT_INIT.
DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR005119; LysR_subst.
DR Pfam: PF00126; HTH_1; 1.
DR PRINTS: PR00039; HTHLYSR
DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
KW Transcription regulation; DNA-binding; Activator.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
FT CONFLICT 270 270 G -> AR (IN REF. 2).
SQ SEQUENCE 344 AA; 37415 MW; 485C82C813B52312 CRC64;
Query Match 30.4%; Score 7; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
|||||

Db 104 ALAGWLR 110

RESULT 5
V120_EBV
ID V120_EBV STANDARD; PRT; 1239 AA.
AC P03189;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Capsid assembly protein BOLF1.
GN BOLF1.
OS Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tufnell P.S., Bartell B.G.;
RA "Data sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
CC SHV-1 23, EBV BOLFI, VZV 21, HVS-1 63, AND HCMV UL47.
CC -----
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CC -----
CC EMBL; V01555; CA24841.1; -
CC PIR; A43041; Q0BE10.
CC Capsid assembly.
CC SEQUENCE 1239 AA; 132748 MW; 6C5DBFC55F2FF729 CRC64;

Query Match 30.48; Score 7; DB 1; Length 1239;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AEGAED 20
DB 596 AEGAED 702
IIIIIII

RESULT 6
ID GHRL_CANFA STANDARD; PRT; 117 AA.
AC Q9BEF8; Q9BEF7;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide).
GN GHRL OR MTLRP
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Gastric fundus;
RA Tonasetto C., Wendling C., Rio M.-C., Poitras P.;
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
RT fundus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9BEF8-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9BEF8-2; Sequence=VSP_003244;
CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
CC EMBL; AJ298295; CAC29155.1; -
CC EMBL; AJ298296; CAC29156.1; -
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC Pfam; PF04643; motilin_assoc.1.
CC Pfam; PF04644; motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN.
CC PRODOM; PD332162; Preproghrelin; 1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPPLIC 37 37 Missing (in isoform 2).
FT /FTid=VSP_003244.
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Query Match 26.18; Score 6; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AEDELE 22
DB 68 AEDELE 73
IIIIII

RESULT 7
ID EFAB_CHICK STANDARD; PRT; 178 AA.
AC P21760; P21928; Q9PWN9;
DT 01-MAY-1991 (Rel. 18, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Extracellular fatty acid binding protein precursor (Ex-FABP)
DE (Quiescence-specific protein) (p20K) (Ch21 protein).
GN EXFABP
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89261749; PubMed=2498647;
RA Bedard P.-A., Vannoni Y., Simmons D.L., Erikson R.L.;
RT "Rapid repression of quiescence-specific gene expression by epidermal
RT growth factor, insulin, and pp60v-src.";
RL Mol. Cell. Biol. 9:1371-1375(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92147639; PubMed=1737754;
RA Dozin B., Descalzi F., Briata L., Hayashi M., Gentili C.,
RA Hayashi K., Quarto R., Cancedda R.;
RT "Expression, regulation, and tissue distribution of the Ch21 protein
RT during chicken embryogenesis.";
RL J. Biol. Chem. 267:2979-2985(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Leghorn;
RA Giannoni P., Dozin B., Zambotti A., Neri M., Cancedda R.;
RT "Differentiation-dependent activation of the extracellular fatty acid
RT binding protein (EXFABP) gene in chicken embryo chondrocytes.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 25-178 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91035433; PubMed=2229062;
RA Cancedda F.D., Dozin B., Rossi F., Molina F., Cancedda R.,
RA Negri A., Ronchi S.;
RT "The Ch21 protein, developmentally regulated in chick embryo, belongs

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to the superfamily of lipophilic molecule carrier proteins.";
 J. Biol. Chem. 265:19060-19064(1990).
 [5]
 RX MEDLINE-90267487; PubMed-2346493;
 RA Cancedda F.D., Asaro D., Molina F., Cancedda R., Caruso C.,
 Camardella L., Negri A., Ronchi S.;
 RT "The amino terminal sequence of the developmentally regulated Ch21
 protein shows homology with amino terminal sequences of low molecular
 weight proteins binding hydrophobic molecules.";
 Biochem. Biophys. Res. Commun. 168:933-938(1990).
 [6]
 RX SEQUENCE OF 103-178 FROM N.A.
 STRAIN-White leghorn; TISSUE-Bone marrow;
 RX MEDLINE-92195690; PubMed-1549365;
 RA Nakano T., Graf T.;
 RT "Identification of genes differentially expressed in two types of
 v-myb-transformed avian myelomonocytic cells.";
 Oncogene 7:527-534(1992).
 [7]
 RX CHARACTERIZATION.
 RX MEDLINE-96355330; PubMed-8702740;
 RA Cancedda F.D., Malpeli M., Gentili C., Di Marzo V., Bet P.,
 Carlevaro M., Cermelli S., Cancedda R.;
 RT "The developmentally regulated avian Ch21 lipocalin is an
 extracellular fatty acid-binding protein.";
 J. Biol. Chem. 271:20163-20169(1996).
 [8]
 RX CHARACTERIZATION.
 RX MEDLINE-20513977; PubMed-11058755;
 RA Descalzi Cancedda F., Dozin B., Zeraga B., Cermelli S., Cancedda R.;
 RT "Ex-FABP: a fatty acid binding lipocalin developmentally regulated in
 chicken endochondral bone formation and myogenesis.";
 Biochim. Biophys. Acta 1482:127-135(2000).
 CC -!- FUNCTION: Preferentially binds long-chain unsaturated fatty acids
 such as linoleic acid, oleic acid, arachidonic acid. Also binds
 with a lower affinity long chain saturated fatty acids such as
 stearic acid. May act as survival protein by playing a role in
 maintaining cell viability.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: PREFERENTIALLY SYNTHESIZED IN NONPROLIFERATING
 CELLS.
 CC -!- PTM: Does not seem to be glycosylated.
 CC -!- MISCELLANEOUS: Developmentally regulated in chick embryo.
 CC -!- SIMILARITY: Belongs to the lipocalin family.

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 DR EMBL: M25371.1;
 DR EMBL: M55644; AAA48677.1;
 DR EMBL: AF121346; RAD23569.1;
 DR EMBL: X61199; NOT_ANNOTATED_CDS.
 DR PIR: A30230; A30230.
 DR InterPro: IPR002345; Lipocalin.
 DR InterPro: IPR000566; Lipocalin_cytFABP.
 DR Pfam: PF00061; Lipocalin; 1.
 DR PRINTS: PR00179; LIPOCALIN.
 DR PROSITE: PS00213; LIPOCALIN; 1.
 KW Lipocalin; Transport; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 178 EXTRACELLULAR FATTY ACID BINDING PROTEIN.
 FT MOD_RES 21 21 BLOCKED.
 FT DISULFID 80 173 BY SIMILARITY.
 FT CONFLICT 4 4 L -> S (IN REF. 2).
 FT CONFLICT 27 27 R -> S (IN REF. 2 AND 4).
 FT CONFLICT 45 45 F -> S (IN REF. 2 AND 4).

FT CONFLICT 62 62 F -> S (IN REF. 1).
 FT CONFLICT 96 96 L -> V (IN REF. 1).
 SQ SEQUENCE 178 AA; 20201 MW; 0DDBDC33C1A0C6B8 CRC64;
 Query Match 26.1%; Score 6; DB 1; Length 178;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 EDELEV 23
 I I I I I I
 Db 65 EDELEV 70
 RESULT 8
 HIS5_METTH STANDARD; PRT; 198 AA.
 AC 027568;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP
 synthase glutamine amidotransferase subunit) (IGP synthase subunit
 hisH) (tmgp synthase subunit hisH) (IGPS subunit hisH).
 DE HISH OR MTH1524.
 GN Methanobacterium thermoautotrophicum.
 OS Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE-98037514; PubMed-9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
 Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 Jiwni N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 deltaH: functional analysis and comparative genomics.";
 J. Bacteriol. 179:7135-7155(1997).
 CC -!- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine to
 IGP, AICAR and glutamate. The hisH subunit provides the glutamine
 amidotransferase activity that produces the ammonia necessary to
 hisP for the synthesis of IGP and AICAR (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-
 ylamino)methylidenesamino]-1-[(5-phosphoribosyl)imidazole-4-
 carboxamide + L-glutamine -> imidazole-glycerol phosphate + 5-
 aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
 CC -!- PATHWAY: Histidine biosynthesis; fifth step.
 CC -!- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.

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 DR EMBL: AF000912; BAB85999.1;
 DR PIR: D69070; D69070.
 DR HAMAP: MF_00278; 1.
 DR InterPro: IPR000991; GATase_1.
 DR Pfam: PF00117; GATase; 1.
 DR PROSITE: PS00442; GATASE_TYPE1; 1.
 KW Histidine biosynthesis; Transferrase; Glutamine amidotransferase;
 Complete proteome.
 FT ACT_SITE 77 77 BY SIMILARITY.
 FT ACT_SITE 177 177 BY SIMILARITY.

FT ACT_SITE 179 179 BY SIMILARITY.
SQ SEQUENCE 198 AA; 21348 MW; E8EFA43EC9163AEF CRC64;

Query Match 26.18; Score 6; DB 1; Length 198;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 EGADE 20
|||||
Db 130 EGADE 135

RESULT 9
COLI_PIG STANDARD; PRT; 267 AA.

AC P01192: Q95246;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Corticotropin-lipotropin precursor (Pro-opiomelanocortin) (POMC)
DE [Contains: NPP; Melanotropin gamma (Gamma-MSH); Corticotropin
DE (Adrenocorticotrophic hormone) (ACTH); Melanotropin alpha (Alpha-MSH);
DE Corticotropin-like intermediary peptide (CLIP); Lipotropin beta (Beta-
DE LPH); Lipotropin gamma (Gamma-LPH); Melanotropin beta (Beta-MSH);
DE Beta-endorphin; Met-enkephalin].
GN POMC.
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86131687; PubMed=3753882;
RA Gossard F.J., Chang A.C.Y., Cohen S.N.;
RT "Sequence of the cDNA encoding porcine pro-opiomelanocortin.";
RL Biochim. Biophys. Acta 866:68-74(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84069823; PubMed=6196724;
RA Bolleau G., Barbeau C., Jeannotte L., Chretien M., Drouin J.;
RT "Complete structure of the porcine pro-opiomelanocortin mRNA derived
RL from the nucleotide sequence of cloned cDNA.";
RN Nucleic Acids Res. 11:8063-8071(1983).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95046835; PubMed=7958386;
RA Gen K., Hirai T., Kato T., Kato Y.;
RT "Presence of the same transcript of pro-opiomelanocortin (POMC) genes
RL in the porcine anterior and intermediate pituitary lobes.";
RN Mol. Cell. Endocrinol. 103:101-108(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=84239667; PubMed=6547437;
RA Oates E., Herbert E.;
RT "5' sequence of porcine and rat pro-opiomelanocortin mRNA. One porcine
RL and two rat forms.";
RN J. Biol. Chem. 259:7421-7425(1984).
RN [5]
RP SEQUENCE OF 136-174.
RA Shepherd R.G., Willson S.D., Howard K.S., Bell P.H., Davies D.S.,
RA Davis S.B., Eigner E.A., Shakespear N.E.;
RT "Studies with corticotropin. III. Determination of the structure of
RL beta-corticotropin and its active degradation products.";
RN J. Am. Chem. Soc. 78:5067-5076(1956).
RN [6]
RP REVISIONS TO 160 AND 165.
RX MEDLINE=72114902; PubMed=4334191;
RA Riniker B., Sieber P., Rittel W., Zuber H.;
RT "Revised amino-acid sequences for porcine and human
RL adrenocorticotrophic hormone.";
RN Nature New Biol. 235:114-115(1972).
RN [7]
RP REVISIONS (CORTICOTROPIN).

RX MEDLINE=74306590; PubMed=4369114;
RA Graf L.;
RT "Re-examination of the sequence of the C-terminal tryptic fragment
RL from porcine adrenocorticotrophic hormone.";
RN Acta Biochim. Biophys. Acad. Sci. Hung. 7:293-297(1972).
RN [8]
RP SEQUENCE OF 136-174.
RX MEDLINE=91071194; PubMed=2174774;
RA Volgt K., Stegmaier W., McGregor G.P., Roesch H., Seliger H.;
RT "Isolation and full structural characterisation of six
RL adrenocorticotropin-like peptides from porcine pituitary gland.
RT Identification of three novel fragments of adrenocorticotropin and of
RL two forms of a novel adrenocorticotropin-like peptide.";
RN Eur. J. Biochem. 194:225-236(1990).
RN [9]
RP SEQUENCE OF 136-148.
RA Harris J.I., Lerner A.B.;
RT "Amino-acid sequence of the alpha-melanocyte-stimulating hormone.";
RL Nature 179:1346-1347(1957).
RN [10]
RP SEQUENCE OF 177-267.
RX MEDLINE=7111231; PubMed=5543613;
RA Graf L., Barat E., Cseh G., Sajgo M.;
RT "Amino acid sequence of porcine beta-lipotrophic hormone.";
RL Biochim. Biophys. Acta 229:276-278(1971).
RN [11]
RP REVISIONS (LIPOTRPIN).
RA Gilardeau C., Chretien M.;
RT "Complete amino acid sequence of porcine beta-lipotrophic hormone
RL (beta-LPH).";
RL (In) Meienhofer J. (eds.);
RL Chemistry and biology of peptides, pp.609-611, Ann Arbor Sci. Pub.,
RL Ann Arbor (1972).
RN [12]
RP REVISION TO 211.
RX MEDLINE=73048217; PubMed=4673865;
RA Pankov Y.A., Yudaev N.A.;
RT "Complete amino acid sequence in the molecule of porcine beta-
RL lipotropin.";
RL Biochimia 37:991-1004(1972).
RN [13]
RP SEQUENCE OF 217-234.
RA Harris J.I., Roos P.;
RT "The structure of the beta-melanocyte-stimulating hormone.";
RL Nature 178:90-90(1956).
RN [14]
RP SEQUENCE OF 217-234.
RA Geschwind I.I., Li C.H., Barnafi L.;
RT "The structure of the beta-melanocyte-stimulating hormone.";
RN J. Am. Chem. Soc. 79:620-625(1957).
RN [15]
RP SEQUENCE OF 237-241.
RX MEDLINE=76100762; PubMed=1207728;
RA Hughes J., Smith T.W., Kosterlitz H.W., Fothergill L.A., Morgan B.A.,
RA Morris H.R.;
RT "Identification of two related pentapeptides from the brain with
RL potent opiate agonist activity.";
RN Nature 258:577-579(1975).
RN [16]
RP SEQUENCE OF 237-267.
RX MEDLINE=77084500; PubMed=1007884;
RA Graf L., Barat E., Pathy A.;
RT "Isolation of a COOH-terminal beta-lipotropin fragment (residues
RL 61-91) with morphine-like analgesic activity from porcine pituitary
RL glands.";
RL Acta Biochim. Biophys. Acad. Sci. Hung. 11:121-122(1976).
CC -1- FUNCTION: ACTH STIMULATES THE ADRENAL GLANDS TO RELEASE CORTISOL.
CC -1- FUNCTION: MSH (MELANOCYTE-STIMULATING HORMONE) INCREASES THE
CC PIGMENTATION OF SKIN BY INCREASING MELANIN PRODUCTION IN
CC MELANOCYTES.
CC -1- FUNCTION: BETA-ENDORPHIN AND MET-ENKEPHALIN ARE ENDOGENOUS
CC OPIATES.
CC -1- TISSUE SPECIFICITY: ACTH AND MSH ARE PRODUCED BY THE PITUITARY

CC GLAND.
CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
CC THE DIFFERENT ACTIVE PEPTIDES.
CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
CC -----
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CC -----
CC EMBL: X03561; CAA27248.1; -
CC DR EMBL: X00135; CAA24968.1; -
CC DR EMBL: S73519; AAB32312.1; -
CC DR EMBL: K01879; AAA31104.1; -
CC DR FIC: A93496; CTPGP.
CC DR InterPro: IPR001941; Mcoitin_ACTH.
CC DR Pfam: PF00976; ACTH_domain; 1.
CC DR PRINTS: PR00383; MELANOCORTIN.
CC DR Endorphin: Hormone: Cleavage on pair of basic residues: Amidation;
CC KW Glycoprotein; Signal.
CC FT SIGNAL 1 26 BY SIMILARITY.
CC FT PEPTIDE 27 106 NPP.
CC FT PEPTIDE 77 87 MELANOTROPIN GAMMA.
CC FT PEPTIDE 136 174 CORTICOTROPIN.
CC FT PEPTIDE 136 148 MELANOTROPIN ALPHA.
CC FT PEPTIDE 154 174 CORTICOTROPIN-LIKE INTERMEDIARY PEPTIDE.
CC FT PEPTIDE 177 267 LIPOTRIPIN BETA.
CC FT PEPTIDE 177 234 LIPOTRIPIN GAMMA.
CC FT PEPTIDE 217 234 MELANOTROPIN BETA.
CC FT PEPTIDE 237 267 BETA-ENDORPHIN.
CC FT PEPTIDE 237 241 MET-ENKEPHALIN.
CC FT MOD_RES 87 87 AMIDATION (G-88 PROVIDE AMIDE GROUP).
CC FT MOD_RES 148 148 AMIDATION (G-149 PROVIDE AMIDE GROUP).
CC FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARIANT 143 143 R -> T.
CC FT CONFLICT 6 6 G -> S (IN REF. 3 AND 4).
CC FT CONFLICT 15 15 T -> A (IN REF. 3 AND 4).
CC FT CONFLICT 23 23 G -> E (IN REF. 3 AND 4).
CC FT CONFLICT 49 49 A -> S (IN REF. 4).
CC SQ SEQUENCE 267 AA; 28894 MW; A6DB487A5032B648 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GADEL 21
| | | | |
Db 161 GADEL 166

RESULT 10
TPM2_DROME STANDARD; PRT; 284 AA.
AC P09491; P09490; Q24408; Q24427; Q24428; Q8S265; Q9VF95;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tropomyosin 2 (tropomyosin I).
GN TM2 OR TMI OR CG4843.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxID=7227;
OX [1]
RP SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
RC TISSUE=Embryo, Larva, and Pupae;
RX MEDLINE=84205681; PubMed=6202423;
RA Karlik C.C., Mahaffey J.W., Coutu M.D., Fyrberg E.A.;
RT "Organization of contractile protein genes within the 88F subdivision

RT of the D. melanogaster third chromosome.";
RL Cell 37:469-481(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
RX MEDLINE=86085920; PubMed=3079761;
RA Basi G.S., Storti R.V.;
RT "Structure and DNA sequence of the tropomyosin I gene from Drosophila
RT melanogaster.";
RL J. Biol. Chem. 261:817-827(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler C., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]
RP REVISIONS.
RC STRAIN=Berkeley;
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM EMBRYONIC).
RC STRAIN=Berkeley; TISSUE=Embryo;
RX PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";


```
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
RN [6]
RP SEQUENCE OF 258-284 FROM N.A. (ISOFORM EMBRYONIC).
RX MEDLINE=85215579; PubMed=4000944;
RA Boardman M., Basi G.S., Storti R.V.;
RT "Multiple polyadenylation sites in a Drosophila tropomyosin gene are
RL used to generate functional mRNAs.";
RL Nucleic Acids Res. 13:1763-1776(1985).
CC -1- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Thoracic; Synonyms=127; t;
CC IsoId=p09491-1; Sequence=Displayed;
CC Name=Embryonic; Synonyms=129; A, B, e;
CC IsoId=p09491-2; Sequence=VSP_006616;
CC -1- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE
CC EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
CC -1- SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY.
CC -1- CAUTION: Ref.6 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K02622; AAA28970.1; -
DR EMBL; K02623; AAA28971.1; -
DR EMBL; K02622; AAA28971.1; JOINED.
DR EMBL; K03277; AAA28973.1; -
DR EMBL; K03277; AAA28974.1; -
DR EMBL; AE003708; AAN13652.1; -
DR EMBL; AY071087; AAL48709.1; -
DR EMBL; X02220; CAA26142.1; ALT_SEQ.
DR PIR; A25624; A25624.
DR PIR; B25624; B25624.
DR FlyBase; FBgn004117; Tm2.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS00326; TROPOMYOSIN; 1.
KW Muscle protein; Coiled coil; Repeat; Alternative splicing;
KW Multigene family.
FT VARSPPLIC 259 284 RLFNEKEKYKAICDDLDQTFEAELTGY -> ELGINKDRYKS
FT LADMDSTFAELAGY (in isoform Embryonic).
FT /FTId=VSP_006616
FT M -> V (IN REF. 1).
FT Q -> L (IN REF. 1).
FT I -> T (IN REF. 1).
FT R -> D (IN REF. 1).
FT SEQUENCE 284 AA; 32981 MW; 07AD03FDD304EA5F CRC64;
Oy Query Match 26.1%; Score 6; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 18 EDELEV 23
111111
173 EDELEV 178
RESULT 11
PCD1_HUMAN STANDARD; PRT; 288 AA.
ID Q15116; Q00517;
AC Q15116; Q00517;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Programmed cell death protein 1 precursor (Protein PD-1) (hpd-1).
GN PCD1 OR PDI.
OS Homo sapiens (Human).
```

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OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95154844; PubMed=7851902;
RA Shinohara T., Taniwaki M., Ishida Y., Kawalch M., Honjo T.;
RT "Structure and chromosomal localization of the human PD-1 gene
RT (PDCD1).";
RL Genomics 23:704-706(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97473511; PubMed=9332365;
RA Finger L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,
RA Burrows P.D., Billips L.D.;
RA Burrows P.D., Billips L.D.;
RT "The human PD-1 gene: complete cDNA, genomic organization, and
RT developmentally regulated expression in B cell progenitors.";
RL Gene 197:177-187(1997).
RN [3]
RP ERRATUM.
RA Finger L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,
RA Burrows P.D., Billips L.D.;
RL Gene 203:253-253(1997).
CC -1- FUNCTION: POSSIBLE CELL DEATH INDUCER, IN ASSOCIATION WITH
CC OTHER FACTORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DEVELOPMENTAL STAGE: INDUCED AT PROGRAMMED CELL DEATH.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC -----
DR EMBL; L27440; AAC41700.1; -
DR EMBL; U64863; AAC51773.1; -
DR PIR; A55737; A55737.
DR HSSP; P01607; IRE1.
DR Genew; HGNC:8760; PDCD1.
DR MIM; 600244; -
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0006959; P:humoral immune response; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; Apoptosis.
FT SIGNAL 1 288
FT CHAIN 21 288 PROGRAMMED CELL DEATH PROTEIN 1.
FT DOMAIN 21 170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 191 POTENTIAL.
FT DOMAIN 192 288 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 35 145 IG-LIKE V-TYPE.
FT DISULFID 54 123 POTENTIAL.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 38 38 F -> S (IN REF. 1).
FT CONFLICT 162 162 P -> S (IN REF. 1).
FT SEQUENCE 288 AA; 31707 MW; A5210AD50C3046C7 CRC64;
Oy Query Match 26.1%; Score 6; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 LRPEDG 11
Db 277 LRPEDG 282

RESULT 12
OPSD_LIMPA
ID OPSD_LIMPA STANDARD; PRT; 289 AA.
AC Q42431;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Rhodopsin (Fragment).
GN RHO.
OS Limnococtus pallidus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoldei; Abyssocottidae; Limnococtus.
OX NCBI_TaxID=61634;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98086781; PubMed=9417898;
RA Hunt D.M., Fitzgibbon J., Slobodyanyuk S.J., Bowmaker J.K.,
RA Dulai K.S.;
RT "Molecular evolution of the cottoid fish endemic to Lake Baikal
RT deduced from nuclear DNA evidence.";
RL Mol. Phylogenet. Evol. 8:415-422(1997).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC LINKED TO CIS-RETINAL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES
CC VISION IN DIM LIGHT.
CC -!- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
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CC -----
CC EMBL: U97271; AAB61725.1; -.
CC HSSP: P02699; IBOJ.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC InterPro: IPR001760; Opsin.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS: PR00237; GPCR_RHODPSN.
CC PROSITE: PS00237; G-PROTEIN_RECEP_FL1; FALSE_NEG.
CC PROSITE: PS02362; G-PROTEIN_RECEP_FL2; 1.
CC PROSITE: PS00238; OPSIN; 1.
CC Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
FT NON_TER 1 1
FT DOMAIN <1 7 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 8 32 1 (POTENTIAL).
FT DOMAIN 33 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 69 2 (POTENTIAL).
FT DOMAIN 70 84 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 85 104 3 (POTENTIAL).
FT DOMAIN 105 123 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 124 147 4 (POTENTIAL).
FT DOMAIN 148 173 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 174 201 5 (POTENTIAL).
FT DOMAIN 202 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 247 6 (POTENTIAL).
FT DOMAIN 248 255 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 256 280 7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
RETINAL CHROMOPHORE (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
>289
DOMAIN 281
DISULFID 81
BINDING 158
CARBOHYD 267
NON_TER 171
SEQUENCE 289
MW: 160D08E17E5E1280 CRC64;
Query Match 26.1%; Score 6; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAGWLR 7
Db 143 LAGWLR 148

RESULT 13
PARB_HELPJ
ID PARB_HELPJ STANDARD; PRT; 290 AA.
AC Q92K75;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable chromosome partitioning protein parB.
GN PARB OR JHP1066.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: INVOLVED IN CHROMOSOME PARTITION. LOCALIZE TO BOTH POLES
CC OF THE PREDIVISIONAL CELL FOLLOWING COMPLETION OF DNA REPLICATION.
CC BINDS TO THE DNA ORIGIN OF REPLICATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARB FAMILY.
CC -----
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CC -----
CC EMBL: AE001534; AAD06646.1; -.
CC PIR: H71852; H71852.
CC InterPro: IPR004437; ParB_part.
CC InterPro: IPR003115; ParBc.
CC Pfam: PF02195; ParBc; 1.
CC SMART: SM00470; ParB; 1.
CC TIGRFAMs: TIGR00180; parB_part; 1.
CC Chromosome partitioning; DNA-binding; Complete proteome.
KW Chromosome partitioning; DNA-binding; Complete proteome.
SQ SEQUENCE 290 AA; 33405 MW; 6709BA0547A55A4F CRC64;

Query Match 26.1%; Score 6; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AEDELE 22
Db 245 AEDELE 250

RESULT 14

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MTSA_STRP8
ID MTSA_STRP8 STANDARD; PRT; 310 AA.
AC QBP280;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metal ABC transporter substrate-binding lipoprotein precursor.
GN MTSA OR SPYM18_0494.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OC NCBI_TaxID=186103;
RX SEQUENCE FROM N.A.
RP STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21977593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RA "Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC -|- FUNCTION: Part of an ATP-driven transport system for a metal; this
CC protein has affinity for Zn(II), Fe(III) and Cu(II).
CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC -|- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC 9. Lipoprotein receptor antigen (Lrai) subfamily.
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CC -----
CC EMBL; AE009988; AAL97215.1; -.
CC InterPro; IPR006128; Lipoprotein_4.
CC InterPro; IPR006127; SBP_bac_9.
CC Pfam; PF01297; SBP_bac_9; 1.
CC PRINTS; PR00690; ADHESFAMILY.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
CC Transport; Zinc transport; Iron transport; Copper; Membrane;
CC Lipoprotein; Signal; Complete proteome.
CC SIGNAL 1 20
CC CHAIN 21 310
CC METAL ABC TRANSPORTER SUBSTRATE-
CC BINDING LIPOPROTEIN.
CC FT LIPID 21 21 N-ACYL DIGLYCERIDE (PROBABLE).
CC FT SEQUENCE 310 AA; 34330 MW; 40F613659AAD1768 CRC64;
SQ
Query Match 26.1%; Score 6; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 EDGGQA 14
Dd |||||
Db 94 EDGGQA 99
RESULT 15
MTSA_STRPY
ID MTSA_STRPY STANDARD; PRT; 310 AA.
AC Q9A157; Q9RN17; Q9RNJ0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Metal ABC transporter substrate-binding lipoprotein precursor.
GN MTSA OR SPY0453 OR SPYM3_0318 OR SPS1539.
OS Streptococcus pyogenes, and
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
```

```
OC Streptococcus.
OX NCBI_TaxID=1314, 198466;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 30-39, AND CHARACTERIZATION.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1; and API / Serotype M1;
RX MEDLINE=20032372; PubMed=10564500;
RA Janulczyk R., Pallon J., Bjoerck L.;
RT "Identification and characterization of a Streptococcus pyogenes ABC
RT transporter with multiple specificity for metal cations.";
RL Mol. Microbiol. 34:596-606(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes: a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232".
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Part of an ATP-driven transport system for a metal; this
CC protein has affinity for Zn(II), Fe(III) and Cu(II).
CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC -|- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC 9. Lipoprotein receptor antigen (Lrai) subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF180520; AAD56936.1; -.
CC EMBL; AF180521; AAD56939.1; -.
CC EMBL; AE006505; AAK33468.1; -.
CC EMBL; AE014143; AAM78925.1; ALT_INIT.
CC EMBL; AP005145; BAC64634.1; ALT_INIT.
CC HSP; P96116; ITOA.
CC InterPro; IPR006128; Lipoprotein_4.
CC InterPro; IPR006127; SBP_bac_9.
CC Pfam; PF01297; SBP_bac_9; 1.
CC PRINTS; PR00690; ADHESFAMILY.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
CC Transport; Zinc transport; Iron transport; Copper; Membrane;
CC Lipoprotein; Signal; Complete proteome.
CC SIGNAL 1 20
CC CHAIN 21 310
CC METAL ABC TRANSPORTER SUBSTRATE-
CC BINDING LIPOPROTEIN
CC FT LIPID 21 21 N-ACYL DIGLYCERIDE (PROBABLE).
CC FT VARIANT 77 77 V -> A (IN STRAIN API).
```

```

FT CONFLICT 26 26 T -> A (IN REF. 1).
FT CONFLICT 30 30 K -> E (IN REF. 1).
FT CONFLICT 44 44 A -> G (IN REF. 1).
FT CONFLICT 49 50 AI -> VM (IN REF. 1).
SQ SEQUENCE 310 AA: 34358 MW: B0F829EF1C72CADC CRC64;

Query Match 26.1%; Score 6; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 EDGGOA 14
Db 94 EDGGOA 99

```

Search completed: September 11, 2003, 17:52:41
Job time : 4.42781 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:02 ; Search time 22.016 seconds
(without alignments)
269.586 Million cell updates/sec

Title: US-09-853-253-6
Perfect score: 23
Sequence: 1 ALAGWLRPDGGQAEDELEV 23

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	20	87.0	117 4 Q8TAT9	Q8tat9 homo sapien
2	11	47.8	117 11 Q8CH53	Q8ch53 meriones un
3	8	34.8	433 10 Q93ZV7	Q93zv7 arabidopsis
4	8	34.8	433 10 Q8L7E4	Q8l7e4 arabidopsis
5	8	34.8	483 10 Q65529	Q65529 arabidopsis
6	7	30.4	103 16 Q9L063	Q9l063 streptomyce
7	7	30.4	313 2 Q8VP52	Q8vp52 streptomyce
8	7	30.4	433 16 Q8CNY4	Q8cny4 staphylococ
9	7	30.4	887 16 Q8XY49	Q8xy49 ralstonia s
10	7	30.4	910 16 Q9I3F5	Q9i3f5 pseudomonas
11	7	30.4	2376 5 Q9V5J0	Q9v5j0 drosophila
12	7	30.4	2376 5 Q966V1	Q966v1 drosophila
13	6	26.1	69 16 Q9A542	Q9a542 caulobacter
14	6	26.1	88 17 Q8ZZR1	Q8zzr1 pyrobaculum
15	6	26.1	98 5 P91785	P91785 onchocerca
16	6	26.1	100 16 Q8PBN4	Q8pbn4 xanthomonas

17	6	26.1	106 10 P93359	P93359 nicotiana t
18	6	26.1	110 2 Q87801	Q87801 pseudomonas
19	6	26.1	112 5 Q26847	Q26847 trypanosoma
20	6	26.1	113 16 Q8G7N5	Q8g7n5 bifidobacte
21	6	26.1	117 12 Q85548	Q85548 bovine herp
22	6	26.1	129 4 Q43180	Q43180 homo sapien
23	6	26.1	133 13 Q8JFY6	Q8jfy6 litoria cae
24	6	26.1	137 4 Q8N8H9	Q8n8h9 homo sapien
25	6	26.1	138 16 Q9RD30	Q9rd30 streptomyce
26	6	26.1	142 16 Q8ZBU1	Q8zbu1 yersinia pe
27	6	26.1	147 5 Q25622	Q25622 onchocerca
28	6	26.1	148 5 Q8WT59	Q8wt59 onchocerca
29	6	26.1	154 5 Q8WT58	Q8wt58 onchocerca
30	6	26.1	154 5 Q8WT56	Q8wt56 litomosolde
31	6	26.1	154 5 Q8WT57	Q8wt57 onchocerca
32	6	26.1	159 3 Q05697	Q05697 saccharomyc
33	6	26.1	159 4 Q8N9A4	Q8n9a4 homo sapien
34	6	26.1	161 10 Q9LWY4	Q9lwy4 oryza sativ
35	6	26.1	165 2 Q9RNJ3	Q9rnj3 zymomonas m
36	6	26.1	165 16 Q8XXY6	Q8xyx6 ralstonia s
37	6	26.1	171 5 Q25624	Q25624 onchocerca
38	6	26.1	175 13 Q8JFY7	Q8jfy7 litoria cae
39	6	26.1	175 16 Q9KQ90	Q9kq90 vibrio chol
40	6	26.1	177 11 Q8CIQ8	Q8ciq8 rattus norv
41	6	26.1	178 5 Q25619	Q25619 onchocerca
42	6	26.1	178 5 Q8MZJ8	Q8mzj8 acanthochei
43	6	26.1	178 16 Q98IM5	Q98im5 rhizobium l
44	6	26.1	180 2 Q50344	Q50344 lactobacill
45	6	26.1	186 5 Q9UIY0	Q9uiy0 caenorhabdi

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY; PRT; 117 AA.
AC Q8TAT9:
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025791; AAH25791.1; -
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR pfam; PF04643; motilin_assoc; 1.
DR pfam; PF04644; motilin_ghrelin; 1.
SQ SEQUENCE 117 AA; 12939 MW; 25B0572EBECB7610 CRC64;

Query Match 87.0%; Score 20; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.4e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAEDE 20
|||||
DB 52 ALAGWLRPDGGQAEDE 71

RESULT 2

Q8CH53 PRELIMINARY; PRT; 117 AA.
ID Q8CH53:
AC Q8CH53;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)

```
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Chrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoka T., Miyazawa M., Anagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF42491; AAO06965.1; -;
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 47.8%; Score 11; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QOAGAEDELE 22
Db 63 QOAGAEDELE 73

RESULT 3
Q932V7 PRELIMINARY; PRT; 433 AA.
AC Q932V7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative RNA-binding protein LAH1.
GN A74G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koesena E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene A74g32720 (GI:7270219).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY056237; AAL07086.1; -;
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR PROSITE; PS50102; RRM; 1.
SQ SEQUENCE 433 AA; 48095 MW; E58EBAF51C35A8F7 CRC64;

Query Match 34.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAEDE 20
Db 287 QAEGAEDE 294

RESULT 4
Q8L7E4 PRELIMINARY; PRT; 433 AA.
AC Q8L7E4
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN A74G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Shinn P., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
RA Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sekano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY136302; AAM96968.1; -;
DR EMBL; BT000396; AAN15715.1; -;
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR PROSITE; PS00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 433 AA; 48126 MW; CFFF611A29AA0318 CRC64;

Query Match 34.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAEDE 20
Db 287 QAEGAEDE 294

RESULT 5
O65529 PRELIMINARY; PRT; 483 AA.
AC O65529
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 54.1 kDa protein.
GN F4D11.80 OR A74G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoerge W., Hohseisel J.,
RA Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
```

RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W., Lemcke K.,
RL Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL022537; CAA18589.1; -;
DR EMBL: AL161582; CAB79989.1; -;
DR InterPro: IPR002344; Lupus_La.
DR InterPro: IPR006630; Lupus_La_dom.
DR InterPro: IPR00504; RNA_rec_mot.
DR Pfam: PF00076; rrm; 1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA; 1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS50102; RRM; 1.
DR Hypothetical protein.
SQ SEQUENCE 483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;
Query Match 34.8%; Score 8; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 QAEGAED 20
|||||
Db 302 QAEGAED 309
|||||
RESULT 6
Q9L063
ID Q9L063 PRELIMINARY; PRT; 103 AA.
AC Q9L063
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SC02791.
GN SC02791 OR SC0105.22C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL939114; CAB87228.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;

Query Match 30.4%; Score 7; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DGGQAE 16
|||||
Db 48 DGGQAE 54
|||||

RESULT 7

Q8VP52
ID Q8VP52 PRELIMINARY; PRT; 313 AA.
AC Q8VP52
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE LysR-like transcriptional activator SnpR.
OS Streptomyces sp. C5.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=45212;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C5;
RA Desanti C.L., Strohl W.R.;
RT "Characterization of the Streptomyces sp. strain C5 snp locus and
development of an snp-derived expression vector family.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL: AY072041; AAL61992.1; -;
DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR005119; LysR_subst.
DR Pfam: PF00126; HTH_1; 1.
DR Pfam: PF03466; LysR_substrate; 1.
DR PRINTS: PR00039; HTHLYSR
DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; transcription; transcription regulation.
SQ SEQUENCE 313 AA; 34258 MW; C907C8AF51C3FA13 CRC64;
Query Match 30.4%; Score 7; DB 23; Length 313;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ALAGWLR 7
|||||
Db 103 ALAGWLR 109
|||||
RESULT 8
Q8CNY4
ID Q8CNY4 PRELIMINARY; PRT; 433 AA.
AC Q8CNY4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Trigger factor.
GN SE1350.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren Y.;
RA Chen Z., Wen Y.;
RA Zhang Y., Ren Y., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE016748; AAO04949.1; -;
KW Complete proteome.
SQ SEQUENCE 433 AA; 48732 MW; FF2490AD097F437D CRC64;
Query Match 30.4%; Score 7; DB 16; Length 433;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 DGGQAE 16
|||||
Db 180 DGGQAE 186
|||||
RESULT 9
Q8XY49
ID Q8XY49 PRELIMINARY; PRT; 887 AA.

AC Q8XY49;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Probable phage-related tail transmembrane protein.
 GN RSC1914 OR R503483.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646067; CABL5616.1; -;
 KW Complete proteome.
 SQ SEQUENCE 887 AA; 94105 MW; 9A8840E5362E740E CRC64;
 Query Match 30.4%; Score 7; DB 16; Length 887;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 QOAEAG 18
 Db 290 QOAEAG 296
 ID Q913F5 PRELIMINARY; PRT; 910 AA.
 AC Q913F5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Aconitate hydratase 1.
 GN ACNA OR PA1562.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Huynh W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen";
 RL Nature 406:959-964(2000).
 DR EMBL; AE004584; AAG04951.1; -;
 DR HSSP; P20004; IACO.
 DR InterPro; IPR006249; Aconitase_1.
 DR InterPro; IPR000573; Aconitase_C.
 DR InterPro; IPR001030; Aconitase_N.
 DR Pfam; PF00330; aconitase; 1.
 DR Pfam; PF00694; Aconitase_C; 1.
 DR PRINTS; PR00415; ACONITASE.
 DR ProDom; PD000511; Aconitase_N; 1.
 DR TIGRFAMS; TIGR01341; aconitase_1; 1.
 DR PROSITE; PS00450; ACONITASE_1; 1.
 DR PROSITE; PS01244; ACONITASE_2; 1.

KW Complete proteome.
 SQ SEQUENCE 910 AA; 99147 MW; C65F23CDB6FA0E1C CRC64;
 Query Match 30.4%; Score 7; DB 16; Length 910;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLR 7
 Db 65 ALAGWLR 71
 ID Q9V5J0 PRELIMINARY; PRT; 2376 AA.
 AC Q9V5J0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG18408 protein.
 GN REXIN OR CG3451 OR CG18408 OR CG18409.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Fertaz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busan D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalaali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Brydson R., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Dwydale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003830; AAF58816.2; -;
DR FlyBase; FBgn0033504; rexin.
DR InterPro; IPR001452; SH3.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 3.
DR SMART; SM00326; SH3; 3.
DR PROSITE; PS50002; SH3; 3.
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Query Match 30.4%; Score 7; DB 5; Length 2376;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 QAEGAEED 19
Db 37 QAEGAEED 43
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DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Rexin L1.
GN REXIN OR RXN OR CG3451 OR CG18408 OR CG18409.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki H.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamazaki H., Willert K., Fish M., Nusse R.;
RT "Drosophila Rexin, a Novel SH3 Adaptor Protein of Axin and Arrow that
RT is Essential for Living in Late Stage Embryo.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 3 SH3 DOMAINS.
DR EMBL; AB053478; BAB62017.1; -;
DR FlyBase; FBgn0033504; rexin.
DR InterPro; IPR002965; P_Rich_extensn.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 3.
DR PRINTS; PR01217; PRICHEXTENS.
DR ProDom; PD000066; SH3; 3.
DR SMART; SM00326; SH3; 3.
DR PROSITE; PS50002; SH3; 3.
KW SH3 domain.
SQ SEQUENCE 2376 AA; 267657 MW; 9C7BD6C7A705C888 CRC64;
Query Match 30.4%; Score 7; DB 5; Length 2376;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 QAEGAEED 19
Db 37 QAEGAEED 43
RESULT 13
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AC Q9A542;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cold-shock domain family protein.
GN CC2623.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR EMBL; AE005930; AAK24591.1; -;
DR HSP; P15277; 1MJC.
DR TIGR; CC2623; -;
DR InterPro; IPR002059; Cold_shock.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold_shock; 1.
DR SMART; SM00357; CSP; 1.
KW Activator; DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 69 AA; 7450 MW; 8EA80BE9EE56853C CRC64;
Query Match 26.1%; Score 6; DB 16; Length 69;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 PEDGGQ 13
Db 20 PEDGGQ 25
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Q8ZXR1 ID Q8ZXR1 PRELIMINARY; PRT; 88 AA.

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AC Q82ZRI; 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PAE0124.
GN PAE0124.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RL aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009752; AAL62578.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 88 AA; 9492 MW; 22091651B45CADD1 CRC64;

Query Match 26.1%; Score 6; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
DB 45 ALAGWL 50

RESULT 15
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ID P91785 PRELIMINARY; PRT; 98 AA.
AC P91785;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Antigen maltose binding protein (Fragment).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=94336252; PubMed=8058358;
RA Trenholme K.R., Tree T.I., Gillespie A.J., Guderian R., Maizels R.M.,
RA Bradley J.E.;
RT "Heterogeneity of IgG antibody responses to cloned Onchocerca volvulus
RT antigens in microfiladermia positive individuals from Esmeraldas
RT Province, Ecuador.";
RL Parasite Immunol. 16:201-209(1994).
DR EMBL; S71371; AAC60510.2; -
FT NON_TER 1
FT NON_TER 98
SQ SEQUENCE 98 AA; 11165 MW; 221BEFEBFE14DC76 CRC64;

Query Match 26.1%; Score 6; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LRPEDG 11
DB 51 LRPEDG 56
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Search completed: September 11, 2003, 17:55:49
Job time : 22.016 secs

GenCore version 5.1.6
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OM protein ~ protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 23.984 Seconds
(without alignments)
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Title: US-09-853-253-6

Perfect score: 121

Sequence: 1 ALAGWLRPEDGGAEGAEDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121	100.0	23	AAE23840	Human zsig33-linker
2	121	100.0	23	AAE23841	Human zsig33-linker
3	121	100.0	23	AAE15885	Human zsig33-linker
4	121	100.0	23	AAE15886	Human zsig33-linker
5	121	100.0	24	AAE23839	Human zsig33-linker
6	121	100.0	24	AAE15884	Human zsig33-linker
7	121	100.0	91	AAE33410	Human exon 3-delet
8	121	100.0	116	AAE60517	Human des-Gln14-gh
9	121	100.0	117	AAW87991	Protein designated

10	121	100.0	117	21	AAV87236	Human signal pepti
11	121	100.0	117	22	AAW38890	Human polypeptide
12	121	100.0	117	22	AAW62649	Human zsig33 poly
13	121	100.0	117	22	AAW20101	zsig33 protein. H
14	121	100.0	117	22	AAW60511	Human ghrelin prep
15	121	100.0	117	23	AAW78319	Amino acid sequenc
16	121	100.0	117	23	AAE23838	Human zsig33 prote
17	121	100.0	117	23	AAE15883	Human zsig33 prote
18	121	100.0	117	24	AAW6790	Human PRO polypept
19	121	100.0	117	24	AAW67066	Human secreted/tr
20	121	100.0	117	24	AAW59871	Novel secreted and
21	121	100.0	117	24	AAW59124	Novel human secret
22	121	100.0	117	24	AAW59271	Human secreted/tr
23	121	100.0	117	24	AAW59420	Novel human secret
24	121	100.0	117	24	AAW60555	Human secreted/tr
25	121	100.0	117	24	AAW58046	Human PRO polypept
26	121	100.0	117	24	AAW58977	Human secreted/tr
27	121	100.0	117	24	AAE33409	Human preproghreli
28	121	100.0	117	24	AAW13937	Human PRO1066 poly
29	121	100.0	117	24	AAW10892	Human PRO polypept
30	121	100.0	118	21	AAV66708	Membrane-bound pro
31	121	100.0	118	22	AAW12392	Human PRO1066 poly
32	121	100.0	118	22	AAW65231	Human PRO1066 (UNG
33	121	100.0	126	22	AAW40676	Human polypeptide
34	90	74.4	90	23	ABP08975	Human ORFX protein
35	90	74.4	116	22	AAW60516	Rat des-Gln14-ghre
36	90	74.4	117	22	AAW60510	Rat ghrelin prepro
37	87	71.9	117	22	AAW60521	Porcine des-Gln14-
38	87	71.9	118	22	AAW60520	Porcine ghrelin pr
39	62.5	51.7	89	22	AAW60523	Bovine ghrelin pre
40	54	44.6	200	24	ABP58240	Xenopus laevis nuc
41	50	41.3	653	17	AAW98903	Murine APLP1. Mus
42	48	39.7	82	22	AAW73526	Human colon cancer
43	48	39.7	287	22	AAW15575	Novel human diagno
44	48	39.7	570	22	AAW20671	Novel human diagno
45	48	39.7	2836	22	AAW62719	Drosophila melanog

ALIGNMENTS

RESULT 1
AAE23840
ID AAE23840 standard; peptide; 23 AA.
AC AAE23840;
XX
XX
10-SEP-2002 (first entry)
DE Human zsig33-linker peptide #2.
XX
KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrolntestinal; endocrine; anabolic.
XX
OS Homo sapiens.
XX
PN US2002055156-A1.
XX
PD 09-MAY-2002.
XX
PF 10-MAY-2001; 2001US-0853253.
XX
PR 11-MAY-2000; 2000US-203300P.
XX
PA (JASP/) JASPERS S R.
PA (SHEP/) SHEPPARD P O.
PA (DEIS/) DEISHER T A.
PA (BISH/) BISHOP P D.
XX
PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX WPI; 2002-443750/47.
DR

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
XX
XX
PS Claim 1; Page 28; 34pp; English.
XX
XX The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 121; DB 23; Length 23;

Best Local Similarity 100.0%; Pred. NO. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23

Db 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 2

AAE23841

ID AAE23841 standard; peptide; 23 AA.

XX AC AAE23841;

XX DT 10-SEP-2002 (first entry)

XX DE Human zsig33-linker peptide #3.

XX Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.
XX
XX

OS Homo sapiens.

XX US200205156-A1.

XX PD 09-MAY-2002.

XX PF 10-MAY-2001; 2001US-0853253.

XX PR 11-MAY-2000; 2000US-203300P.

XX PA (JASP/) JASPERS S R.

XX PA (SHEP/) SHEPPARD P O.

XX PA (DEIS/) DEISHER T A.

XX PA (BISH/) BISHOP P D.

XX PI Jaspers SR, Sheppard PO, Delsher TA, Bishop PD;

XX WPI; 2002-443750/47.

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones -
XX
XX
PS Claim 1; Page 28; 34pp; English.
XX

XX The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones.
CC The sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as
CC DNA probes in diagnostic assays to detect and quantitate the presence
CC of similar nucleic acids in samples, and therefore which patients may be
CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC in the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33-like peptide, zsig33-linker peptide.
XX
XX

SQ Sequence 23 AA;

Query Match 100.0%; Score 121; DB 23; Length 23;

Best Local Similarity 100.0%; Pred. NO. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23

Db 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 3

AAE15885

ID AAE15885 standard; peptide; 23 AA.

XX AC AAE15885;

XX DT 26-MAR-2002 (first entry)

XX DE Human zsig33-linker peptide #2.

XX Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-linker peptide.
XX
XX

OS Homo sapiens.

XX WO200187933-A2.

XX PD 22-NOV-2001.

XX PF 10-MAY-2001; 2001WO-US15091.

XX PR 11-MAY-2000; 2000US-0569271.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-082982/11.

XX DR N-PSDB; AAD25760.

XX New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and
PT treating gastrointestinal and growth related diseases, comprises

PT zsig33-like peptides -
XX Claim 1b; Page 81; 89pp; English.
XX
XX The invention relates to zsig33-like peptides (ZS33LP) including
CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and
CC zsig33-epsilon peptides and nucleic acid molecules encoding such
CC zsig33-like peptides. ZS33LP peptides activate the immune system
CC in boosting immunity to infectious diseases, treating immunocompromised
CC patients such as human immunodeficiency virus (HIV) patients, in
CC improving vaccines and in treatment of bacterial, viral, protozoal and
CC fungal infections. Peptides of the invention are used to identify and
CC isolate receptors involved in growth regulation in the liver, blood
CC vessel formation and other developmental processes. They are useful for
CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
CC growth and/or differentiation of tumour cells, as additives to anti-
CC hypoglycaemic preparations containing glucose and as adsorption
CC enhancers for oral drugs which require fast nutrient action and to
CC stimulate glucose-induced insulin release. They are also useful as
CC research reagents for the expansion, differentiation, growth factor and
CC hormone secretion and/or cell-cell interactions of tissues associated
CC with gastrointestinal system, brain and central nervous system. These
CC molecules are useful for treating dysfunction associated with contractile
CC tissues or to suppress or enhance contractility in vivo and to treat
CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
CC acids and/or antibodies are useful for treating disorders associated
CC with gastrointestinal contractility, secretion of digestive enzymes,
CC hormone and acids, secretion of hormones in the pancreas and/or brain,
CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
CC and regulation of nutrient absorption. Sequences of the invention are
CC useful in gene therapy. The present sequence is human zsig33-linker
CC peptide.
XX Sequence 23 AA;
SQ
Query Match 100.0%; Score 121; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. NO. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQGAEGAEDELEV 23
Db 1 ALAGWLRPEDGGQGAEGAEDELEV 23
RESULT 4
AAE15886
ID AAE15886 standard; peptide; 23 AA.
AC AAE15886;
XX
XX 26-MAR-2002 (first entry)
XX Human zsig33-linker peptide #3.
XX
KW Human; zsig33-like peptide; ZS33LP; Immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-linker peptide.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 23
FT /note= "C-terminal amide"
FT
XX WO200187933-A2.
PN
XX 22-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-US15091.
PF
XX 11-MAY-2000; 2000US-0569271.
PR

(ZYMO) ZYMOGENETICS INC.
Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
WPI; 2002-082982/11.
N-PSDB; AAD25760.
New polypeptides, useful for modulating gastric contractility, nutrient
uptake, pancreatic secretion of hormones, digestive enzymes and
treating gastrointestinal and growth related diseases, comprises
zsig33-like peptides -
Claim 1c; Page 82; 89pp; English.
The invention relates to zsig33-like peptides (ZS33LP) including
zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and
zsig33-epsilon peptides and nucleic acid molecules encoding such
zsig33-like peptides. ZS33LP peptides activate the immune system
in boosting immunity to infectious diseases, treating immunocompromised
patients such as human immunodeficiency virus (HIV) patients, in
improving vaccines and in treatment of bacterial, viral, protozoal and
fungal infections. Peptides of the invention are used to identify and
isolate receptors involved in growth regulation in the liver, blood
vessel formation and other developmental processes. They are useful for
evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
growth and/or differentiation of tumour cells, as additives to anti-
hypoglycaemic preparations containing glucose and as adsorption
enhancers for oral drugs which require fast nutrient action and to
stimulate glucose-induced insulin release. They are also useful as
research reagents for the expansion, differentiation, growth factor and
hormone secretion and/or cell-cell interactions of tissues associated
with gastrointestinal system, brain and central nervous system. These
molecules are useful for treating dysfunction associated with contractile
tissues or to suppress or enhance contractility in vivo and to treat
gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
acids and/or antibodies are useful for treating disorders associated
with gastrointestinal contractility, secretion of digestive enzymes,
hormone and acids, secretion of hormones in the pancreas and/or brain,
gastrointestinal motility, recruitment of digestive enzymes, inflammation
and regulation of nutrient absorption. Sequences of the invention are
useful in gene therapy. The present sequence is human zsig33-linker
peptide.
Sequence 23 AA;
Query Match 100.0%; Score 121; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. NO. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQGAEGAEDELEV 23
Db 1 ALAGWLRPEDGGQGAEGAEDELEV 23
RESULT 5
AAE23839
ID AAE23839 standard; peptide; 24 AA.
XX
AC AAE23839;
XX
XX 10-SEP-2002 (first entry)
XX Human zsig33-linker peptide #1.
XX
KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 7..18
FT

FT XX /note= "Hydrophilic region"

PN XX US2002055156-A1.

XX XX 09-MAY-2002.

PD XX

XX XX 10-MAY-2001; 2001US-0853253.

PF XX

XX XX 11-MAY-2000; 2000US-203300P.

XX XX (JASP/) JASPERS S. R.

PA (SHEP/) SHEPPARD P. O.

PA (DEIS/) DEISHER T. A.

PA (BISH/) BISHOP P. D.

XX XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

PI WPI: 2002-443750/47.

XX N-PSDB; AAD38239.

DR ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

XX contractility, nutrient uptake, growth hormones and/or secretion of

PT digestive/pancreatic enzymes and hormones -

XX

PS Claim 1; Page 28; 34pp; English.

XX The invention relates to zsig33-like peptides and their corresponding

CC nucleic acids and methods for modulating gastric contractility, nutrient

CC uptake, growth hormones, secretion of digestive enzymes and hormones.

CC The sequences of the invention are used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate ZSIG33 expression.

CC The nucleic acids of the invention and their complements are used as

CC DNA probes in diagnostic assays to detect and quantitate the presence

CC of similar nucleic acids in samples, and therefore which patients may be

CC in need of restorative therapy. The ZSIG33 peptides are used as antigens

CC in the production of antibodies against ZSIG33 and in assays to identify

CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies

CC and antagonists are used to down regulate expression and activity. The

CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting

CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent

CC assay (ELISA)). The peptides and nucleic acids of the invention are used

CC to modulate gastric contractility, nutrient uptake, growth hormones, the

CC secretion of digestive enzymes and hormones, and/or secretion of enzymes

CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy

CC and zsig33-like peptide is used in protein therapy. The present sequence

CC is human zsig33-like peptide, zsig33-linker peptide.

XX

SQ Sequence 24 AA;

Query Match 100.0%; Score 121; DB 23; Length 24;

Best Local Similarity 100.0%; Pred. No. 3.8e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEV 23

|||||

Db 1 ALAGWLRPEDGGGAEGAEDELEV 23

RESULT 6

AAE15884

XX AC AAE15884;

XX 26-MAR-2002 (first entry)

XX Human zsig33-linker peptide #1.

DE Human; zsig33-like peptide; ZS33LP; immunity; developmental process;

KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;

KW adsorption enhancer; gastrointestinal disease; growth related disease;

KW inflammation; gene therapy; growth regulation; blood vessel formation;

KW HIV; zsig33-linker peptide.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

PH Region 6..22

FT /note= "Hydrophilic antigenic site"

FT Region 7..18

FT /note= "Hydrophilic region"

XX

PN WO200187933-A2.

XX

XX 22-NOV-2001.

PD

XX 10-MAY-2001; 2001WO-US15091.

PF

XX 11-MAY-2000; 2000US-0569271.

PR

XX (ZYMO) ZYMOGENETICS INC.

PA Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

PI WPI: 2002-082982/11.

XX N-PSDB; AAD25760.

DR

XX New polypeptides, useful for modulating gastric contractility, nutrient

PT uptake, pancreatic secretion of hormones, digestive enzymes and

PT treating gastrointestinal and growth related diseases, comprises

PT zsig33-like peptides -

XX

PS Claim 1a; Page 81; 89pp; English.

XX The invention relates to zsig33-like peptides (ZS33LP) including

CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and

CC zsig33-epsilon peptides and nucleic acid molecules encoding such

CC zsig33-like peptides. ZS33LP peptides activate the immune system

CC in boosting immunity to infectious diseases, treating immunocompromised

CC patients such as human immunodeficiency virus (HIV) patients, in

CC improving vaccines and in treatment of bacterial, viral, protozoal and

CC fungal infections. Peptides of the invention are used to identify and

CC isolate receptors involved in growth regulation in the liver, blood

CC vessel formation and other developmental processes. They are useful for

CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate

CC growth and/or differentiation of tumour cells, as additives to anti-

CC hypoglycaemic preparations containing glucose and as adsorption

CC enhancers for oral drugs which require fast nutrient action and to

CC stimulate glucose-induced insulin release. They are also useful as

CC research reagents for the expansion, differentiation, growth factor and

CC hormone secretion and/or cell-cell interactions of tissues associated

CC with gastrointestinal system, brain and central nervous system. These

CC molecules are useful for treating dysfunction associated with contractile

CC tissues or to suppress or enhance contractility in vivo and to treat

CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic

CC acids and/or antibodies are useful for treating disorders associated

CC with gastrointestinal contractility, secretion of digestive enzymes,

CC hormone and acids, secretion of hormones in the pancreas and/or brain,

CC gastrointestinal motility, recruitment of digestive enzymes, inflammation

CC and regulation of nutrient absorption. Sequences of the invention are

CC useful in gene therapy. The present sequence is human zsig33-linker

CC peptide.

XX

SQ Sequence 24 AA;

Query Match 100.0%; Score 121; DB 23; Length 24;

Best Local Similarity 100.0%; Pred. No. 3.8e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEV 23

|||||

Db 1 ALAGWLRPEDGGGAEGAEDELEV 23

RESULT 7

AAE33410

ID AAE33410 standard; Protein; 91 AA.
 AC AAE33410;
 XX
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human exon 3-deleted ghrelin protein.
 XX
 XX Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
 KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
 KW cancer; human.
 XX
 OS Homo sapiens.
 XX
 XX WO200290387-A1.
 PN
 XX
 PD 14-NOV-2002.
 XX
 XX 10-MAY-2002; 2002WO-AU00582.
 PF
 XX
 PR 10-MAY-2001; 2001AU-0004919.
 PR
 PR 17-DEC-2001; 2001AU-0009567.
 XX
 PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 XX Choplin LK, Jeffery PL, Herington AC;
 PI
 XX
 XX WPI: 2003-111957/10.
 DR
 DR N-PSDB; AAD50726.
 XX
 XX Identifying a cancer cell or tissue for treating prostate, ovarian,
 PT breast cancer, or benign prostatic hyperplasia, by detecting the
 PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
 PT 1b proteins or nucleic acids -
 XX
 PS Claim 14; Page 34; 50pp; English.
 XX
 CC The invention relates to a method for identifying a cancer cell or
 CC tissue of the reproductive system by detecting expression of a ghrelin,
 CC an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic
 CC acids. The antibodies, exon 3-deleted form of preproghrelin and
 CC antagonists are useful for treating cancer of the reproductive system
 CC such as prostate, ovarian, breast, cervical or uterine cancer,
 CC choriocarcinoma or benign prostatic hyperplasia. The present sequence
 CC is human exon 3-deleted ghrelin protein.
 XX
 SQ Sequence 91 AA;
 Query Match 100.0%; Score 121; DB 24; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 8
 AAB60517
 ID AAB60517 standard; Protein; 116 AA.
 XX
 AC AAB60517;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
 XX
 XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX

PN WO200107475-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-JP04907.
 XX
 XX 23-JUL-1999; 99JP-0210002.
 PR
 PR 29-NOV-1999; 99JP-0338841.
 PR
 PR 26-APR-2000; 2000JP-0126623.
 XX
 PA (KANG/) KANGAWA K.
 XX
 XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 PI
 XX WPI: 2001-159704/16.
 DR
 DR N-PSDB; AAF59647.
 XX
 XX New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 XX
 XX Claim 3; Page 186-187; 210pp; Japanese.
 CC
 CC The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 SQ Sequence 116 AA;
 Query Match 100.0%; Score 121; DB 22; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 51 ALAGWLRPEDGGQAGAEDELEV 73
 RESULT 9
 AAW87991
 ID AAW87991 standard; Protein; 117 AA.
 XX
 AC AAW87991;
 XX
 DT 07-APR-1999 (first entry)
 XX
 DE Protein designated zsig33.
 XX
 XX Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
 KW nutrient absorption regulation; obesity; metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..23 /note= "signal peptide"
 FT Protein 24..117 /note= "mature protein"
 FT
 XX

PN W09842840-A1.
 XX 01-OCT-1998.
 XX 23-MAR-1998; 98WO-US05620.
 XX 24-MAR-1997; 97US-0822897.
 PR 24-MAR-1997; 97US-0041102.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Delsher TA, Sheppard PO;
 XX WPI; 1999-070071/06.
 DR N-PSDB; AAX04550.
 XX Human polypeptide having homology to motilin, zsig33 - useful e.g.
 PT to treat gastrointestinal motility disorders, obesity etc. and to
 PT identify antagonists to treat gastrointestinal hypermotility
 XX
 PS Claim 13; Page 55-56; 69pp; English.
 XX The present sequence represents a protein designated Zsig33. The nucleic
 CC acids are strongly expressed in stomach tissue. The polypeptide (or
 CC allelic variants/orthologs) can be used to stimulate gastric motility,
 CC measured as increased transit time or gastric emptying of an ingested
 CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. Zsig33 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC and CNS functions. They may therefore be used e.g. to regulate satiety
 CC or treat obesity and other metabolic disorders where neurological
 CC feedback modulates nutritional absorption. They are useful to identify
 CC zsig33 agonists, antagonists and ligands and to produce antibodies.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 121; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
 |||||
 Db 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 10
 AAY87236
 ID AAY87236 standard; Protein; 117 AA.
 XX
 AC AAY87236;
 XX
 DT 11-MAY-2000 (first entry)
 DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
 DE
 XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX Homo sapiens.
 OS
 XX W0200000610-A2.
 PN
 XX

PD 06-JAN-2000.
 XX 25-JUN-1999; 99WO-US14484.
 XX 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX (INCYTE) INCYTE PHARM INC.
 XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX WPI; 2000-160673/14.
 DR N-PSDB; AAZ98121.
 XX New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease -
 PT
 PS Claim 1; Page 168-169; 327pp; English.
 XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPP
 CC from natural sources.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 121; DB 21; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
 |||||
 Db 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 11
 AAM38890
 ID AAM38890 standard; Protein; 117 AA.
 XX
 AC AAM38890;
 XX 22-OCT-2001 (first entry)
 DT Human polypeptide SEQ ID NO 2035.
 DE
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

OS Homo sapiens.

PN WO200153312-A1.

XX 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-052317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI: 2001-442253/47.

DR N-PSDB; AAI58046.

XX Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -

XX Example 3; SEQ ID NO 2035; 10078pp; English.

PS The invention relates to human nucleic acids (AAI57798-AAI61369) and

XX the encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: Immune system suppression,

CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

XX Sequence 117 AA;

SQ Query Match 100.0%; Score 121; DB 22; Length 117;

XX Best Local Similarity 100.0%; Pred. No. 2.2e-10;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEV 23

DB 52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 12

AAB62649

ID AAB62649 standard; Protein: 117 AA.

XX AAB62649;

XX 23-JUL-2001 (first entry)

XX Human zsig33 polypeptide.

XX

KW zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
 KW G-protein coupled receptor.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 24..37

FT /note= "specifically claimed fragment that binds to
 the GHS-R"

XX WO200138355-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US32074.

XX 22-NOV-1999; 99US-0166765.

XX (ZYMO) ZYMOGENETICS INC.

PA Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

XX WPI: 2001-355879/37.

XX N-PSDB; AAF83678.

XX Forming reversible peptide receptor complex for purifying cell and

PT peptides, stimulating signal transduction and modulating hormone

XX secretion, involves contacting a receptor with zsig33 polypeptide -

XX Claim 1; Page 93-94; 111pp; English.

PS The invention relates to a method of forming a reversible peptide-

XX receptor complex that involves providing an immobilized receptor, and

CC contacting the receptor with a zsig33 peptide (comprising residues 24-37

CC of AAB62649), where the receptor binds to the zsig33 peptide. The method

CC is useful for purifying cells, purifying a peptide, stimulating signal

CC transduction in a cell expressing a receptor. It is also useful for

CC modulating secretion of hormones, neural development and/or utilization,

CC gastric contractility, nutrient uptake, secretion of digestive and

CC pancreatic enzymes and hormones, secretion of insulin-like growth factor

CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth

CC hormone secretion in a mammal having a disease associated with abnormal

CC levels of growth hormone, such as osteoporosis, bone repair, bone

CC remodeling, low osteoblast levels, cartilage repair and remodeling,

CC skeletal dysplasia, immune suppression, obesity, growth retardation,

CC protein catabolic responses after surgery, cachexia, protein loss,

CC dwarfism, wound healing and ovulation induction, treating a mammal having

CC a metabolic disorder requiring neurological feedback, such as satiety

CC regulation, glucose absorption and metabolism and neuropathy-associated

CC gastrointestinal disorders, and stimulating glucose-induced insulin

CC release in a mammal. The present sequence represents the human zsig33

XX polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.

XX Sequence 117 AA;

SQ Query Match 100.0%; Score 121; DB 22; Length 117;

XX Best Local Similarity 100.0%; Pred. No. 2.2e-10;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEV 23

DB 52 ALAGWLRPEDGGGAEGAEDELEV 74

RESULT 13

AAB20101

ID AAB20101 standard; Protein: 117 AA.

XX AAB20101;

XX

DT 23-APR-2001 (first entry)
 XX zsig33 protein.
 DE
 KW SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
 KW nutritional absorption modulator; growth hormone secretagogue;
 KW therapy; human.
 XX
 OS Homo sapiens.
 XX
 PH Location/Qualifiers
 FT Peptide
 FT 1..23
 FT /label= Signal_peptide
 FT Protein
 FT 24..117
 FT /label= Mature_protein
 FT Peptide
 FT 24..34
 FT /label= SGIP_peptide
 FT /note= "this peptide is claimed in Claim 1"
 XX
 PN WO200100830-A1.
 XX
 PD 04-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-US18306.
 XX
 PR 30-JUN-1999; 99US-0345157.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 XX
 DR WPI; 2001-123010/13.
 DR N-PSDB; AAF30033.
 XX
 XX Novel variants of SGIP peptides for modulating contractility in
 PT duodenum or jejunum tissue, pancreatic secretion of hormones and
 PT digestive enzymes, inducing growth hormone secretion or modulating
 PT gastric emptying -
 XX
 PS Disclosure; 54; 61pp; English.
 XX
 CC The present sequence is that of zsig33, a secreted protein with
 CC homology to motilin (see AAB20102). zsig33 is expressed at high
 CC levels in the stomach, and at lower levels in the small intestine
 CC and pancreas. A novel peptide fragment of zsig33, termed SGIP (see
 CC AAB20100), is claimed. SGIP is a ligand for growth hormone
 CC secretagogue receptor, and is therefore useful for modulating
 CC secretion of growth hormone and insulin like growth factor 1.
 CC SGIP, and variant SGIP peptides, are used in claimed methods for
 CC stimulating contractility in duodenum or jejunum tissue,
 CC modulating pancreatic secretion of hormones and digestive enzymes,
 CC inducing growth hormone secretion, and modulating gastric emptying.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 121; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGAEGAEDEV 23
 DB 52 ALAGWLRPEDGGGAEGAEDEV 74
 RESULT 14
 AAB60511
 ID AAB60511 standard; Protein; 117 AA.
 XX
 AC AAB60511;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human ghrelin preproprotein, SEQ ID NO:5.

XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX
 PN WO200107475-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-JP04907.
 XX
 PR 23-JUL-1999; 99JP-0210002.
 PR 29-NOV-1999; 99JP-0338841.
 PR 26-APR-2000; 2000JP-0126623.
 XX
 PA (KANG/) KANGAWA K.
 XX
 XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 XX
 DR WPI; 2001-159704/16.
 DR N-PSDB; AAF59645.
 XX
 XX New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 XX
 PS Claim 3; Page 182; 210pp; Japanese.
 XX
 CC The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating the peptides. The peptides
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 121; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGAEGAEDEV 23
 DB 52 ALAGWLRPEDGGGAEGAEDEV 74
 RESULT 15
 ABB78319
 ID ABB78319 standard; Protein; 117 AA.
 XX
 AC ABB78319;
 XX
 DT 05-DEC-2002 (first entry)
 XX
 DE Amino acid sequence of a human zsig33.
 XX
 KW Short gastrointestinal peptide; SGIP; zsig33; motilin.
 XX
 OS Homo sapiens.
 XX

```

FH Key      Location/Qualifiers
FT Peptide  1..23
FT          /note= "signal peptide"
FT Protein  24..119
FT          /note= "mature protein"
XX
PN US6420521-B1.
XX
XX 16-JUL-2002.
XX
XX 30-JUN-2000; 2000US-0608810.
XX
XX 30-JUN-1999; 99US-141592P.
XX
XX (Zymo ) ZYMOGENETICS INC.
XX
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
XX WPI; 2002-634794/68.
XX N-PSDB; ABV72214.
XX
XX New Short Gastrointestinal Peptide, which has homology to motilin,
XX useful for preventing, diagnosing and treating gastrointestinal
XX disorders
XX
XX Disclosure; Columns 39-40; 23pp; English.
XX
XX The present sequence represents human zsig33. The specification describes
XX a short gastrointestinal peptide (SGIP), which is derived from zsig33.
XX SGIP has homology to motilin. The SGIP peptide may be used in the
XX prevention, diagnosis and treatment of diseases associated with
XX inappropriate SGIP expression. For example, SGIP may be used to treat
XX disorders associated with decreased expression by rectifying mutations
XX or deletions in a patient's genome that affect the activity of Scip by
XX expressing inactive proteins or to supplement the patients own production
XX of SGIP. SGIP may also be used as an antigen in the production of
XX antibodies against SGIP and in assays to identify modulators of SGIP
XX expression and activity. The anti-SGIP antibodies, agonists and
XX antagonists may also be used to regulate expression and activity. The
XX anti-SGIP antibodies may also be used as diagnostic agents for detecting
XX the presence of SGIP in samples.
XX
SQ Sequence 117 AA;
    Query Match      100.0%; Score 121; DB 23; Length 117;
    Best Local Similarity 100.0%; Pred. No. 2.2e-10;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 ALAGWLRPEDGGQAGAEDELEV 23
       |||
    Db 52 ALAGWLRPEDGGQAGAEDELEV 74
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Job time : 23.984 secs

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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-853-253-6

Perfect score: 121

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Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	117	3	US-09-046-479-2
2	121	100.0	117	4	US-08-822-897C-2
3	121	100.0	117	4	US-09-608-810A-4
4	121	100.0	117	4	US-09-996-243-268
5	52	43.0	233	4	US-09-252-991A-27758
6	50	41.3	634	1	US-08-339-152A-17
7	50	41.3	653	1	US-08-339-152A-16
8	50	41.3	653	2	US-08-007-999B-3
9	50	41.3	653	2	US-08-689-276A-3
10	49	40.5	139	2	US-08-039-198B-10
11	48	39.7	518	4	US-09-252-991A-23604
12	47	38.8	283	4	US-09-252-991A-29700
13	46	38.0	341	4	US-09-252-991A-27327
14	46	38.0	428	4	US-09-252-991A-19723
15	46	38.0	517	4	US-09-252-991A-25921
16	46	38.0	1044	4	US-09-252-991A-18853
17	45.5	37.6	579	3	US-08-704-711A-1
18	45.5	37.6	579	4	US-09-521-220-1
19	45.5	37.6	582	3	US-08-704-711A-2
20	45.5	37.6	582	3	US-08-448-489-1
21	45.5	37.6	582	3	US-09-211-704A-9
22	45.5	37.6	582	4	US-09-521-220-2
23	45.5	37.6	582	4	US-09-391-104-28
24	45.5	37.6	591	2	US-08-889-402-1
25	45	37.2	174	4	US-09-252-991A-18600
26	45	37.2	494	1	US-08-464-340A-4
27	45	37.2	494	5	PCT-US94-08449A-4

28	45	37.2	1059	4	US-09-394-272-5	Sequence 5, Appli
29	44	36.4	405	4	US-09-252-991A-20326	Sequence 20326, A
30	43	35.4	118	3	US-08-482-304-12	Sequence 12, Appl
31	43	35.5	118	3	US-08-483-474-12	Sequence 12, Appl
32	43	35.5	140	3	US-08-482-304-9	Sequence 9, Appli
33	43	35.5	140	3	US-08-483-474-9	Sequence 9, Appli
34	43	35.5	162	4	US-09-252-991A-24838	Sequence 24838, A
35	43	35.5	191	4	US-09-252-991A-21437	Sequence 21437, A
36	43	35.5	212	3	US-09-154-083-4	Sequence 4, Appli
37	43	35.5	247	4	US-09-252-991A-27419	Sequence 27419, A
38	43	35.5	268	4	US-09-252-991A-27950	Sequence 27950, A
39	43	35.5	311	4	US-09-252-991A-28068	Sequence 28068, A
40	43	35.5	380	3	US-08-765-743-2	Sequence 2, Appli
41	43	35.5	380	4	US-09-341-446B-2	Sequence 2, Appli
42	43	35.5	424	4	US-09-341-446B-6	Sequence 6, Appli
43	43	35.5	424	4	US-09-341-446B-8	Sequence 8, Appli
44	43	35.5	427	4	US-09-341-446B-4	Sequence 4, Appli
45	43	35.5	450	4	US-09-252-991A-25523	Sequence 25523, A

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046.479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 121; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 2

US-08-822-897C-2
; Sequence 2, Application US/0822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,897C
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-822-897C-2

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 3

US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608,810A
; CURRENT FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEV 74

RESULT 4

US-09-996-243-268
; Sequence 268, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600

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3	PRIOR FILING DATE: 1998-05-28	
4	PRIOR APPLICATION NUMBER: 60/087607	
5	PRIOR FILING DATE: 1998-06-02	
6	PRIOR APPLICATION NUMBER: 60/087609	
7	PRIOR FILING DATE: 1998-06-02	
8	PRIOR APPLICATION NUMBER: 60/087759	
9	PRIOR FILING DATE: 1998-06-02	
10	PRIOR APPLICATION NUMBER: 60/087827	
11	PRIOR FILING DATE: 1998-06-03	
12	PRIOR APPLICATION NUMBER: 60/088021	
13	PRIOR FILING DATE: 1998-06-04	
14	PRIOR APPLICATION NUMBER: 60/088025	
15	PRIOR FILING DATE: 1998-06-04	
16	PRIOR APPLICATION NUMBER: 60/088026	
17	PRIOR FILING DATE: 1998-06-04	
18	PRIOR APPLICATION NUMBER: 60/088028	
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20	PRIOR APPLICATION NUMBER: 60/088029	
21	PRIOR FILING DATE: 1998-06-04	
22	PRIOR APPLICATION NUMBER: 60/088030	
23	PRIOR FILING DATE: 1998-06-04	
24	PRIOR APPLICATION NUMBER: 60/088033	
25	PRIOR FILING DATE: 1998-06-04	
26	PRIOR APPLICATION NUMBER: 60/088326	
27	PRIOR FILING DATE: 1998-06-04	
28	PRIOR APPLICATION NUMBER: 60/088167	
29	PRIOR FILING DATE: 1998-06-05	
30	PRIOR APPLICATION NUMBER: 60/088202	
31	PRIOR FILING DATE: 1998-06-05	
32	PRIOR APPLICATION NUMBER: 60/088212	
33	PRIOR FILING DATE: 1998-06-05	
34	PRIOR APPLICATION NUMBER: 60/088217	
35	PRIOR FILING DATE: 1998-06-05	
36	PRIOR APPLICATION NUMBER: 60/088655	
37	PRIOR FILING DATE: 1998-06-09	
38	PRIOR APPLICATION NUMBER: 60/088734	
39	PRIOR FILING DATE: 1998-06-10	
40	PRIOR APPLICATION NUMBER: 60/088738	
41	PRIOR FILING DATE: 1998-06-10	
42	PRIOR APPLICATION NUMBER: 60/088742	
43	PRIOR FILING DATE: 1998-06-10	
44	PRIOR APPLICATION NUMBER: 60/088810	
45	PRIOR FILING DATE: 1998-06-10	
46	PRIOR APPLICATION NUMBER: 60/088824	
47	PRIOR FILING DATE: 1998-06-10	
48	PRIOR APPLICATION NUMBER: 60/088826	
49	PRIOR FILING DATE: 1998-06-10	
50	PRIOR APPLICATION NUMBER: 60/088858	
51	PRIOR FILING DATE: 1998-06-11	
52	PRIOR APPLICATION NUMBER: 60/088861	
53	PRIOR FILING DATE: 1998-06-11	
54	PRIOR APPLICATION NUMBER: 60/088876	
55	PRIOR FILING DATE: 1998-06-11	
56	PRIOR APPLICATION NUMBER: 60/089105	
57	PRIOR FILING DATE: 1998-06-12	
58	PRIOR APPLICATION NUMBER: 60/089154	
59	PRIOR FILING DATE: 1998-06-15	
60	PRIOR APPLICATION NUMBER: 60/089532	
61	PRIOR FILING DATE: 1998-06-17	
62	PRIOR APPLICATION NUMBER: 60/089538	
63	PRIOR FILING DATE: 1998-06-17	
64	PRIOR APPLICATION NUMBER: 60/089598	
65	PRIOR FILING DATE: 1998-06-17	
66	PRIOR APPLICATION NUMBER: 60/089599	
67	PRIOR FILING DATE: 1998-06-17	
68	PRIOR APPLICATION NUMBER: 60/089600	
69	PRIOR FILING DATE: 1998-06-17	

1	PRIOR APPLICATION NUMBER: 60/089551
2	PRIOR FILING DATE: 1998-06-17
3	PRIOR APPLICATION NUMBER: 60/089801
4	PRIOR FILING DATE: 1998-06-18
5	PRIOR APPLICATION NUMBER: 60/089907
6	PRIOR FILING DATE: 1998-06-18
7	PRIOR APPLICATION NUMBER: 60/089908
8	PRIOR FILING DATE: 1998-06-18
9	PRIOR APPLICATION NUMBER: 60/089947
10	PRIOR FILING DATE: 1998-06-19
11	PRIOR APPLICATION NUMBER: 60/089948
12	PRIOR FILING DATE: 1998-06-19
13	PRIOR APPLICATION NUMBER: 60/089952
14	PRIOR FILING DATE: 1998-06-19
15	PRIOR APPLICATION NUMBER: 60/090246
16	PRIOR FILING DATE: 1998-06-22
17	PRIOR APPLICATION NUMBER: 60/090252
18	PRIOR FILING DATE: 1998-06-22
19	PRIOR APPLICATION NUMBER: 60/090255
20	PRIOR FILING DATE: 1998-06-22
21	PRIOR APPLICATION NUMBER: 60/090349
22	PRIOR FILING DATE: 1998-06-23
23	PRIOR APPLICATION NUMBER: 60/090355
24	PRIOR FILING DATE: 1998-06-23
25	PRIOR APPLICATION NUMBER: 60/090429
26	PRIOR FILING DATE: 1998-06-24
27	PRIOR APPLICATION NUMBER: 60/090431
28	PRIOR FILING DATE: 1998-06-24
29	PRIOR APPLICATION NUMBER: 60/090435
30	PRIOR FILING DATE: 1998-06-24
31	PRIOR APPLICATION NUMBER: 60/090444
32	PRIOR FILING DATE: 1998-06-24
33	PRIOR APPLICATION NUMBER: 60/090445
34	PRIOR FILING DATE: 1998-06-24
35	PRIOR APPLICATION NUMBER: 60/090472
36	PRIOR FILING DATE: 1998-06-24
37	PRIOR APPLICATION NUMBER: 60/090535
38	PRIOR FILING DATE: 1998-06-24
39	PRIOR APPLICATION NUMBER: 60/090540
40	PRIOR FILING DATE: 1998-06-24
41	PRIOR APPLICATION NUMBER: 60/090542
42	PRIOR FILING DATE: 1998-06-24
43	PRIOR APPLICATION NUMBER: 60/090557
44	PRIOR FILING DATE: 1998-06-24
45	PRIOR APPLICATION NUMBER: 60/090676
46	PRIOR FILING DATE: 1998-06-25
47	PRIOR APPLICATION NUMBER: 60/090678
48	PRIOR FILING DATE: 1998-06-25
49	PRIOR APPLICATION NUMBER: 60/090690
50	PRIOR FILING DATE: 1998-06-25
51	PRIOR APPLICATION NUMBER: 60/090694
52	PRIOR FILING DATE: 1998-06-25
53	PRIOR APPLICATION NUMBER: 60/090695
54	PRIOR FILING DATE: 1998-06-25
55	PRIOR APPLICATION NUMBER: 60/090696
56	PRIOR FILING DATE: 1998-06-25
57	PRIOR APPLICATION NUMBER: 60/090862
58	PRIOR FILING DATE: 1998-06-26
59	PRIOR APPLICATION NUMBER: 60/090863
60	PRIOR FILING DATE: 1998-06-26
61	PRIOR APPLICATION NUMBER: 60/091360
62	PRIOR FILING DATE: 1998-07-01
63	PRIOR APPLICATION NUMBER: 60/091478
64	PRIOR FILING DATE: 1998-07-02
65	PRIOR APPLICATION NUMBER: 60/091544
66	PRIOR FILING DATE: 1998-07-01
67	PRIOR APPLICATION NUMBER: 60/091519
68	PRIOR FILING DATE: 1998-07-02
69	PRIOR APPLICATION NUMBER: 60/091626
70	PRIOR FILING DATE: 1998-07-02
71	PRIOR APPLICATION NUMBER: 60/091633
72	PRIOR FILING DATE: 1998-07-02
73	PRIOR APPLICATION NUMBER: 60/091978

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPDGGGAEGAEDLEV 23
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Db 52 ALAGWLRPDGGGAEGAEDLEV 74

RESULT 5
US-09-252-991A-27758
; Sequence 27758, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27758
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27758

Query Match 43.0%; Score 52; DB 4; Length 233;
Best Local Similarity 72.7%; Pred. No. 2.7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWLRPDGGGA 14
|||||
Db 203 GWLRPDGSGRA 213

RESULT 6
US-08-339-152A-17
; Sequence 17, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzil, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-152A-17

Query Match 41.3%; Score 50; DB 1; Length 634;
Best Local Similarity 76.9%; Pred. No. 16;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGOAEGAEDLEV 23
|||||
Db 213 GGRAEGEEDLEV 225

RESULT 7
US-08-339-152A-16
; Sequence 16, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzil, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-152A-16

Query Match 41.3%; Score 50; DB 1; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGOAEGAEDLEV 23
|||||
Db 233 GGRAEGEEDLEV 245

RESULT 8
US-08-007-999B-3
; Sequence 3, Application US/08007999B
; Patent No. 5851787
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/007,999B
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION NUMBER: US 07/930,022
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: 0609.3520002/JAG/GKT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-007-999B-3
Query Match 41.3%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 11 GGOAGGADELEV 23
||:|||||
Db 233 GGRAEGGEDEEV 245
RESULT 9
US-08-689-276A-3
; Sequence 3, Application US/08689276A
; Patent No. 5891991
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/689,276A
; FILING DATE: 06-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/007,999
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,022
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3520003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-689-276A-3
Query Match 41.3%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 11 GGOAGGADELEV 23
||:|||||
Db 233 GGRAEGGEDEEV 245
RESULT 10
US-08-039-198B-10
; Sequence 10, Application US/08039198B
; Patent No. 5858725
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/039,198B
; FILING DATE: 29-JUL-1993
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01744
; FILING DATE: 08-OCT-91
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-039-1988-10

Query Match 40.5%; Score 49; DB 2; Length 139;
Best Local Similarity 61.5%; Pred. No. 4.4;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGQAG 16
||: ||||| |
Db 68 GWIDPEDGGTKY 80

RESULT 11

US-09-252-991A-23604
; Sequence 23604, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23604
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-23604

Query Match 39.7%; Score 48; DB 4; Length 518;
Best Local Similarity 47.4%; Pred. No. 26;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 3 AGWLRPEDGGQAGADEL 21
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Db 412 AGWAQPEPGCGGCAERL 430

RESULT 12

US-09-252-991A-29700
; Sequence 29700, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29700
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-29700

Query Match 38.8%; Score 47; DB 4; Length 283;
Best Local Similarity 58.8%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 AGWLRPEDGGQAG 19
| |||| |
Db 86 AAGLRQEDGADGTGAED 102

RESULT 13

US-09-252-991A-27327
; Sequence 27327, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27327
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-27327

Query Match 38.0%; Score 46; DB 4; Length 341;
Best Local Similarity 52.4%; Pred. No. 33;
Matches 11; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

Qy 7 RPEDGGQAGAE----DELEV 23
: || ||| | : |
Db 181 QPEGGGQGEHAQADRPDHEV 201

RESULT 14

US-09-252-991A-19723
; Sequence 19723, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19723
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-19723

Query Match 38.0%; Score 46; DB 4; Length 428;
Best Local Similarity 55.0%; Pred. No. 42;
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDEL 21
 ||| ||| |:
 Db 293 LALWSLPEDPRPADWADEL 312

RESULT 15

US-09-252-991A-25921
 ; Sequence 25921, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25921
 ; LENGTH: 517
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25921

Query Match 38.0%; Score 46; DB 4; Length 517;
 Best Local Similarity 47.6%; Pred. No. 52;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDELE 22
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 Db 338 LAGLDPHPGIQAQCPHOQLQ 358

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 Job time : 7.14973 secs

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OM protein - protein search, using sw model

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(without alignments)
239.348 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 121

Sequence: 1 ALAGWLRPEDGGQAGAEDELEV 23

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	121	100.0	23	US-09-853-253-6	Sequence 6, Appli
3	121	100.0	24	US-09-853-253-4	Sequence 4, Appli
4	121	100.0	117	US-09-794-987-2	Sequence 2, Appli
5	121	100.0	117	US-09-853-253-2	Sequence 2, Appli
6	121	100.0	117	US-09-989-722-268	Sequence 268, App
7	121	100.0	117	US-09-989-723-268	Sequence 268, App
8	121	100.0	117	US-09-989-279-268	Sequence 268, App
9	121	100.0	117	US-09-989-727-268	Sequence 268, App
10	121	100.0	117	US-09-989-731-268	Sequence 268, App
11	121	100.0	117	US-09-989-732-268	Sequence 268, App
12	121	100.0	117	US-09-991-073-268	Sequence 268, App
13	121	100.0	117	US-09-990-442-268	Sequence 268, App
14	121	100.0	117	US-09-991-163-268	Sequence 268, App
15	121	100.0	117	US-09-993-604-268	Sequence 268, App

16	121	100.0	117	10	US-09-990-456-268	Sequence 268, App
17	121	100.0	117	10	US-09-989-721-268	Sequence 268, App
18	121	100.0	117	10	US-09-992-598-268	Sequence 268, App
19	121	100.0	117	10	US-09-989-293A-268	Sequence 268, App
20	121	100.0	117	10	US-09-989-735-268	Sequence 268, App
21	121	100.0	117	10	US-09-990-444-268	Sequence 268, App
22	121	100.0	117	10	US-09-991-181-268	Sequence 268, App
23	121	100.0	117	10	US-09-989-730-268	Sequence 268, App
24	121	100.0	117	10	US-09-990-436-268	Sequence 268, App
25	121	100.0	117	10	US-09-993-687-268	Sequence 268, App
26	121	100.0	117	11	US-09-989-734-268	Sequence 268, App
27	121	100.0	117	11	US-09-997-653-268	Sequence 268, App
28	121	100.0	117	11	US-09-993-667-268	Sequence 268, App
29	121	100.0	117	11	US-09-997-428-268	Sequence 268, App
30	121	100.0	117	11	US-09-997-666-268	Sequence 268, App
31	121	100.0	117	11	US-09-990-438-268	Sequence 268, App
32	121	100.0	117	11	US-09-990-562-268	Sequence 268, App
33	121	100.0	117	11	US-09-990-711-268	Sequence 268, App
34	121	100.0	117	11	US-09-989-726-268	Sequence 268, App
35	121	100.0	117	11	US-09-998-156-268	Sequence 268, App
36	121	100.0	117	11	US-09-990-437-268	Sequence 268, App
37	121	100.0	117	11	US-09-991-157-268	Sequence 268, App
38	121	100.0	117	11	US-09-997-514-268	Sequence 268, App
39	121	100.0	117	11	US-09-997-573-268	Sequence 268, App
40	121	100.0	117	11	US-09-991-172-268	Sequence 268, App
41	121	100.0	117	11	US-09-990-726-268	Sequence 268, App
42	121	100.0	117	11	US-09-997-559-268	Sequence 268, App
43	121	100.0	117	11	US-09-997-601-268	Sequence 268, App
44	121	100.0	117	11	US-09-990-443-268	Sequence 268, App
45	121	100.0	117	11	US-09-991-854-268	Sequence 268, App

ALIGNMENTS

RESULT 1
US-09-853-253-5
; Sequence 5, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-5

Query Match 100.0%; Score 121; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAGWLRPEDGGQAGAEDELEV 23
Db 1 ALAGWLRPEDGGQAGAEDELEV 23

RESULT 2
US-09-853-253-6
; Sequence 6, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN

1

Qy 1 ALAGWLRPEDGGQAEAGAEDELEV 23

Db 52 ALAGWLRPEDGGQAEGBDELEV 74

RESULT 6

US-09-989-722-268

; Sequence 268, Application US/09989722

; Patent No. US20020072067A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730PIC63

; CURRENT APPLICATION NUMBER: US/09/989,722

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

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; PRIOR APPLICATION NUMBER: 60/090246

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: 60/090252

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: 60/090254

RESULT 7
US-09-989-723-268
; Sequence 268, Application US/09989723
; Patent No.US20020072092A1

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;	PRIOR APPLICATION NUMBER:	60/088167
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7	PRIOR FILING DATE: 1998-07-02
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7	PRIOR FILING DATE: 1998-07-02
7	PRIOR APPLICATION NUMBER: 60/091978
7	PRIOR FILING DATE: 1998-07-07
7	PRIOR APPLICATION NUMBER: 60/091982
7	PRIOR FILING DATE: 1998-07-07
7	PRIOR APPLICATION NUMBER: 60/092182
7	PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 121; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels

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Db	52	ALAGWLRPEDGGQGAEGAEDELEV
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RESULT 8
US-09-989-279-268
; Sequence 268, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: ASHkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrari, Napoleone

```

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerbitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
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Query Match 100.0%; Score 121; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-989-727-268
; Sequence 268, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10

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; Sequence 268, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
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Query Match 100.0%; Score 121; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.2e-09; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11

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 ; Sequence 268, Application US/09989732
 ; Patent No. US20020123463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730P1C57

; CURRENT APPLICATION NUMBER: US/09/989,732
 ; CURRENT FILING DATE: 2001-11-19
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;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR APPLICATION NUMBER: 60/091626
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;;
Query Match 100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred No. 4, 2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;;
QY 1 ALAGWLRPEDGGGAEGAEDELEV 23
Db 52 ALAGWLRPEDGGGAEGAEDELEV 74
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RESULT 12
US-09-991-073-268
;; Sequence 268, Application US/09991073
;; Patent No. US20020127576A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC15
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186

1	PRIOR APPLICATION NUMBER: 60/089514
2	PRIOR FILING DATE: 1998-06-16
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4	PRIOR FILING DATE: 1998-06-17
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6	PRIOR FILING DATE: 1998-06-17
7	PRIOR APPLICATION NUMBER: 60/089598
8	PRIOR FILING DATE: 1998-06-17
9	PRIOR APPLICATION NUMBER: 60/089599
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11	PRIOR APPLICATION NUMBER: 60/089600
12	PRIOR FILING DATE: 1998-06-17
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25	PRIOR APPLICATION NUMBER: 60/089952
26	PRIOR FILING DATE: 1998-06-19
27	PRIOR APPLICATION NUMBER: 60/090246
28	PRIOR FILING DATE: 1998-06-22
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30	PRIOR FILING DATE: 1998-06-22
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34	PRIOR FILING DATE: 1998-06-23
35	PRIOR APPLICATION NUMBER: 60/090355
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40	PRIOR FILING DATE: 1998-06-24
41	PRIOR APPLICATION NUMBER: 60/090435
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43	PRIOR APPLICATION NUMBER: 60/090444
44	PRIOR FILING DATE: 1998-06-24
45	PRIOR APPLICATION NUMBER: 60/090445
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54	PRIOR FILING DATE: 1998-06-24
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56	PRIOR FILING DATE: 1998-06-24
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62	PRIOR FILING DATE: 1998-06-25
63	PRIOR APPLICATION NUMBER: 60/090694
64	PRIOR FILING DATE: 1998-06-25
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67	PRIOR APPLICATION NUMBER: 60/090696
68	PRIOR FILING DATE: 1998-06-25
69	PRIOR APPLICATION NUMBER: 60/090862
70	PRIOR FILING DATE: 1998-06-26
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72	PRIOR FILING DATE: 1998-06-26
73	PRIOR APPLICATION NUMBER: 60/091360

;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAGAEDELEV 23
Db 52 ALAGWLRPDGGQAGAEDELEV 74

RESULT 13
US-09-990-442-268
; Sequence 268, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25

;; PRIOR APPLICATION NUMBER: 60/078910
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;; PRIOR FILING DATE: 1998-04-28
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;; PRIOR FILING DATE: 1998-05-07
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; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score
Best Local Similarity 100.0%; Pred.
Matches 23; Conservative

QY 1 ALAGWLRLPDDGQAGAEDELEV 23
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Db 52 ALAGWLRLPDDGQAGAEDELEV 74
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RESULT 14
US-09-991-163-268
; Sequence 268, Application US/09991163
; Patent No. US2002013253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napter, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Trans
; TITLE OF INVENTION: Acids Encoding th
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/0495787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106

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;	PRIOR APPLICATION NUMBER:	60/089801
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;	PRIOR FILING DATE:	1998-06-26
;	PRIOR APPLICATION NUMBER:	60/091360
;	PRIOR FILING DATE:	1998-07-01
;	PRIOR APPLICATION NUMBER:	60/091478
;	PRIOR FILING DATE:	1998-07-02
;	PRIOR APPLICATION NUMBER:	60/091544
;	PRIOR FILING DATE:	1998-07-01
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;	PRIOR APPLICATION NUMBER:	60/091633
;	PRIOR FILING DATE:	1998-07-02
;	PRIOR APPLICATION NUMBER:	60/091978
;	PRIOR FILING DATE:	1998-07-07
;	PRIOR APPLICATION NUMBER:	60/091982

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%   Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. NO. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      52 ALAGWLRPDGGQGAEGAEDELEV 74

RESULT 15
US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
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1 PRIOR FILING DATE: 1998-06-19
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5 PRIOR FILING DATE: 1998-06-19
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7 PRIOR FILING DATE: 1998-06-22
8 PRIOR APPLICATION NUMBER: 60/090252
9 PRIOR FILING DATE: 1998-06-22
10 PRIOR APPLICATION NUMBER: 60/090254
11 PRIOR FILING DATE: 1998-06-22
12 PRIOR APPLICATION NUMBER: 60/090349
13 PRIOR FILING DATE: 1998-06-23
14 PRIOR APPLICATION NUMBER: 60/090355
15 PRIOR FILING DATE: 1998-06-23
16 PRIOR APPLICATION NUMBER: 60/090429
17 PRIOR FILING DATE: 1998-06-24
18 PRIOR APPLICATION NUMBER: 60/090431
19 PRIOR FILING DATE: 1998-06-24
20 PRIOR APPLICATION NUMBER: 60/090435
21 PRIOR FILING DATE: 1998-06-24
22 PRIOR APPLICATION NUMBER: 60/090444
23 PRIOR FILING DATE: 1998-06-24
24 PRIOR APPLICATION NUMBER: 60/090445
25 PRIOR FILING DATE: 1998-06-24
26 PRIOR APPLICATION NUMBER: 60/090472
27 PRIOR FILING DATE: 1998-06-24
28 PRIOR APPLICATION NUMBER: 60/090535
29 PRIOR FILING DATE: 1998-06-24
30 PRIOR APPLICATION NUMBER: 60/090540
31 PRIOR FILING DATE: 1998-06-24
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34 PRIOR APPLICATION NUMBER: 60/090557
35 PRIOR FILING DATE: 1998-06-24
36 PRIOR APPLICATION NUMBER: 60/090676
37 PRIOR FILING DATE: 1998-06-25
38 PRIOR APPLICATION NUMBER: 60/090678
39 PRIOR FILING DATE: 1998-06-25
40 PRIOR APPLICATION NUMBER: 60/090690
41 PRIOR FILING DATE: 1998-06-25
42 PRIOR APPLICATION NUMBER: 60/090694
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44 PRIOR APPLICATION NUMBER: 60/090695
45 PRIOR FILING DATE: 1998-06-25
46 PRIOR APPLICATION NUMBER: 60/090696
47 PRIOR FILING DATE: 1998-06-25
48 PRIOR APPLICATION NUMBER: 60/090862
49 PRIOR FILING DATE: 1998-06-26
50 PRIOR APPLICATION NUMBER: 60/090863
51 PRIOR FILING DATE: 1998-06-26
52 PRIOR APPLICATION NUMBER: 60/091360
53 PRIOR FILING DATE: 1998-07-01
54 PRIOR APPLICATION NUMBER: 60/091478
55 PRIOR FILING DATE: 1998-07-02
56 PRIOR APPLICATION NUMBER: 60/091544
57 PRIOR FILING DATE: 1998-07-01
58 PRIOR APPLICATION NUMBER: 60/091519
59 PRIOR FILING DATE: 1998-07-02
60 PRIOR APPLICATION NUMBER: 60/091626
61 PRIOR FILING DATE: 1998-07-02
62 PRIOR APPLICATION NUMBER: 60/091633
63 PRIOR FILING DATE: 1998-07-02
64 PRIOR APPLICATION NUMBER: 60/091978
65 PRIOR FILING DATE: 1998-07-07
66 PRIOR APPLICATION NUMBER: 60/091982
67 PRIOR FILING DATE: 1998-07-07
68 PRIOR APPLICATION NUMBER: 60/092182
69 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 121; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGQAEDELEV 74

Search completed: September 11, 2003, 17:48:33
Job time : 15.0214 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 : Search time 3.32086 Seconds
(without alignments)
325.703 Million cell updates/sec

Title: US-09-853-253-6
Perfect score: 121
Sequence: 1 ALAGWLPRPDGGQAEGBEDEV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	121	100.0	117	1	GHRL_HUMAN		Q9ubu3 homo sapien
2	90	74.4	117	1	GHRL_RAT		Q9dyh7 rattus norv
3	87	71.9	118	1	GHRL_PIG		Q9gky5 sus scrofa
4	86	71.1	117	1	GHRL_MOUSE		Q9eqx0 mus musculu
5	72	59.5	116	1	GHRL_BOVIN		Q9bdj6 bos taurus
6	68	56.2	117	1	GHRL_CANFA		Q9bef8 canis faml
7	54	44.6	200	1	NUPL_XENLA		P05221 xenopus lae
8	51	42.1	91	1	ACYP_BACSU		Q35031 bacillus su
9	50	41.3	653	1	APPL_MOUSE		Q03157 mus musculu
10	48	39.7	300	1	NKX1_BISBI		O46383 bison bison
11	48	39.7	668	1	SYM_METKA		O8tx28 methanopyru
12	48	39.7	1216	1	NKX1_BOVIN		Q28i39 bos taurus
13	47	38.8	380	1	OPRK_CAVPO		P41144 cavia porce
14	47	38.8	1168	1	DDX8_ARATH		Q38953 arabidopsis
15	45.5	37.6	580	1	MM14_PIG		Q9xt90 sus scrofa
16	45.5	37.6	582	1	MM14_HUMAN		P50281 homo sapien
17	45.5	37.6	582	1	MM14_MOUSE		P53690 mus musculu
18	45.5	37.6	582	1	MM14_RAT		Q10739 rattus norv
19	45.5	37.6	591	1	PAXI_HUMAN		P49023 homo sapien
20	45	37.2	190	1	RS9A_SCHPO		Q09757 schizosacch
21	45	37.2	242	1	HAP5_YEAST		Q02516 saccharomyc
22	45	37.2	494	1	KCF1_HUMAN		Q9h3m0 homo sapien
23	45	37.2	544	1	PRG_DEIRA		Q9ru23 deinococcus
24	45	37.2	992	1	SNXJ_HUMAN		Q92543 homo sapien
25	45	37.2	1059	1	SPS_VICFA		Q43876 vicia faba
26	44.5	36.8	777	1	RGL2_HUMAN		O15211 homo sapien
27	44.5	36.8	1233	1	VLI_REOVD		P15024 reovirus (t
28	44	36.4	115	1	INS_VERMO		Q9w7r2 verasper mo
29	44	36.4	168	1	TCTP_BRAOL		Q944w6 brassica ol
30	44	36.4	273	1	NK22_MOUSE		P42586 mus musculu
31	44	36.4	449	1	CMGA_BOVIN		P05059 bos taurus
32	44	36.4	4447	1	PKSK_BACSU		P40803 bacillus su
33	43.5	36.0	525	1	SYK_DEIRA		Q9rxel deinococcus

ALIGNMENTS

RESULT 1

ID	GHRL_HUMAN	STANDARD;	PRT;	117 AA.
AC	Q9UBU3; Q8TAT9; Q9H3R3;			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).			
DE	releasing peptide) (Motilin-related peptide) (M46 protein).			
GN	GHRL OR MTLRP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.			
RX	MEDLINE=20067959; PubMed=10604470;			
RA	Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;			
RT	"Ghrelin is a growth-hormone-releasing acylated peptide from stomach."			
RL	Nature 402:656-660(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Kojima M.;			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Stomach;			
RA	Tomasetto C., Karam S.M., Rio M.-C.;			
RT	"Identification of a novel gastric protein m46.";			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Wajhrach M.P., Ten I.S., Gertner J.M., Leibel R.L.;			
RT	"Genomic organization of the human Ghrelin gene.";			
RL	J. Endocrinol. Genet. 1:231-233(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Blood;			
RX	MEDLINE=22388957; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			

Q95220 oryctolagus
Q9d5v6 mus musculu
P41145 homo sapien
Q8pnz5 xanthomonas
P16230 oryctolagus
P96142 thermus the
P29376 homo sapien
P54423 bacillus su
P38631 saccharomyc
P01341 lophius pis
P05019 homo sapien
P27484 nicotiana s

34 43.5 36.0 582 1 MM14_RABIT
35 43 35.5 365 1 SYAP_MOUSE
36 43 35.5 380 1 OPRK_HUMAN
37 43 35.5 579 1 SYQ_XANAC
38 43 35.5 852 1 SRCH_RABIT
39 43 35.5 862 1 SYV_THETH
40 43 35.5 864 1 KLTK_HUMAN
41 43 35.5 894 1 WPRB_BACSU
42 43 35.5 1876 1 GLS1_YEAST
43 42.5 35.1 116 1 INS_LOPPI
44 42.5 35.1 195 1 IGFB_HUMAN
45 42.5 35.1 214 1 GRP2_NICSY

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [6]
RQ SEQUENCE OF 24-33.
RX TISSUE=Stomach;
RY MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide
RL hormone: the motilin-related peptide.";
RN Gastroenterology 119:395-405(2000).
RP [7]
RQ REVIEW.
RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RL hormone secretagogue receptor.";
RN Trends Endocrinol. Metab. 12:118-122(2001).
RQ -1- FUNCTION: Specific ligand for the growth hormone secretagogue
RX receptor type 1 (GHSR) inducing the release of growth hormone from
RA the pituitary. Has an appetite-stimulating effect, induces
RT adiposity and stimulates gastric acid secretion. Involved in
RL growth regulation.
RN -1- SUBCELLULAR LOCATION: Secreted.
RQ -1- ALTERNATIVE PRODUCTS:
RX Event-Alternative splicing; Named isoforms=2;
RA Name=1; Synonyms=ghrelin;
RY IsoId=Q9UBU3-1; Sequence=Displayed;
RQ Name=2; Synonyms=del-Gln14-ghrelin;
RX IsoId=Q9UBU3-2; Sequence=VSP_003245;
RA -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
RQ -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
RX WWW="http://www.infobiogen.fr/services/chronocancer/Genes/GhrelinID327.html".
RQ -----
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RA or send an email to license@isb-sib.ch).
RQ -----
RX EMBL: AB029434; BAA89371.1; -
DR EMBL: AB035700; BAB19045.1; -
DR EMBL: AJ252278; CAB65733.1; -
DR EMBL: AF296558; AAG10300.1; -
DR EMBL: BC025791; AAH25791.1; -
DR PIR: A59316; AAH25791.1; -
DR MIM: 605353; -
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0005625; C:soluble fraction; TAS.
DR GO: GO:0005131; F:growth hormone receptor ligand activity; TAS.
DR GO: GO:0007467; P:cell-cell signaling; TAS.
DR GO: GO:0007186; P:G-protein coupled receptor protein signaling. . .; TAS.
DR InterPro: IPR006737; motilin_assoc.
DR InterPro: IPR006738; motilin_ghrelin.
DR InterPro: IPR005441; Preproghrelin.
DR Pfam: PF04643; motilin_assoc; 1.
DR Pfam: PF04644; motilin_ghrelin; 1.
DR PRINTS: PR01624; GHRELIN.
DR PRODOM: PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
FT Alternative splicing.
FT SIGNAL 1 23
FT PEPTIDE 24 51 GHRELIN.
FT PROPEP 52 117 REMOVED IN MATURE FORM.
FT LIPID 26 26 N-OCTANOATE.
FT VARSPLIC 37 37 Missing (in isoform 2).
FT /FTId=VSP_003245.
FT CONFLICT 72 72 L -> M (IN REF. 5).

SQ SEQUENCE 117 AA; 12911 MW; 39C0572BECA2755 CRC64;
Query Match 100.0%; Score 121; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ALAGWLRPEDGGQAGAEDELEV 23
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEV 74
RESULT 2
GHRL_RAT
ID GHRL_RAT STANDARD; PRT; 117 AA.
AC Q9QYH7; O9ET69;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide).
GN GHRL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,
RP AND ACYLATION OF SER-26.
RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from
RT stomach.";
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS
RP SPECTROMETRY, AND ACYLATION OF SER-26.
RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX MEDLINE=20357315; PubMed=10801861;
RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT "Purification and characterization of rat des-Gln14-ghrelin, a second
RT endogenous ligand for the growth hormone secretagogue receptor.";
RL J. Biol. Chem. 275:21995-22000(2000).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=21092536; PubMed=11162448;
RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
RT in gastrointestinal tissue.";
RL Biochem. Biophys. Res. Commun. 279:909-913(2000).
RN [4]
RP STRUCTURE-ACTIVITY RELATIONSHIP.
RX MEDLINE=21433488; PubMed=11549267;
RA Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
RT "Structure-activity relationship of ghrelin: pharmacological study of
RT ghrelin peptides.";
RL Biochem. Biophys. Res. Commun. 287:142-146(2001).
RN [5]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RL hormone secretagogue receptor.";
RN Trends Endocrinol. Metab. 12:118-122(2001).
RQ -1- FUNCTION: Specific ligand for the growth hormone secretagogue
RX receptor type 1 (GHSR) inducing the release of growth hormone from
RA the pituitary. Has an appetite-stimulating effect, induces
RT adiposity and stimulates gastric acid secretion. Involved in
RL growth regulation.
RN -1- SUBCELLULAR LOCATION: Secreted.
RQ -1- ALTERNATIVE PRODUCTS:
RX Event-Alternative splicing; Named isoforms=2;


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CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9QYH7-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9QYH7-2; Sequence=VSP_003248;
CC TISSUE SPECIFICITY: Broadly expressed with higher expression in
CC the stomach. Very low levels are detected in the hypothalamus,
CC heart, lung, pancreas, intestine and adipose tissue.
CC -! PTM: O-n-octanoylation is essential for activity. The replacement
CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.
CC -! MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;
CC RANGE=24-51.
CC -! MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;
CC RANGE=24-36, 38-51.
CC -! SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; AB029433; BAA89370.1; -;
CC EMBL; AB035699; BAB11956.1; -;
CC PIR; B59316; B59316.
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc; 1.
CC Pfam; PF04644; motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN.
CC ProDom; PD332162; Preproghrelin; 1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
KW SIGNAL 1 23
FT PEPTIDE 24 51 GHRELIN.
FT PROPEP 52 117 REMOVED IN MATURE FORM.
FT LIPID 26 26 N-OCTANOATE.
FT VARSPLIC 37 37 Missing (in isoform 2).
FT /FTID=VSP_003248.
SQ SEQUENCE 117 AA; 13176 MW; 8857546FE51A7691 CRC64;

Query Match 74.4%; Score 90; DB 1; Length 117;
Best Local Similarity 73.9%; Pred. No. 4.1e-06;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
DB 52 ALEGWLHPDRGQAEAEDELEI 74

RESULT 3
GHRL_PIG
ID GHRL_PIG STANDARD; PRT; 118 AA.
AC Q9GKY5; Q9BDG8; Q9GKY4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide).
GN GHRL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Stomach;

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RA Rousselle J., Lacroix D., Dubreuil P.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -! SUBCELLULAR LOCATION: Secreted (By similarity).
CC -! ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9GKY5-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9GKY5-2; Sequence=VSP_003247;
CC -! PTM: O-n-octanoylation is essential for activity (By similarity).
CC -! SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB035703; BAB19048.1; -;
CC EMBL; AB035704; BAB19049.1; -;
CC EMBL; AF308930; AAK19243.1; -;
CC EMBL; AY028942; AAK30002.1; -;
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc; 1.
CC Pfam; PF04644; motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN.
CC ProDom; PD332162; Preproghrelin; 1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
KW SIGNAL 1 24 BY SIMILARITY.
FT PEPTIDE 25 52 GHRELIN.
FT PROPEP 53 118 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 27 27 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC 38 38 Missing (in isoform 2).
FT /FTID=VSP_003247.
FT CONFLICT 17 17 L -> P (IN REF. 2; AAK30002).
FT CONFLICT 72 72 K -> E (IN REF. 2; AAK30002).
SQ SEQUENCE 118 AA; 12785 MW; 85603E1D6DAB1A76 CRC64;

Query Match 71.9%; Score 87; DB 1; Length 118;
Best Local Similarity 65.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
DB 53 ALEGWLGPDSGEVEGTEKLEI 75

RESULT 4
GHRL_MOUSE
ID GHRL_MOUSE STANDARD; PRT; 117 AA.
AC Q9EQX0; Q9WU21;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRL OR MTLRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
RP

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CC TISSUE=Stomach;
RX MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide
RL hormone: the motilin-related peptide.";
RN Gastroenterology 119:395-405(2000).
RP [2]
RA Kojima M.;
RA "Mouse mRNA for preproghrelin.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RA SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gajobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RL hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
CC -1- RECEPTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC Name=2; Synonyms=del-gln14-ghrelin;
CC IsoId=Q9EQX0-1; Sequence=Displayed;
CC IsoId=Q9EQX0-2; Sequence=VSP_003246;
CC -1- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
CC with higher levels in the stomach, medium levels in the duodenum,
CC jejunum, ileum and colon. Low expression in the testis and brain.
CC Not detected in the salivary gland, pancreas, liver and lung.
CC -1- PPM: O-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC
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CC
CC EMBL; AJ243503; CAB46500.1; -
CC EMBL; AB035701; BAB19046.1; -
CC EMBL; AB060078; BAB69857.1; -
CC EMBL; AK008658; BAB25814.1; -
CC EMBL; AK008860; BAB25934.1; -
CC MGD; MGI:1930008; Ghrl.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005576; C:extracellular; IDA.
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin-ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc; 1.
CC Pfam; PF04644; motilin-ghrelin; 1.
CC PRINTS; PR01624; GHRELIN.
CC PRODOM; PD332162; Preproghrelin; 1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23 GHRELIN
FT PEPTIDE 24 51 REMOVED IN MATURE FORM (BY SIMILARITY).
FT PROPEP 52 117 N-OCTANOATE (BY SIMILARITY).
FT LIPID 26 26 Missing (in isoform 2).
FT VARSPLIC 37 37 /FTID=VSP_003246.
FT SQ SEQUENCE 117 AA; 13207 MW; EACBA49D2E3CA7203 CRC64;
Query Match 71.18; Score 86; DB 1; Length 117;
Best Local Similarity 69.68; Pred. No. 1.5e-05;
Matches 16; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ALAGWLRPEDGGGAEGAEDELEV 23
Db 52 ALEGWLHPEDRGQAEEETELEEI 74
RESULT 5
GHRL_BOVIN STANDARD; PRT; 116 AA.
AC Q9BDJ6; Q9GKV6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ghrelin precursor (growth hormone secretagogue) (growth hormone
DE releasing peptide).
GN GHRL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Kita K., Harada K., Yokota H.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-99 FROM N.A.
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- PPM: O-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC
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CC -----
DR EMBL: AF350329; AAK18612.1; -.
DR EMBL: AB035702; BAB19047.1; -.
DR InterPro: IPR006737; motilin_ghrelin.
DR InterPro: IPR005441; Preproghrelin.
DR Pfam: PF04643; motilin_ghrelin; 1.
DR PRINTS: PR01624; GHRELIN.
DR ProDom: PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 50 GHRELIN (BY SIMILARITY).
FT PROPEP 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT CONFLICT 34 34 K -> E (IN REF. 2).
SQ SEQUENCE 116 AA; 12792 MW; F55536DAC3FA59B6 CRC64;

Query Match 59.5%; Score 72; DB 1; Length 116;
Best Local Similarity 68.2%; Pred. No. 0.0015;
Matches 15; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDELEV 23
   | | | | | | | | | | | | | |
Db 52 LKQFDPVGVGQAGAEDELEI 73

RESULT 6
GHRL_CANFA
ID GHRL_CANFA STANDARD; PRT; 117 AA.
AC Q9BEF8; Q9BEF7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
  releasing peptide) (Motilin-related peptide).
GN GHRL OR MTLRP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Gastric fundus;
RA Tomasetto C., Wendling C., Rio M.-C., Poltras P.;
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
  fundus."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
  receptor type 1 (GHSR) inducing the release of growth hormone from
  the pituitary. Has an appetite-stimulating effect, induces
  adiposity and stimulates gastric acid secretion. Involved in
  growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9BEF8-1; Sequences=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9BEF8-2; Sequences=VSP_003244;
CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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  or send an email to license@lsb-sib.ch).
CC EMBL: AJ298295; CAC29155.1; -.

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DR EMBL: AJ298296; CAC29156.1; -.
DR InterPro: IPR006737; motilin_ghrelin.
DR InterPro: IPR005441; Preproghrelin.
DR Pfam: PF04643; motilin_ghrelin; 1.
DR PRINTS: PR01624; GHRELIN.
DR ProDom: PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC 37 37 Missing (in isoform 2).
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Query Match 56.2%; Score 68; DB 1; Length 117;
Best Local Similarity 65.2%; Pred. No. 0.0058;
Matches 15; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23
   | | | | | | | | | | | | | |
Db 52 ALEGLSPEDTSQVGEAEDELEI 74

RESULT 7
NUPL_XENLA
ID NUPL_XENLA STANDARD; PRT; 200 AA.
AC P05221;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nucleoplasmin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218476; PubMed=2884102;
RA Dingwall C., Dillworth S.M., Black S.J., Kearsley S.E., Cox L.S.,
RA Laskey R.A.;
RT "Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and a
  cluster of sequences homologous to putative nuclear localization
  signals."
RT signals."
RL EMBO J. 6:69-74(1987).
RN [2]
RP SEQUENCE OF 7-200 FROM N.A.
RX MEDLINE=88112783; PubMed=3428591;
RA Buergrlin T.R., Mattaj J.W., Newmeyer D.D., Zeller R.,
RA de Robertis E.M.;
RT "Cloning of nucleoplasmin from Xenopus laevis oocytes and analysis of
  its developmental expression."
RL Genes Dev. 1:97-107(1987).
CC -1- FUNCTION: NUCLEOPLASMIN IS AN ACIDIC, PENTAMERIC, THERMOSTABLE
  PROTEIN WHICH IS ABLE TO ASSEMBLE NUCLEOSOMES BY BINDING HISTONES
  AND TRANSFERRING THEM TO DNA.
CC -1- SUBUNIT: Homopentamer.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.
CC -----
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CC EMBL: X04766; CAA28460.1; -.

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DR EMBL; Y00204; CAA68363.1; -
 DR PIR; A26169;
 DR PDB; 1EE5; 26-SEP-01.
 DR PDB; 1EJY; 24-APR-00.
 DR PDB; 1K5J; 21-NOV-01.
 DR InterPro; IPR004301; Nucleoplasmalmin.
 DR Pfam; PF03066; Nucleoplasmalmin; 1.
 KW Nuclear protein; Phosphorylation; 3D-structure.
 FT DOMAIN 138 145 POLY-GLU (PROBABLE HISTONE BINDING SITE).
 FT CONFLICT 11 11 L -> V (IN REF. 2).
 FT CONFLICT 27 27 D -> N (IN REF. 2).
 FT CONFLICT 31 31 E -> A (IN REF. 2).
 FT CONFLICT 34 34 V -> I (IN REF. 2).
 FT CONFLICT 61 61 N -> H (IN REF. 2).
 FT CONFLICT 72 72 A -> K (IN REF. 2).
 FT CONFLICT 75 75 S -> P (IN REF. 2).
 FT CONFLICT 80 80 T -> S (IN REF. 2).
 FT CONFLICT 111 111 L -> V (IN REF. 2).
 FT CONFLICT 134 137 MISSING (IN REF. 2).
 FT CONFLICT 147 147 Q -> P (IN REF. 2).
 SQ SEQUENCE 200 AA; 22023 MW; A91DD110F2965812 CRC64;
 Query Match 44.6%; Score 54; DB 1; Length 200;
 Best Local Similarity 55.6%; Pred. No. 1;
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Qy 5 WLRPEDGGQAFGEDELE 22
 Db 126 WAEEDEGEAGEEEEE 143
 RESULT 8
 ID ACYP_BACSU STANDARD; PRT; 91 AA.
 AC O35031;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative acylphosphatase (EC 3.6.1.7) (Acylphosphate
 DE phosphohydrolase).
 GN YFLL.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AC327;
 RC MEDLINE=97417488; PubMed=9272861;
 RX Yamamoto H., Uchiyama S., Nigroho F.A., Sekiguchi J.;
 RA "Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region
 RT of the Bacillus subtilis genome reveal genes for a new two-component
 RT system, three spore germination proteins, an iron uptake system and a
 RT general stress response protein."
 RL Gene 194:191-199(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RC MEDLINE=98044033; PubMed=9384377;
 RX Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Entian K.D., Errington J., Fabbret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandl G.,
 RA Gulseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis".
 RL Nature 390:249-256(1997).
 CC -1- CATALYTIC ACTIVITY: An acyl phosphate + H(2)O -> a fatty acid anion
 CC + phosphate.
 CC -1- SIMILARITY: BELONGS TO THE ACYLPHOSPHATASE FAMILY.
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 DR EMBL; D86417; BAA22305.1; -
 DR EMBL; Z98108; CAB12593.1; -
 DR PIR; B69811; B69811.
 DR HSP; P00818; IAPS.
 DR Subtilist; BG12947; yfll.
 DR InterPro; IPR01792; Acylphosphatase.
 DR Pfam; PF00708; Acylphosphatase; 1.
 DR PRINTS; PR00112; ACYLPHPHATASE.
 DR ProDom; PD001884; Acylphosphatase; 1.
 DR PROSITE; PS00150; ACYLPHOSPHATASE_1; 1.
 DR PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.
 KW Hypothetical protein; Hydrolase; Complete proteome.
 SQ SEQUENCE 91 AA; 10318 MW; 50795631BF3310F4 CRC64;
 Query Match 42.1%; Score 51; DB 1; Length 91;
 Best Local Similarity 44.0%; Pred. No. 1.2;
 Matches 11; Conservative 5; Mismatches 5; Indels 4; Gaps 1;
 Qy 2 LAGWLRPEDGGQ----AEGAEDELE 22
 Db 30 LAGWVKRRDDGRVEILAEGPENALQ 54
 RESULT 9
 ID APPL_MOUSE STANDARD; PRT; 653 AA.
 AC Q03157; Q8VC38;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
 GN APLP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=93066322; PubMed=1279693;
 RX Masco W., Bupp K., Magendanz M., Gusella J.F., Tanzi R.E.,
 RA Solomon F.;
 RA "Identification of a mouse brain cDNA that encodes a protein related
 RT to the Alzheimer disease-associated amyloid beta protein precursor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).

RN [2] SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP COLLAGEN-BINDING.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I";
 RL J. Biol. Chem. 271:1613-1620(1996).
 RN [4]
 RP INTERACTION WITH DAB1.
 RX MEDLINE=99389880; PubMed=10460257;
 RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
 RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
 RT protein 1";
 RL J. Neurosci. 19:7507-7515(1999).
 RN [5]
 RP INTERACTION WITH MAPK8IP1.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niihara T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/Islet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [6]
 RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APPB1, AND MUTAGENESIS OF
 RP TYR-641.
 RX MEDLINE=22313598; PubMed=12228233;
 RA Scheinfeld M.H., Gherzi E., Laky K., Fowlkes B.J., D'Adamo L.;
 RA "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
 RA secretase regulates transcription";
 RL J. Biol. Chem. 277:44195-44201(2002).
 CC -1- FUNCTION: May play a role in postsynaptic function. The C-terminal
 CC gamma-secretase processed fragment, ALIDI, activates transcription
 CC activation through APPB1 (Re65) binding. Couples to JIP signal
 CC transduction through C-terminal binding. May interact with
 CC cellular G-protein signaling pathways. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I.
 CC -1- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
 CC neuronal apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APPB and APBA family members,
 CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
 CC serine phosphorylation.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
 CC processed in the Golgi complex.
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-

CC terminal to the NPXY motif are often required for complete
 CC interaction. The NPXY site is also involved in clathrin-mediated
 CC endocytosis.
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal
 CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
 CC similarity).
 CC -1- PTM: N-glycosylated.
 CC -1- PTM: O-glycosylated.
 CC -1- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
 CC Zinc-binding increases heparin binding. No Cu(II) reducing
 CC activity with copper-binding.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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 CC -----
 CC EMBL; L04538; AAA37247.1; -;
 CC EMBL; BC021877; AAH21877.1; -;
 CC PIR; A46362; A46362.
 CC HSP; P05067; 1MWP.
 CC MGD; MGI:88046; Aipl1.
 CC InterPro: IPR001868; A4_APP.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC PRINTS; PR00203; AMYLOIDA4.
 CC SMART; SM00006; A4_EXTRA; 1.
 CC PROSITE; PS00319; A4_EXTRA; 1.
 CC PROSITE; PS00320; A4_INTRA; 1.
 CC KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
 KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
 KW Glycoprotein.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 653 AMYLOID-LIKE PROTEIN 1.
 FT CHAIN 624 653 C30 (BY SIMILARITY).
 FT DOMAIN 38 583 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 584 606 POTENTIAL.
 FT DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 157 177 COPPER-BINDING.
 FT DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 263 271 POLY-GLU.
 FT DOMAIN 535 538 POLY-SER.
 FT DOMAIN 601 606 POLY-LEU.
 FT SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY
 FT SIMILARITY).
 FT SITE 607 618 BASOLATERAL SORTING SIGNAL (BY
 FT SIMILARITY).
 FT SITE 623 624 CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
 FT SITE 641 644 ENDOCYTOSIS SIGNAL.
 FT SITE 643 646 NPXY MOTIF.
 FT CARBOHYD 464 464 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 554 554 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOTIF 641 641 Y->G: REDUCED BINDING OF APBBL.
 FT CONFLICT 17 17 P -> PP (IN REF. 2).
 SQ SEQUENCE 653 AA; 72750 MW; 56516DC3EA40E4B0 CRC64;
 Query Match 41.3%; Score 50; DB 1; Length 653;
 Best Local Similarity 76.9%; Pred. No. 12;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 11 GGQAGGADEDELEV 23
 ||:||| ||| ||
 Db 233 GGRAGGEDDEEV 245
 RESULT 10
 NKX1_BISBI

```
ID NKX1_BISBI STANDARD PRT; 300 AA.
AC O46383;
AT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 (Na(+)/K(+)/Ca(2+)-
DE exchange protein 1) (Retinal rod Na-Ca+K exchanger) (Fragment).
GN SLC24A1 OR NCKX1.
OS Bison bison (American bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bison.
OX NCBI_TaxID=9901;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98138491; PubMed=9478004;
RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison
RT with a revised bovine sequence.";
RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
CC -1- FUNCTION: Critical component of the visual transduction cascade,
CC controlling the calcium concentration of outer segments during
CC light and darkness. Light causes a rapid lowering of cytosolic
CC free calcium in the outer segment of both retinal rod and cone
CC photoreceptors and the light-induced lowering of calcium is caused
CC by extrusion via this protein which plays a key role in the
CC process of light adaptation. Transports one Ca(2+) and one K(+) in
CC exchange for four Na(+) (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
-----
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-----
DR EMBL; AF025480; AAC13320.1; -
KW Vision; transport; Antiport; Symport; Calcium transport;
KW Potassium transport; Sodium transport; Transmembrane.
FT NON_TER 1
FT TRANSMEM 259 275 POTENTIAL.
FT DOMAIN 218 242 POLY-GLU.
FT NON_TER 300 300
FT SEQUENCE 300 AA; 31671 MW; 2BE592DA5AB9781E CRC64;
Query Match 39.7%; Score 48; DB 1; Length 300;
Best Local Similarity 45.0%; Pred. No. 11;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Qy 4 GWLPEGGGAGAEDELEV 23
I :: :||: || ||| :|
Db 84 GEIQAGEGEGEVEGEDEGEI 103
RESULT 11
SYM_METKA STANDARD PRT; 668 AA.
AC Q8TX28;
AT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
DE (MetrS).
OS Methanopyrus kandleri.
OS Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozayavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -1- FUNCTION: is required not only for elongation of protein synthesis
CC but also for the initiation of all mRNA translation through
CC initiator tRNA(fMet) aminoacylation (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) -> AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC MetG subfamily 1.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
-----
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-----
DR EMBL; AE010375; AAM02063.1; -
DR HAMAP; MF_00098; fused; 1.
DR InterPro; IPR004495; MetG_Cterm.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002304; tRNA-synt_met.
DR InterPro; IPR002547; tRNA_bind.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR Pfam; PF01588; tRNA_bind; 1.
DR PIRSF; PIRSF001528; MetRS_dimerising; 1.
DR TIGRFAMs; TIGR00398; metg; 1.
DR TIGRFAMs; TIGR00399; metg_Cterm; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
DR PROSITE; PS00886; TRBD; 1.
DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW RNA-binding; tRNA-binding; Metal-binding; Zinc; Complete proteome.
FT SITE 11 21 "HIGH" REGION.
FT SITE 332 336 "KMSKS" REGION.
FT DOMAIN 567 668 tRNA-BINDING.
FT METAL 146 146 ZINC (BY SIMILARITY).
FT METAL 149 149 ZINC (BY SIMILARITY).
FT METAL 159 159 ZINC (BY SIMILARITY).
FT METAL 162 162 ZINC (BY SIMILARITY).
SQ SEQUENCE 668 AA; 77386 MW; FBC5734FF5FEF015 CRC64;
Query Match 39.7%; Score 48; DB 1; Length 668;
Best Local Similarity 53.3%; Pred. No. 24;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 6 LRPEGGGAGAEDE 20
I ||: ||: ||: |||
Db 547 LLPESGEGEQDDE 561
RESULT 12
NKX1_BOVIN STANDARD PRT; 1216 AA.
ID NKX1_BOVIN
AC Q28139; O46384;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+) -
DE exchange protein 1) (Retinal rod Na-Ca+K exchanger).
GN SLC24A1 OR NCKX1.
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CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; U04092; AAA67171.1; -.
CC PIR; A55259; A55259.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN
CC PROSITE; PS00237; G_PROTEIN_RECIP_FL_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECIP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC phosphorylation; Lipoprotein; Palmitate.
CC DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 59 85 1 (POTENTIAL).
CC DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 96 117 2 (POTENTIAL).
CC DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 133 154 3 (POTENTIAL).
CC DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 174 196 4 (POTENTIAL).
CC DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 223 247 5 (POTENTIAL).
CC DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 276 299 6 (POTENTIAL).
CC DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 312 333 7 (POTENTIAL).
CC DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
CC DISULFID 131 210 BY SIMILARITY.
CC LIPID 345 345 PALMITATE (POTENTIAL).
CC CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 380 AA; 42736 MW; 4FF053834DBBA623 CRC64;

Query Match 38.8%; Score 47; DB 1; Length 380;
Best Local Similarity 38.1%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGARDELE 22
D 30 LPGAEPDGNAGPQDEQLE 50
D 30 LPGAEPDGNAGPQDEQLE 50

RESULT 14
DDX8_ARATH STANDARD; PRT; 1168 AA.
AC Q38953; Q9LRV0;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative pre-mRNA splicing factor ATP-dependent RNA helicase.
GN AT3G26560 OR MPE16.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
ON NCBI_TaxID=3702;
[1]
CC SEQUENCE FROM N.A.
CC STRAIN=cv. Columbia;
CC MEDLINE=97086699; PubMed=8932388;
CC Quigley F., Dao P., Cottet A., Mache R.;
CC "Sequence analysis of an 81 kb contig from Arabidopsis thaliana
CC chromosome III.";
CC Nucleic Acids Res. 24:4313-4318(1996).
CC [2]

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RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
CC -1- FUNCTION: COULD ACT LATE IN THE SPLICING OF PRE-MRNA AND MEDIATE
CC THE RELEASE OF THE SPLICED MRNA FROM SPLICEOSOMES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. DEAD
CC SUBFAMILY. DDX8/PRP22 ORTHOLOG.
CC -1- SIMILARITY: Contains 1 S1 motif domain.
CC -1- CAUTION: Ref.1 sequences differ from that shown due to a
CC frameshift in position 57.
CC -----
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CC -----
CC EMBL; X98130; CAA66825.1; ALT_FRAME.
CC EMBL; X97970; CAA66613.1; ALT_FRAME.
CC EMBL; AB028611; BAB01838.1; -.
CC HSP; P05055; 1SRO.
CC InterPro; IPR001410; DEAD.
CC InterPro; IPR002464; DEAD_BOX.
CC InterPro; IPR001650; Helicase_C.
CC InterPro; IPR003029; S1.
CC Pfam; PF00271; helicase_C; 1.
CC Pfam; PF00575; S1; 1.
CC SMART; SM00487; DEXDC; 1.
CC SMART; SM00490; HELIC; 1.
CC SMART; SM00316; S1; 1.
CC PROSITE; PS00690; DEAD_ATP_HELICASE; 1.
CC PROSITE; PS50126; S1; 1.
CC Hypothetical protein; mRNA processing; mRNA splicing; Helicase;
KW ATP-binding; Nuclear protein.
KW DOMAIN 214 283 S1 MOTIF.
FT NP_BIND 538 545 ATP (POTENTIAL).
FT SITE 635 638 DEAD_BOX.
FT DOMAIN 777 780 POLY-PRO.
SQ SEQUENCE 1168 AA; 134156 MW; B3632DE4A7A7690C CRC64;

Query Match 38.8%; Score 47; DB 1; Length 1168;
Best Local Similarity 57.9%; Pred. No. 59;
Matches 11; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

QY 9 EDGG----QAEGAEDELEV 23
D 372 EDGGDMLYQEGAELEEI 390
D 372 EDGGDMLYQEGAELEEI 390

RESULT 15
MM14_PIG STANDARD; PRT; 580 AA.
AC Q9XT90;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Matrix metalloproteinase-14 precursor (EC 3.4.24.-) (MMP-14)
DE (Membrane-type matrix metalloproteinase 1) (MT-MMP 1) (MTMMP1)
DE NCBI_TaxID=9823;
[1]
CC Sus scrofa (Pig).
CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CC NCBI_TaxID=9823;
CC [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=99095929; PubMed=9881602;
RA Caron C., Xue J., Bartlett J.D.;
RT "Expression and localization of membrane type 1 matrix
RT metalloproteinase in tooth tissues.";
RL Matrix Biol. 17:501-511(1998).
CC -!- FUNCTION: SEEMS TO SPECIFICALLY ACTIVATE OF PRO-GELATINASE A. MAY
CC THUS TRIGGER INVASION BY TUMOR CELLS BY ACTIVATING PRO-GELATINASE
CC A ON THE TUMOR CELL SURFACE (BY SIMILARITY). MAY PLAY A ROLE IN
CC THE BIOMINERALIZATION OF ENAMEL AND DENTIN.
CC -!- COFACTOR: Binds 1 zinc ion per subunit, calcium (By similarity).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein (potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN DEVELOPING TOOTH TISSUES
CC AND MAY PLAY A ROLE IN THE BIOMINERALIZATION OF ENAMEL AND DENTIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC -----
DR EMBL; AF067419; AAD38324.1; -.
DR HSSP; P08254; 1HFS.
DR MEROPS; M10.014; -.
DR InterPro; IPR000595; Hemopexin.
DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR006026; Zn_MTpeptdse.
DR InterPro; IPR006025; Zn_MTpeptdse.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolase; Metalloprotease; Zinc; Zymogen; Calcium; Signal;
KW Transmembrane.
FT SIGNAL 1 28 POTENTIAL.
FT PROPEP 29 109 ACTIVATION PEPTIDE.
FT CHAIN 110 580 MATRIX METALLOPROTEINASE-14.
FT DOMAIN 110 539 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 540 560 POTENTIAL.
FT DOMAIN 561 580 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 314 509 HEMOPEXIN-LIKE.
FT SITE 91 91 CYSTEINE SWITCH (POTENTIAL).
FT METAL 237 237 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 238 238 BY SIMILARITY.
FT METAL 241 241 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 247 247 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 317 506 BY SIMILARITY.
SQ SEQUENCE 580 AA; 65934 MW; B7B2C2C569A96CAC CRC64;

Query Match 37.6%; Score 45.5; DB 1; Length 580;
Best Local Similarity 45.8%; Pred. No. 48;
Matches 11; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 ALAGNLRPEDGGA-EGAEDELEY 23
|| | : || : || : ||
Db 499 ALRDMWGPCSGGRPDGTEETEY 522

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Search completed: September 11, 2003, 17:21:45
Job time : 4.32086 secs

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 21.893 seconds
(without alignments)
271.100 Million cell updates/sec

Title: US-09-853-253-6

Perfect score: 121

Sequence: 1 ALAGWLRPDGGQAEDELEV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	119	98.3	117	4 Q8TAT9	Q8tat9 homo sapien
2	92	76.0	117	11 Q8CH53	Q8ch53 meriones un
3	59	48.8	1208	5 Q815T3	Q815t3 plasmodium
4	59	48.8	1264	5 Q9U445	Q9u445 plasmodium
5	55	45.5	183	10 Q8LNL6	Q8lnl6 oryza sativ
6	53	43.8	202	15 Q90P58	Q90p58 human immun
7	53	43.8	1228	5 Q27724	Q27724 plasmodium
8	52	43.0	201	15 Q90P50	Q90p50 human immun
9	52	43.0	232	16 Q916L1	Q916l1 pseudomonas
10	52	43.0	249	12 Q82036	Q82036 hirame rhab
11	52	43.0	392	12 Q9QL89	Q9ql89 hirame rhab
12	52	43.0	977	6 Q95169	Q95169 capra hircu
13	51.5	42.6	436	5 Q9N638	Q9n638 caenorhabdi
14	51	42.1	158	6 Q8XW90	Q8xw90 raistonia s
15	51	42.1	201	15 Q90NL5	Q90nl5 human immun
16	51	42.1	604	16 Q8UFA5	Q8ufa5 agrobacteri

17	51	42.1	609	2 Q9RH77	Q9rh77 bradyrhizob
18	50	41.3	131	16 Q9RV90	Q9rv90 deinococcus
19	50	41.3	202	15 Q90P76	Q90p76 human immun
20	50	41.3	202	15 Q90P77	Q90p77 human immun
21	50	41.3	472	10 Q8LRD5	Q8lrd5 oryza sativ
22	50	41.3	582	6 Q9XSP0	Q9xsp0 capra hircu
23	50	41.3	582	6 Q9GLE4	Q9gle4 bos taurus
24	49.5	40.9	484	16 Q9R2L7	Q9r2l7 deinococcus
25	49	40.5	201	15 Q90P55	Q90p55 human immun
26	49	40.5	201	15 Q90N8	Q90nk8 human immun
27	49	40.5	286	12 Q8QRU5	Q8qr5 chimpanzee
28	48.5	40.1	110	10 Q93VB3	Q93vb3 oryza sativ
29	48.5	40.1	172	2 Q9RBY2	Q9rby2 pseudomonas
30	48.5	40.1	172	2 Q9R2S2	Q9r2s2 pseudomonas
31	48.5	40.1	269	2 Q9FTM8	Q9etm8 pseudomonas
32	48	39.7	106	16 Q8ELH4	Q8elh4 oceanobacil
33	48	39.7	115	10 Q8LI79	Q8li79 oryza sativ
34	48	39.7	120	15 Q78494	Q78494 human immun
35	48	39.7	201	15 Q90P53	Q90p53 human immun
36	48	39.7	201	15 Q90NL3	Q90nl3 human immun
37	48	39.7	201	15 Q90NL6	Q90nl6 human immun
38	48	39.7	201	15 Q90NL0	Q90nl0 human immun
39	48	39.7	201	15 Q90NL1	Q90nl1 human immun
40	48	39.7	201	15 Q90NM1	Q90nm1 human immun
41	48	39.7	201	15 Q90NM2	Q90nm2 human immun
42	48	39.7	201	15 Q90NL9	Q90nl9 human immun
43	48	39.7	202	15 Q90P31	Q90p31 human immun
44	48	39.7	202	15 Q90P37	Q90p37 human immun
45	48	39.7	211	10 Q943L4	Q943l4 oryza sativ

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY; PRT; 117 AA.
AC Q8TAT9;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025791; AAH25791.1; -
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc.1;
DR Pfam; PF04644; motilin_ghrelin.1;
SQ SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;

Query Match 98.3%; Score 119; DB 4; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.6e-09;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAEDELEV 23
|||||
DB 52 ALAGWLRPDGGQAEDEMEV 74

RESULT 2

Q8CH53 PRELIMINARY; PRT; 117 AA.
ID Q8CH53;
AC Q8CH53;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
ON NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoaka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AA006965.1; -.
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 76.0%; Score 92; DB 11; Length 117;
Best Local Similarity 73.9%; Pred. No. 1.3e-05;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEV 23
Db 52 ALEGWLRPDGGRGAEGAEDELEI 74

RESULT 3
Q815T3 PRELIMINARY; PRT; 1208 AA.
AC Q815T3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase, putative.
GN Plasmodium falciparum (isolate 3D7).
OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=36329;
ON [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Perteaux M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014846; AAN36207.1; -.
SQ SEQUENCE 1208 AA; 133873 MW; 25AA7752E707E621 CRC64;

Query Match 48.8%; Score 59; DB 5; Length 1208;
Best Local Similarity 52.6%; Pred. No. 8.2;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGGAEGAEDELE 22
Db 1072 GWCRPKDNKTSQGYNDELE 1090

RESULT 4
Q90445 PRELIMINARY; PRT; 1264 AA.
AC Q90445;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase4.

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GN ATPASE4.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21179120; PubMed=11145964;
RA Krishna S., Woodrow C., Webb R., Penny J., Takeyasu K., Kimura M.,
RA East J.M.;
RT "Expression and Functional Characterization of a Plasmodium falciparum
RT Ca2+-ATPase (PfATP4) Belonging to a Subclass Unique to Apicomplexan
RT Organisms.";
RL J. Biol. Chem. 276:10782-10787(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
CC ATPASES).
DR EMBL; AF203980; AAF17245.1; -.
DR HSP; P04191; IEUL.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 5.
DR PROSITE; PS00154; ATPase_E1-E2; 1.
KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SQ SEQUENCE 1264 AA; 140261 MW; 638142BB1B433640 CRC64;

Query Match 48.8%; Score 59; DB 5; Length 1264;
Best Local Similarity 52.6%; Pred. No. 8.6;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGGAEGAEDELE 22
Db 1128 GWCRPKDNKTSQGYNDELE 1146

RESULT 5
Q8LNL6 PRELIMINARY; PRT; 183 AA.
AC Q8LNL6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0071120.2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA McCombie W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,
RA Kuit K., Nascimento L., Zutavern T., Ballja V., Bell M., Baker J.,
RA Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,
RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone
RT OSJNBA0071120, from chromosome 10, complete sequence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC074355; AAM74240.1; -.
DR Gramene; Q8LNL6; -.
KW Hypothetical protein.
SQ SEQUENCE 183 AA; 20492 MW; DE73BD8607292D7B CRC64;

Query Match 45.5%; Score 55; DB 10; Length 183;
Best Local Similarity 47.6%; Pred. No. 4.2;
Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

```


RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 RL opportunistic pathogen".
 CC Nature 406:959-964(2000).
 CC -1- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: AE004466; AAC03668.1; -;
 DR InterPro: IPR001845; HTH_ArsR.
 DR Pfam: PF01022; HTH_5; 1.
 DR PRINTS: PR00778; HTHARSR.
 DR SMART: SM00418; HTH_ArsR; 1.
 KW DNA-binding; Transcription regulation; Complete proteome.
 SQ SEQUENCE 232 AA; 24440 MW; E3C29187694CF936 CRC64;

Query Match 43.0%; Score 52; DB 16; Length 232;
 Best Local Similarity 72.7%; Pred. No. 15;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GWLRPEDGGQA 14
 |||||:|:|

Db 202 GWLRPQDGSRA 212

RESULT 10

Q82036 PRELIMINARY; PRT; 249 AA.
 ID Q82036
 AC Q82036;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Nucleocapsid protein.
 GN N.
 OS Hirame rhabdovirus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Novirhabdovirus.
 OX NCBI_TaxID=38142;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8401-H;
 RA Nishizawa T.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D45422; BAA08261.1; -;
 DR InterPro: IPR004902; Rhabdo_ncap_2.
 DR Pfam: PF03216; Rhabdo_ncap_2; 1.
 SQ SEQUENCE 249 AA; 26936 MW; 62FF2BFA5D47DB89 CRC64;

Query Match 43.0%; Score 52; DB 12; Length 249;
 Best Local Similarity 75.0%; Pred. No. 16;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 EDGGQAEAGDE 20
 |||||:|:|

Db 235 EDGGEDEGE 246

RESULT 11

Q9QL89 PRELIMINARY; PRT; 392 AA.
 ID Q9QL89
 AC Q9QL89;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Nucleocapsid protein.
 GN N.
 OS Hirame rhabdovirus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Novirhabdovirus.
 OX NCBI_TaxID=38142;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CA 9703;
 RA Oh H.K., Choi T.J.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF104985; AAF14116.1; -;

DR InterPro: IPR004902; Rhabdo_ncap_2.
 DR Pfam: PF03216; Rhabdo_ncap_2; 1.
 SQ SEQUENCE 392 AA; 42465 MW; CSA282238FC7A638 CRC64;

Query Match 43.0%; Score 52; DB 12; Length 392;
 Best Local Similarity 75.0%; Pred. No. 26;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 EDGGQAEAGDE 20
 |||||:|:|

Db 378 EDGGEDEGE 389

RESULT 12

Q95169 PRELIMINARY; PRT; 977 AA.
 ID Q95169
 AC Q95169;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Skeletal muscle voltage-gated chloride channel gCLC-1 (Fragment).
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97008165; PubMed=8855341;
 RA Beck C.L., Fahlike C., George A.L.;
 RT "Molecular basis for decreased muscle chloride conductance in the
 RT myotonic goat".
 RL Proc. Natl. Acad. Sci. U.S.A. 93:11248-11252(1996).
 DR EMBL: U60275; AAC48666.1; -;
 DR InterPro: IPR000644; CBS_domain.
 DR InterPro: IPR001807; Cl-channel_volt.
 DR InterPro: IPR005829; Sug_transporter.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00654; voltage_CLC; 1.
 DR PRINTS: PR00762; CLCHANNEL.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
 FT NON_TER
 SQ SEQUENCE 977 AA; 107894 MW; 1E462B3CB307A148 CRC64;

Query Match 43.0%; Score 52; DB 6; Length 977;
 Best Local Similarity 62.5%; Pred. No. 67;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GWLRPEDGGQAEAGD 19
 |||||:|:|

Db 895 GWSLPEDGAGATCAGD 910

RESULT 13

Q9N638 PRELIMINARY; PRT; 436 AA.
 ID Q9N638
 AC Q9N638;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE F37D6.6 protein.
 GN F37D6.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilkenson J.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;

RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT Investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA McMurray A.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z79600; CAB70221.1; -;
 DR EMBL; Z75540; CAB70221.1; JOINED.
 DR EMBL; Z75540; CAB70215.1; -;
 DR EMBL; Z79600; CAB70215.1; JOINED.
 DR WormPep; F37D6.6; CE24960.
 DR InterPro: IPR001132; DwarfIn.
 DR InterPro: IPR003619; DwarfIn_A.
 DR Pfam; PF03166; MH2; 1.
 DR SMART; SM00523; DWA; 1.
 DR SMART; SM00524; DWA; 1.
 SQ SEQUENCE 436 AA; 49496 MW; E0C71263BC580EEE CRC64;

Query Match 42.6%; Score 51.5; DB 5; Length 436;
 Best Local Similarity 52.9%; Pred. No. 34;
 Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 5 WLRPE-DGGQAGAEDE 20
 I:III :II :I:II:
 Db 169 WIRPETNGGDDGSEDK 185

RESULT 14

Q8XW90
 ID Q8XW90 PRELIMINARY; PRT; 158 AA.
 AC Q8XW90;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein RSC2585.
 GN RSC2585 OR RS00797.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_Taxid=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choigne N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646070; CAD16292.1; -;
 DR InterPro: IPR002145; HTH_CopG.
 DR Pfam; PF01402; HTH 4; 1
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 158 AA; 17814 MW; C9BA42BF9C10E1BC CRC64;

Query Match 42.1%; Score 51; DB 16; Length 158;
 Best Local Similarity 58.8%; Pred. No. 14;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGA 17
 III II I: I I I
 Db 36 ALASWLSPDAGDQREA 52

RESULT 15

Q90NL5
 ID Q90NL5 PRELIMINARY; PRT; 201 AA.
 AC Q90NL5;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nickle D.C.;
 RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF371104; AAK66503.1; -;
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR AIDS; Coat protein; Glycoprotein.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 201
 SQ SEQUENCE 201 AA; 22470 MW; E1993A2A412EC118 CRC64;

Query Match 42.1%; Score 51; DB 15; Length 201;
 Best Local Similarity 40.9%; Pred. No. 18;
 Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDELEV 23
 : I I III I : I I:
 Db 179 ITGLLTRDGGGGNGTDTNETEI 200

Search completed: September 11, 2003, 17:30:28
 Job time : 21.893 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:48:42 ; Search time 40.0428 Seconds
(without alignments)
123.627 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 117

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	100.0	117	3	US-09-046-479-2
2	117	100.0	117	4	US-08-822-897C-2
3	117	100.0	117	4	US-09-608-810A-4
4	117	100.0	117	4	US-09-996-243-268
5	11	9.4	11	4	US-09-608-810A-2
6	7	6.0	442	4	US-09-134-001C-3033
7	7	6.0	502	2	US-08-481-337A-8
8	7	6.0	502	3	US-09-382-256-18
9	7	6.0	502	3	US-09-395-115-18
10	7	6.0	502	3	US-08-123-934A-4
11	7	6.0	502	4	US-08-436-265-18
12	7	6.0	502	4	US-09-679-187-18
13	7	6.0	502	5	PCT-US94-10080-4
14	7	6.0	502	5	PCT-US95-05467-8
15	7	6.0	552	4	US-09-252-991A-27032
16	7	6.0	599	4	US-09-252-991A-20368
17	7	6.0	662	4	US-09-252-991A-22861
18	7	6.0	981	4	US-09-252-991A-16798
19	7	6.0	3165	2	US-08-459-146-3
20	7	6.0	3165	2	US-08-459-085-3
21	6	5.1	15	1	US-08-434-705B-18
22	6	5.1	15	2	US-09-086-201-18
23	6	5.1	24	3	US-08-948-782-1
24	6	5.1	24	3	US-09-482-612-1
25	6	5.1	24	4	US-09-677-554-1
26	6	5.1	30	2	US-08-995-927-9
27	6	5.1	30	4	US-09-582-096-9

Sequence 13, Appl
Sequence 104, App
Sequence 104, App
Sequence 11, Appl
Sequence 5646, Ap
Sequence 14, Appl
Sequence 21677, A
Sequence 325, App
Sequence 234, App
Sequence 2, Appl
Sequence 3, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 31, Appl
Sequence 6022, Ap
Sequence 1, Appl
Sequence 275, App

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
US-09-046-479-2

Query Match 100.0%; Score 117; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e-109;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVQQRKESKPKPPAKLQPRALAGWLRLPE 60
Db 1 MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVQQRKESKPKPPAKLQPRALAGWLRLPE 60
Oy 61 DGGQGAEGAEDLEVRFNAPFDVGKLSGVQYQQHSQLGKFLQDILWEEAKEAPADK 117
Db 61 DGGQGAEGAEDLEVRFNAPFDVGKLSGVQYQQHSQLGKFLQDILWEEAKEAPADK 117

RESULT 2

US-08-822-897C-2

; Sequence 2, Application US/08822897C

; Patent No. 6380158

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Delsher, Theresa A.

; TITLE OF INVENTION: MOTILIN HOMOLOGS

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZymoGenetics, Inc.,

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/822.897C

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sawislak, Deborah A.

; REGISTRATION NUMBER: 37,438

; REFERENCE/DOCKET NUMBER: 97-04

; TELEPHONE: 206-442-6672

; TELEFAX: 206-442-6678

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 117 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

US-08-822-897C-2

Query Match 100.0%; Score 117; DB 4; Length 117;

Best Local Similarity 100.0%; Pred. No. 1e-109;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVQQRKESKPKPPAKLQPRALAGWLRLPE 60
Db 1 MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVQQRKESKPKPPAKLQPRALAGWLRLPE 60

Oy 61 DGGQGAEGAEDLEVRFNAPFDVGKLSGVQYQQHSQLGKFLQDILWEEAKEAPADK 117
Db 61 DGGQGAEGAEDLEVRFNAPFDVGKLSGVQYQQHSQLGKFLQDILWEEAKEAPADK 117

RESULT 3

US-09-608-810A-4

; Sequence 4, Application US/09608810A

; Patent No. 6420521

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Delsher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608.810A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4

Query Match 100.0%; Score 117; DB 4; Length 117;

Best Local Similarity 100.0%; Pred. No. 1e-109;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVQQRKESKPKPPAKLQPRALAGWLRLPE 60
Db 1 MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVQQRKESKPKPPAKLQPRALAGWLRLPE 60

Oy 61 DGGQGAEGAEDLEVRFNAPFDVGKLSGVQYQQHSQLGKFLQDILWEEAKEAPADK 117
Db 61 DGGQGAEGAEDLEVRFNAPFDVGKLSGVQYQQHSQLGKFLQDILWEEAKEAPADK 117

RESULT 4

US-09-996-243-268

; Sequence 268, Application US/09996243

; Patent No. 6478825

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gertsens, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C13

; CURRENT APPLICATION NUMBER: US/09/996.243

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 117; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e-109;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSGTVCSTLLLLGMLDLAMAGSSFLSPHQVQQRKSKPPAKLQPRALAGWLRPE 60
Db 1 MPSEGTVCSTLLLLGMLDLAMAGSSFLSPHQVQQRKSKPPAKLQPRALAGWLRPE 60
Qy 61 DGGQGAEDLEVRNAPFDVGIKLGVQYQHQHSQLGKFLQDILWEEAKEAPADK 117
Db 61 DGGQGAEDLEVRNAPFDVGIKLGVQYQHQHSQLGKFLQDILWEEAKEAPADK 117

RESULT 5

US-09-608-810A-2
; Sequence 2, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Delsher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608.810A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-810A-2

Query Match 9.4%; Score 11; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GSSFLSPHQH 34
Db 1 GSSFLSPHQH 11

RESULT 6

US-09-134-001C-3033
; Sequence 3033, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C

; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3033
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3033

Query Match 6.0%; Score 7; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 DGGQAEQ 67
Db 189 DGGQAEQ 195

RESULT 7

US-08-481-337A-8
; Sequence 8, Application US/08481337A
; Patent No. 5863738
; GENERAL INFORMATION:
; APPLICANT: TEN DIJKE, Peter
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: MIYAZONO, Kohel
; APPLICANT: SAMPATH, Kuber T.
; TITLE OF INVENTION: Morphogenic Protein-Specific Cell
; TITLE OF INVENTION: Surface Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/481.337A
; APPLICATION NUMBER: US/08/481.337A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-097CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-481-337A-8

Query Match 6.0%; Score 7; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVCSLLL 12
Db 133 TVCSLLL 139

RESULT 8

US-09-382-256-18
; Sequence 18, Application US/09382256A
; Patent No. 6207814
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohel
; TEN DIJKE, Peter
; FRANZEN, Petra
; YAMASHITA, Hidetoshi
; HELDIN, Carl-Henrik
; TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
; HAVING SERINE THREONINE KINASE DOMAINS,
; AND THEIR USE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/382,256A
; FILING DATE: 24-Aug-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: NO. 6207814ember 17, 1993
; APPLICATION NUMBER: GB 9224057.1
; FILING DATE: NO. 6207814ember 17, 1992
; APPLICATION NUMBER: GB 9304677.9
; FILING DATE: March 8, 1993
; APPLICATION NUMBER: GB 9304680.3
; FILING DATE: March 8, 1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: May 28, 1993
; APPLICATION NUMBER: 9313763.6
; FILING DATE: July 2, 1993
; APPLICATION NUMBER: 9316099.2
; FILING DATE: August 3, 1993
; APPLICATION NUMBER: 321344.5
; FILING DATE: October 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6207814man D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5298.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-382-256-18

Query Match 6.0%; Score 7; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVCSLLL 12
| | | | |
Db 133 TVCSLLL 139

RESULT 9

US-09-395-115-18
; Sequence 18, Application US/09395115
; Patent No. 6271365
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohel; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/395,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-NO. 6271365ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-NO. 6271365ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-395-115-18

Query Match 6.0%; Score 7; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVCSLLL 12
| | | | |
Db 133 TVCSLLL 139

RESULT 10
 US-08-123-934A-4
 ; Sequence 4, Application US/08123934A
 ; Patent No. 6291206
 ; GENERAL INFORMATION:
 ; APPLICANT: WOZNEY, John
 ; APPLICANT: CELESTE, Anthony J.
 ; APPLICANT: THIES, R. Scott
 ; APPLICANT: YAMAJI, No. 6291206oru
 ; TITLE OF INVENTION: RECEPTOR PROTEINS
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/123.934A
 ; FILING DATE: 17-SEP-1993
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: LAZAR, Steven R
 ; REGISTRATION NUMBER: 32,618
 ; REFERENCE/DOCKET NUMBER: 5203
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617 876 1170
 ; TELEFAX: 617 876 5851
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-123-934A-4

Query Match 6.0%; Score 7; DB 3; Length 502;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVCSLLL 12
 Db 133 TVCSLLL 139

RESULT 11
 US-08-436-265-18
 ; Sequence 18, Application US/08436265
 ; Patent No. 6316217
 ; GENERAL INFORMATION:
 ; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
 ; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
 ; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
 ; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/436.265
 ; FILING DATE: 30-October-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB93/02367
 ; FILING DATE: 17-No. 6316217ember-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9224057.1
 ; FILING DATE: 17-No. 6316217ember-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9304677.9
 ; FILING DATE: 8-March-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9304680.3
 ; FILING DATE: 8-March-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9311047.6
 ; FILING DATE: 28-May-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9313763.6
 ; FILING DATE: 2-July-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9136099.2
 ; FILING DATE: 3-August-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9321344.5
 ; FILING DATE: 15-October-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kohlei, Vineet
 ; REGISTRATION NUMBER: 37,003
 ; REFERENCE/DOCKET NUMBER: LUD 5298
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-436-265-18

Query Match 6.0%; Score 7; DB 4; Length 502;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVCSLLL 12
 Db 133 TVCSLLL 139

RESULT 12
 US-09-679-187-18
 ; Sequence 18, Application US/09679187
 ; Patent No. 6331621
 ; GENERAL INFORMATION:
 ; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
 ; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
 ; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
 ; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/679,187
;; FILING DATE: 03-OCT-2000
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/436,265
;; FILING DATE: 30-October-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB93/02367
;; FILING DATE: 17-NO. 6331621ember-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9224057.1
;; FILING DATE: 17-NO. 6331621ember-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9304677.9
;; FILING DATE: 8-March-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9304680.3
;; FILING DATE: 8-March-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9311047.6
;; FILING DATE: 28-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9313763.6
;; FILING DATE: 2-July-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9136099.2
;; FILING DATE: 3-August-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 9321344.5
;; FILING DATE: 15-October-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kohlel, Vineet
;; REGISTRATION NUMBER: 37,003
;; REFERENCE/DOCKET NUMBER: LUD 5298
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 502 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-679-187-18

Query Match 6.0%; Score 7; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVCSLLL 12
Db 133 TVCSLLL 139

RESULT 13
PCT-US94-10080-4
;; Sequence 4, Application PC/TUS9410080
;; GENERAL INFORMATION:
;; APPLICANT: GENETICS INSTITUTE, INC.
;; TITLE OF INVENTION: RECEPTOR PROTEINS
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
;; STREET: 87 Cambridgepark Drive
;; CITY: Cambridge
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02140
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/10080
;; FILING DATE: HERewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/123,934
;; FILING DATE: 17-SEP-1993
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LAZAR, Steven R
;; REGISTRATION NUMBER: 32,618
;; REFERENCE/DOCKET NUMBER: 5203-PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 498-8260
;; TELEFAX: (617) 876-5851
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 502 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US94-10080-4
Query Match 6.0%; Score 7; DB 5; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVCSLLL 12
Db 133 TVCSLLL 139

RESULT 14
PCT-US95-05467-8
;; Sequence 8, Application PC/TUS9505467
;; GENERAL INFORMATION:
;; APPLICANT:
;; APPLICANT:
;; TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
;; ADDRESS: THIBEAULT
;; STREET: 53 STATE STREET
;; CITY: BOSTON
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/05467
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: PITCHER, EDMUND R.
;; REGISTRATION NUMBER: 27,829
;; REFERENCE/DOCKET NUMBER: CRP-097PC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 248-7000
;; TELEFAX: (617) 248-7100
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 502 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US95-05467-8

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Query Match      6.0%; Score 7; DB 5; Length 502;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 TVCSLLL 12
Db      133 TVCSLLL 139

RESULT 15
US-09-252-991A-27032
; Sequence 27032, Application US/09252991A
; Patent No. 6351795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27032
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27032

Query Match      6.0%; Score 7; DB 4; Length 552;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 DGGQAE 67
Db      22 DGGQAE 28

Search completed: September 11, 2003, 17:58:12
Job time : 41.0428 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:27:22 ; Search time 123.257 Seconds
(without alignments)
150.669 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 117

Sequence: 1 MPSPTGVCVSLLLGLMLDL.....LGKFLQDLWEAKEAPADK 117

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	100.0	117	20	AAW87991 Protein designated
2	117	100.0	117	21	AA187236 Human signal pepti
3	117	100.0	117	22	AAAM38890 Human polypeptide
4	117	100.0	117	22	AAAB62649 Human zsig33 polyp
5	117	100.0	117	22	AAAB20101 zsig33 protein. H
6	117	100.0	117	22	AAAB60511 Human ghrelin prep
7	117	100.0	117	23	ABH78319 Amino acid sequenc
8	117	100.0	117	23	AAE23838 Human zsig33 prote
9	117	100.0	117	23	AAE15883 Human zsig33 prote

10	117	100.0	117	24	ABU66790 Human PRO polypept
11	117	100.0	117	24	ABU67066 Human secreted/tra
12	117	100.0	117	24	ABU59871 Novel secreted and
13	117	100.0	117	24	ABU59124 Novel human secret
14	117	100.0	117	24	ABU59271 Human secreted/tra
15	117	100.0	117	24	ABU59420 Novel human secret
16	117	100.0	117	24	ABU60555 Human secreted/tra
17	117	100.0	117	24	ABU58046 Human PRO polypept
18	117	100.0	117	24	ABU58977 Human secreted/tr
19	117	100.0	117	24	AAE33409 Human preproghrell
20	117	100.0	117	24	ABU13937 Human PRO1066 poly
21	117	100.0	117	24	ABU10892 Human PRO polypept
22	117	100.0	118	21	AA166708 Membrane-bound pro
23	117	100.0	118	22	AAU12392 Human PRO1066 poly
24	117	100.0	118	22	AAE65231 Human PRO1066 (UNQ
25	117	100.0	126	22	AAW40676 Human polypeptide
26	81	69.2	116	22	AAAB60517 Human des-Gln14-gh
27	75	64.1	91	24	AAE33410 Human exon 3-delet
28	28	23.9	28	22	AAAB60509 Human ghrelin, SEQ
29	28	23.9	28	23	ABB09532 Human ghrelin. Ho
30	28	23.9	28	23	AAE19032 Human ghrelin pept
31	26	22.2	28	23	AAE19039 Human ghrelin pept
32	25	21.4	25	23	AAE23842 Human zsig33-beta
33	25	21.4	25	23	AAE15887 Human zsig33-beta
34	25	21.4	28	23	AAE19021 Human ghrelin pept
35	25	21.4	28	23	AAE19027 Human ghrelin pept
36	25	21.4	28	23	AAE19028 Human ghrelin pept
37	25	21.4	28	23	AAE19029 Human ghrelin pept
38	25	21.4	28	23	AAE19030 Human ghrelin pept
39	25	21.4	28	23	AAE19031 Human ghrelin pept
40	25	21.4	28	23	AAE19033 Human ghrelin pept
41	25	21.4	28	23	AAE19034 Human ghrelin pept
42	25	21.4	28	23	AAE19035 Human ghrelin pept
43	25	21.4	28	23	AAE19036 Human ghrelin pept
44	25	21.4	28	23	AAE19037 Human ghrelin pept
45	25	21.4	28	23	AAE19038 Human ghrelin pept

ALIGNMENTS

RESULT 1
AAW87991
ID AAW87991 standard; Protein; 117 AA.
XX
AC AAW87991;
XX
DT 07-APR-1999 (first entry)
XX
DE Protein designated zsig33.
XX
KW Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
XX nutrient absorption regulation; obesity; metabolic disorder.
OS Homo sapiens.
XX
FH Key
FT Peptide
FT Protein
FT
FT
XX
XX WO9842840-A1.
XX
PD 01-OCT-1998.
XX
PF 23-MAR-1998; 98WO-US05620.
XX
PR 24-MAR-1997; 97US-0822897.
XX 24-MAR-1997; 97US-0041102.
XX (ZYMO) ZYMOGENETICS INC.

PI Delsher TA, Sheppard PO;
 XX WPI; 1999-070071/06.
 DR N-PSDB; AAX04550.
 XX
 XX Human polypeptide having homology to motilin, zsig33 - useful e.g.
 PT to treat gastrointestinal motility disorders, obesity etc. and to
 PT identify antagonists to treat gastrointestinal hypermotility
 XX
 XX Claim 13; Page 55-56; 69pp; English.
 XX
 XX The present sequence represents a protein designated zsig33. The nucleic
 CC acids are strongly expressed in stomach tissue. The polypeptide (or
 CC allelic variants/orthologs) can be used to stimulate gastric motility,
 CC measured as increased transit time or gastric emptying of an ingested
 CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. Zsig33 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC and CNS functions. They may therefore be used e.g. to regulate satiety
 CC or treat obesity and other metabolic disorders where neurological
 CC feedback modulates nutritional absorption. They are useful to identify
 CC zsig33 agonists, antagonists and ligands and to produce antibodies.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 117; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-101;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MPSPTVCSLLLLGMLDLAMAGSFLSPFHQVQQRKESKPPAKLPALAGWLRLPE 60
 DB 1 MPSPTVCSLLLLGMLDLAMAGSFLSPFHQVQQRKESKPPAKLPALAGWLRLPE 60
 OY 61 DGGQAGAEDELEVRNAPFDVGKLSGVQYQHQHSGALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAGAEDELEVRNAPFDVGKLSGVQYQHQHSGALGKFLQDILWEEAKEAPADK 117
 RESULT 2
 AAY87236
 ID AAY87236 standard; Protein; 117 AA.
 XX
 AC AAY87236;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
 XX
 KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nontropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 XX WO200000610-A2.
 PN
 PD 06-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-US14484.
 PF
 XX 26-JUN-1998; 98US-0090762.
 PR
 PR 31-JUL-1998; 98US-0094983.
 PR
 PR 01-OCT-1998; 98US-0102686.

PR 11-DEC-1998; 98US-0112129.
 XX (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX
 DR WPI; 2000-160673/14.
 DR N-PSDB; AAZ98121.
 XX
 XX New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease
 XX
 PS Claim 1; Page 168-169; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, nontropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPP
 CC from natural sources.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 117; DB 21; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-101;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MPSPTVCSLLLLGMLDLAMAGSFLSPFHQVQQRKESKPPAKLPALAGWLRLPE 60
 DB 1 MPSPTVCSLLLLGMLDLAMAGSFLSPFHQVQQRKESKPPAKLPALAGWLRLPE 60
 OY 61 DGGQAGAEDELEVRNAPFDVGKLSGVQYQHQHSGALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAGAEDELEVRNAPFDVGKLSGVQYQHQHSGALGKFLQDILWEEAKEAPADK 117
 RESULT 3
 AAM38890
 ID AAM38890 standard; Protein; 117 AA.
 XX
 AC AAM38890;
 XX
 XX 22-OCT-2001 (first entry)
 DT
 XX Human polypeptide SEQ ID NO 2035.
 DE
 XX Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX OS Homo sapiens.
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US34263.
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 23-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX DR WPI; 2001-442253/47.
XX DR N-PSDB; AAI58046.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries -
XX PS Example 3; SEQ ID NO 2035; 10078pp; English.
XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
XX CC the encoded polypeptides (AAI38642-AAI2213) with nootropic,
XX CC immunosuppressant and cytosolic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC C.N.S disorders.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification.
XX SQ Sequence 117 AA;
Query Match 100.0%; Score 117; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MFSPTVCSLLLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPRLAGWLRLPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEAKAPADK 117
DB 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEAKAPADK 117
RESULT 4
ID AAB62649
ID AAB62649 standard; Protein; 117 AA.
AC AAB62649;
XX DT 23-JUL-2001 (first entry)
XX DE Human zsig33 polypeptide.

XX KW zsig33; signal transduction; hormone; enzyme; neural development;
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
XX OS G-protein coupled receptor.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 24..37
FT /note= "specifically claimed fragment that binds to
XX the GHS-R"
XX WO200138355-A2.
XX PD 31-MAY-2001.
XX PF 22-NOV-2000; 2000WO-US32074.
XX PR 22-NOV-1999; 99US-0166765.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX WPI; 2001-355879/37.
XX DR N-PSDB; AAF83678.
XX PT Forming reversible peptide receptor complex for purifying cell and
XX PT peptides, stimulating signal transduction and modulating hormone
XX PT secretion, involves contacting a receptor with zsig33 polypeptide -
XX Claim 1; Page 93-94; 111pp; English.
XX The invention relates to a method of forming a reversible peptide-
XX receptor complex that involves providing an immobilized receptor, and
XX contacting the receptor with a zsig33 peptide (comprising residues 24-37
XX of AAB62649), where the receptor binds to the zsig33 peptide. The method
XX is useful for purifying cells, purifying a peptide, stimulating signal
XX transduction in a cell expressing a receptor. It is also useful for
XX modulating secretion of hormones, neural development and/or utilization,
XX gastric contractility, nutrient uptake, secretion of digestive and
XX pancreatic enzymes and hormones, secretion of insulin-like growth factor
XX -I, secretion of non-zsig33 proteins. It is useful for modulating growth
XX hormone secretion in a mammal having a disease associated with abnormal
XX levels of growth hormone, such as osteoporosis, bone repair, bone
XX remodeling, low osteoblast levels, cartilage repair and remodeling,
XX skeletal dysplasia, immune suppression, obesity, growth retardation,
XX protein catabolic responses after surgery, cachexia, protein loss,
XX dwarfism, wound healing and ovulation induction, treating a mammal having
XX a metabolic disorder requiring neurological feedback, such as satiety
XX regulation, glucose absorption and metabolism and neuropathy-associated
XX gastrointestinal disorders, and stimulating glucose-induced insulin
XX release in a mammal. The present sequence represents the human zsig33
XX polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
XX SQ Sequence 117 AA;
Query Match 100.0%; Score 117; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFSPTVCSLLLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPRLAGWLRLPE 60
DB 1 MFSPTVCSLLLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPRLAGWLRLPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEAKAPADK 117
DB 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEAKAPADK 117
RESULT 5

AAB20101
ID AAB20101 standard; Protein; 117 AA.
XX
AC AAB20101;
XX
DT 23-APR-2001 (first entry)
XX
DE zsig33 protein.
XX
KW SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
KW nutritional absorption modulator; growth hormone secretagogue;
KW therapy; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Signal_peptide
FT Protein 24..117
FT /label= Mature_protein
FT Peptide 24..34
FT /label= SGIP_peptide
FT /note= "this peptide is claimed in Claim 1"
XX
PN WO200100830-A1.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18306.
XX
PR 30-JUN-1999; 99US-0345157.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
DR WPI; 2001-123010/13.
DR N-PSDB; AAF30033.
XX
PT Novel variants of SGIP peptides for modulating contractility in
PT duodenum or jejunum tissue, pancreatic secretion of hormones and
PT digestive enzymes, inducing growth hormone secretion or modulating
PT gastric emptying -
XX
PS Disclosure; 54; 61pp; English.
XX
CC The present sequence is that of zsig33, a secreted protein with
CC homology to motilin (see AAB20102). zsig33 is expressed at high
CC levels in the stomach, and at lower levels in the small intestine
CC and pancreas. A novel peptide fragment of zsig33, termed SGIP (see
CC AAB20100), is claimed. SGIP is a ligand for growth hormone
CC secretagogue receptor, and is therefore useful for modulating
CC secretion of growth hormone and insulin like growth factor 1.
CC SGIP, and variant SGIP peptides, are used in claimed methods for
CC stimulating contractility in duodenum or jejunum tissue,
CC modulating pancreatic secretion of hormones and digestive enzymes,
CC inducing growth hormone secretion, and modulating gastric emptying.
XX
SQ Sequence 117 AA;
Query Match 100.0%; Score 117; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHORVQQRKESKPPAKLQPRALAGWL RPE 60
Db 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHORVQQRKESKPPAKLQPRALAGWL RPE 60
Qy 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117

RESULT 6
AAB60511
ID AAB60511 standard; Protein; 117 AA.
XX
AC AAB60511;
XX
DT 24-APR-2001 (first entry)
XX
DE Human ghrelin preproprotein, SEQ ID NO:5.
XX
KW Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
KW calcium concentration elevation; infant growth disorder;
KW growth hormone deficiency.
XX
OS Homo sapiens.
XX
PN WO200107475-A1.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-JP04907.
XX
PR 23-JUL-1999; 99JP-0210002.
PR 29-NOV-1999; 99JP-0338841.
PR 26-APR-2000; 2000JP-0126623.
XX
PA (KANG/) KANGAWA K.
XX
PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
XX
DR WPI; 2001-159704/16.
DR N-PSDB; AAF59645.
XX
PT New peptide compounds which induce growth hormone secretion and
PT elevate cell calcium concentrations, useful in treatment and diagnosis
PT of infant growth disorders -
XX
PS Claim 3; Page 182; 210pp; Japanese.
XX
CC The invention relates to a novel peptide compound or its salt which
CC induces the secretion of growth hormone and/or elevates calcium ion
CC concentration in cells. The peptides are ghrelin homologues and are
CC characterised in that at least one amino acid has been substituted by
CC a modified amino acid and/or a non-amino acid compound. The invention
CC also encompasses the unmodified peptides: the DNA encoding the peptides;
CC vectors and host cells comprising such DNA; a method of producing the
CC peptides comprising recombinant production, optionally followed by
CC chemical modification; an antibody specific for a peptide of the
CC invention; and an assay and kit for detecting the peptides. The peptides
CC of the invention are useful for treating and/or diagnosing diseases
CC caused by a deficiency in growth hormone expression or activity. In
CC particular, they are useful for promoting infant growth due to growth
CC hormone deficiency. The compounds of the invention are safe with
CC no accompanying side effects. The present sequence represents a
CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
CC of the invention.
XX
SQ Sequence 117 AA;
Query Match 100.0%; Score 117; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHORVQQRKESKPPAKLQPRALAGWL RPE 60
Db 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHORVQQRKESKPPAKLQPRALAGWL RPE 60
Qy 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQGAEGAEDLEVRFNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117
RESULT 7

ABB78319

ID ABB78319 standard; Protein; 117 AA.

XX AC ABB78319;

XX DT 05-DEC-2002 (first entry)

XX DE Amino acid sequence of a human zsig33.

XX KW Short gastrointestinal peptide; SGIP; zsig33; motilin.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..23

XX FT /note= "signal peptide"

XX FT Protein 24..119

XX FT /note= "mature protein"

XX US6420521-B1.

XX PN 16-JUL-2002.

XX PD 30-JUN-2000; 2000US-0608810.

XX PF 30-JUN-1999; 99US-141592P.

XX PR (ZYMO) ZYMOGENETICS INC.

XX PA Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

XX PI WPI; 2002-634794/68.

XX DR N-PSDB; ABV72214.

XX PT New Short Gastrointestinal Peptide, which has homology to motilin, useful for preventing, diagnosing and treating gastrointestinal disorders

XX PS Disclosure; Columns 39-40; 23pp; English.

XX CC The present sequence represents human zsig33. The specification describes a short gastrointestinal peptide (SGIP), which is derived from zsig33. SGIP has homology to motilin. The SGIP peptide may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SGIP expression. For example, SGIP may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of SGIP by expressing inactive proteins or to supplement the patients own production of SGIP. SGIP may also be used as an antigen in the production of antibodies against SGIP and in assays to identify modulators of SGIP expression and activity. The anti-SGIP antibodies, agonists and antagonists may also be used to regulate expression and activity. The anti-SGIP antibodies may also be used as diagnostic agents for detecting the presence of SGIP in samples.

SQ Sequence 117 AA;

Query Match 100.0%; Score 117; DB 23; Length 117;

Best Local Similarity 100.0%; Pred. No. 2.3e-101;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPERHQVQQRKESKPPAKLQPRALAGWLRLPE 60

Db 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPERHQVQQRKESKPPAKLQPRALAGWLRLPE 60

QY 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKAPADK 117

Db 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKAPADK 117

RESULT 8

AAE23838

ID AAE23838 standard; Protein; 117 AA.

XX

AC AAE23838;

XX DT 10-SEP-2002 (first entry)

XX DE Human zsig33 protein.

XX KW Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.

XX OS Homo sapiens.

XX PN US2002055156-A1.

XX PD 09-MAY-2002.

XX PF 10-MAY-2001; 2001US-0853253.

XX PR 11-MAY-2000; 2000US-203300P.

XX PA (JASP/) JASPERS S R.

XX PA (SHEP/) SHEPPARD P O.

XX PA (DEIS/) DEISHER T A.

XX PA (BISH/) BISHOP P D.

XX PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX DR WPI; 2002-443750/47.

XX DR N-PSDB; AAD38238.

XX PT ZSIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones

XX PS Disclosure; Page 27; 34pp; English.

XX CC The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate zsig33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The zsig33 peptides are used as antigens in the production of antibodies against zsig33 and in assays to identify modulators of zsig33 expression and activity. The anti-zsig33 antibodies and antagonists are used to down regulate expression and activity. The anti-zsig33 antibodies are also used as diagnostic agents for detecting the presence of zsig33 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy and zsig33-like peptide is used in protein therapy. The present sequence is human zsig33 protein.

SQ Sequence 117 AA;

Query Match 100.0%; Score 117; DB 23; Length 117;

Best Local Similarity 100.0%; Pred. No. 2.3e-101;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPERHQVQQRKESKPPAKLQPRALAGWLRLPE 60

Db 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPERHQVQQRKESKPPAKLQPRALAGWLRLPE 60

QY 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKAPADK 117

Db 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKAPADK 117

RESULT 9
AAEL15883
ID AAEL15883 standard; Protein; 117 AA.
XX
AC AAEL15883;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human zsig33 protein.
XX
KW Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
adsorption enhancer; gastrointestinal disease; growth related disease;
inflammation; gene therapy; growth regulation; blood vessel formation;
HIV; zsig33 protein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Signal_peptide
FT Protein 24..117
FT /note= "Human mature zsig33 protein"
XX
PN WO200187933-A2.
XX
PD 22-NOV-2001.
XX
PE 10-MAY-2001; 2001WO-US15091.
XX
PR 11-MAY-2000; 2000US-0569271.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX
DR WPI; 2002-082982/11.
DR N-PSDB; AAD25759.
XX
XX New polypeptides, useful for modulating gastric contractility, nutrient
uptake, pancreatic secretion of hormones, digestive enzymes and
treating gastrointestinal and growth related diseases, comprises
zsig33-like peptides -
XX
PS Disclosure; Page 80-81; 89pp; English.
XX
XX The invention relates to zsig33-like peptides (ZS33LP) including
zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and
zsig33-epsilon peptides and nucleic acid molecules encoding such
zsig33-like peptides. ZS33LP peptides activate the immune system
in boosting immunity to infectious diseases, treating immunocompromised
patients such as human immunodeficiency virus (HIV) patients, in
improving vaccines and in treatment of bacterial, viral, protozoal and
fungal infections. Peptides of the invention are used to identify and
isolate receptors involved in growth regulation in the liver, blood
vessel formation and other developmental processes. They are useful for
evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
growth and/or differentiation of tumour cells, as additives to anti-
hypoglycaemic preparations containing glucose and as adsorption
enhancers for oral drugs which require fast nutrient action and to
stimulate glucose-induced insulin release. They are also useful as
research reagents for the expansion, differentiation, growth factor and
hormone secretion and/or cell-cell interactions of tissues associated
with gastrointestinal system, brain and central nervous system. These
molecules are useful for treating dysfunction associated with contractile
tissues or to suppress or enhance contractility in vivo and to treat
gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
acids and/or antibodies are useful for treating disorders associated
with gastrointestinal contractility, secretion of digestive enzymes,
hormone and acids, secretion of hormones in the pancreas and/or brain,
gastrointestinal motility, recruitment of digestive enzymes, inflammation
and regulation of nutrient absorption. Sequences of the invention are
useful in gene therapy. The present sequence is human zsig33 protein.

XX
SQ Sequence 117 AA;
XX
Query Match 100.0%; Score 117; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MPSPGTVCSTLLGLMLDLAMAGSSFLSPDHQVQQRKESKPKPAKLQPRALAGWLRLPE 60
|||||
DB 1 MPSPGTVCSTLLGLMLDLAMAGSSFLSPDHQVQQRKESKPKPAKLQPRALAGWLRLPE 60
|||||
QY 61 DGGQAEAGDELEVRFNAPFDVGKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117
|||||
DB 61 DGGQAEAGDELEVRFNAPFDVGKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117
|||||
RESULT 10
ABU66790
ID ABU66790 standard; Protein; 117 AA.
XX
AC ABU66790;
XX
DT 23-MAY-2003 (first entry)
XX
DE Human PRO polypeptide #221.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder;
cytostatic.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-0143114.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.

PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 98WO-US00106.
PR 08-MAR-1999; 98WO-US05028.
PR 10-MAR-1999; 98WO-US05190.
PR 20-APR-1999; 98WO-US08615.
PR 14-MAY-1999; 98WO-US10733.
PR 02-JUN-1999; 98WO-US12252.
PR 01-SEP-1999; 98WO-US40111.
PR 08-SEP-1999; 98WO-US20594.
PR 13-SEP-1999; 98WO-US20944.
PR 15-SEP-1999; 98WO-US21090.
PR 15-SEP-1999; 98WO-US21547.
PR 05-OCT-1999; 98WO-US23089.
PR 29-NOV-1999; 98WO-US28214.
PR 30-NOV-1999; 98WO-US28313.
PR 30-NOV-1999; 98WO-US28409.
PR 01-DEC-1999; 98WO-US28301.
PR 01-DEC-1999; 98WO-US28634.
PR 02-DEC-1999; 98WO-US28551.
PR 02-DEC-1999; 98WO-US28564.
PR 02-DEC-1999; 98WO-US28564.
PR 02-DEC-1999; 98WO-US28565.
PR 16-DEC-1999; 98WO-US30095.
PR 20-DEC-1999; 98WO-US30911.
PR 20-DEC-1999; 98WO-US30999.
PR 22-DEC-1999; 98WO-US30720.
PR 30-DEC-1999; 98WO-US31243.
PR 30-DEC-1999; 98WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04144.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23352.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32456.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
PI
XX
DR WPI; 2003-331925/31.
DR N-PSDB; ACA04244.
XX
XX
PT New secreted and transmembrane nucleic acids and polypeptides,
PT designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer -
XX
PS Claim 12; Fig 442; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid
CC further comprises the full-length coding sequence of the DNA deposited
CC under American Type Culture Collection (ATCC) accession number in a list
CC given in the specification. Also included are vectors and host
CC cells for producing PRO proteins. PRO fusion proteins, anti-PRO
CC antibodies, PRO extracellular domains and mature sequences, methods
CC of detecting PRO proteins, methods for stimulating the release of
CC TNF-alpha (tumour necrosis factor alpha) from human blood,
CC and the proliferation of differentiation of chondrocyte cells, the
CC proliferation of, or gene expression in pericyte cells, the release or
CC proteoglycans from cartilage, proliferation of inner ear utricular
CC supporting cells, the proliferation of T-lymphocyte cells, the release
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
CC proliferation of endothelial cells), a method for modulating the uptake
CC of glucose or free fatty acid (PPA) by skeletal muscle cells,
CC a method for inhibiting the binding of A-peptide to factor VIIa,
CC or the differentiation of adipocyte cells, a method for detecting the
CC presence of a tumour in a mammal and an oligonucleotide probe derived
CC from any of the nucleotide sequences cited above. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
CC diabetic complications. The nucleic acids are useful as hybridisation
CC probes, in chromosome and gene mapping, and in generating antisense RNA
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors. Both are useful in tissue typing.
XX
CC The present sequence represents a PRO protein of the invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 117; DB 24; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MPSPCTVCSLLLLGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRLPE 60
 Db 1 MPSPCTVCSLLLLGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRLPE 60

Oy 61 DGGQGAEGADELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 Db 61 DGGQGAEGADELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 12

ABU59871
 ID ABU59871 standard; Protein; 117 AA.

XX AC ABU59871;

XX DT 13-MAY-2003 (first entry)

XX DE Novel secreted and transmembrane protein PRO1066.

XX KW Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.

XX OS Homo sapiens.

XX PN US2003017563-A1.

XX PD 23-JAN-2003.

XX PF 07-MAY-2002; 2002US-0140808.

XX PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US22089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 22-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 10-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806899.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX

DR WPI; 2003-148238/14.
 XX N-PSDB; ABX89361.
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 XX treatments -
 XX
 PS Claim 12; Fig 442; 659pp; English.
 XX
 CC The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC is the amino acid sequence of a novel human PRO protein.
 XX
 SQ Sequence 117 AA:
 Query Match 100.0%; Score 117; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-101;
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 Db 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHEHQVQQRKSKPPAKLQPRALAGWLRLPE 60
 QY 61 DGGQAGAEDELEVRFNAPFDVGKLSGVYQHQSHQALGKFLQDILWEEAKEAPADK 117
 Db 61 DGGQAGAEDELEVRFNAPFDVGKLSGVYQHQSHQALGKFLQDILWEEAKEAPADK 117
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 ID ABU59124 standard; Protein; 117 AA.
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 AC ABU59124;
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 DT 28-APR-2003 (first entry)
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 DE Novel human secreted or transmembrane protein PRO1066.
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 KW Human; PRO: hypertrophy of neonatal heart; angiogenesis: wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosum; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW -chondrocyte redifferentiation; sports injury; arthritis.
 XX Homo sapiens.
 OS
 XX US2002132252-A1.
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 PD 19-SEP-2002.
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 PF 14-NOV-2001; 2001US-0990442.
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 PR 05-NOV-1997; 97WO-US20069.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
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 PR 30-NOV-1999; 99WO-US28313.
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 PR 24-FEB-2000; 2000WO-US04914.
 PR 02-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
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 PR 20-MAR-2000; 2000WO-US07377.
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 PR 24-AUG-2000; 2000WO-US23328.
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PR 01-JUN-2001; 2001WO-USI7800.
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PR 09-JUL-2001; 2001WO-US21735.
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PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
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PR 20-JUL-1998; 98US-093339P.
PR 30-JUL-1998; 98US-094651P.
PR 04-AUG-1998; 98US-095282P.
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PR 17-AUG-1998; 98US-096895P.
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PR 26-AUG-1998; 98US-098014P.
PR 31-AUG-1998; 98US-098525P.

PR	16-SEP-1998;	98US-100634P.	PR	20-MAR-2000;	2000WO-US07377.
PR	17-SEP-1998;	98US-100858P.	PR	30-MAR-2000;	2000WO-US08439.
PR	22-DEC-1998;	98US-113296P.	PR	15-MAY-2000;	2000WO-US13358.
PR	12-MAR-1999;	98US-123957P.	PR	17-MAY-2000;	2000WO-US13705.
PR	23-JUN-1999;	98US-141037P.	PR	22-MAY-2000;	2000WO-US14042.
Query Match 100.0%; Score 117; DB 24; Length 117;			PR	30-MAY-2000;	2000WO-US14941.
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DB	61	DGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117	PR	08-NOV-2000;	2000WO-US30952.
RESULT 15			PR	01-DEC-2000;	2000WO-US32678.
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XX	ABU59420;		PR	01-JUN-2001;	2001WO-US17800.
XX	22-APR-2003 (first entry)		PR	20-JUN-2001;	2001WO-US19692.
XX	Novel human secreted or transmembrane protein PRO1184.		PR	29-JUN-2001;	2001WO-US21066.
XX	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;		PR	09-JUL-2001;	2001WO-US21735.
KW	cardiac insufficiency disorder; cancer; tumour; immune response;		PR	16-JUN-1997;	97US-049787P.
KW	adrenal cortical capillary endothelial growth; c-fos induction;		PR	17-OCT-1997;	97US-062250P.
KW	vascular endothelial growth factor inhibition; VEGF inhibition;		PR	12-NOV-1997;	97US-065186P.
KW	endothelial cell growth inhibitor; T-lymphocytes stimulation;		PR	13-NOV-1997;	97US-065311P.
KW	retinal neurons cell survival; rod photoreceptor cell survival;		PR	24-NOV-1997;	97US-066770P.
KW	retinal disorder; retinitis pigmentosa; kidney disease;		PR	25-FEB-1998;	98US-075945P.
KW	mammalian kidney mesangial cell proliferation; Berger disease;		PR	20-MAR-1998;	98US-078910P.
KW	dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;		PR	28-APR-1998;	98US-083322P.
KW	chondrocyte redifferentiation; sports injury; arthritis.		PR	07-MAY-1998;	98US-084600P.
OS	Homo sapiens.		PR	28-MAY-1998;	98US-087106P.
XX	US200307985-A1.		PR	02-JUN-1998;	98US-087607P.
PN	06-FEB-2003.		PR	02-JUN-1998;	98US-087609P.
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XX	05-NOV-1997;	97WO-US20069.	PR	03-JUN-1998;	98US-087827P.
PR	16-SEP-1998;	98WO-US19330.	PR	04-JUN-1998;	98US-088021P.
PR	17-SEP-1998;	98WO-US19437.	PR	04-JUN-1998;	98US-088025P.
PR	07-OCT-1998;	98WO-US21141.	PR	04-JUN-1998;	98US-088026P.
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PR	10-MAR-2000;	2000WO-US05841.	PR	16-JUN-1998;	98US-089105P.
PR	15-MAR-2000;	2000WO-US06319.	PR	16-JUN-1998;	98US-089440P.
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Job time : 123.257 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:55:57 ; Search time 71.9519 seconds
(without alignments)
237.266 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 117

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Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	117	100.0	117	9 US-09-853-253-2	Sequence 2, Appli
3	117	100.0	117	9 US-09-989-722-268	Sequence 268, App
4	117	100.0	117	9 US-09-989-723-268	Sequence 268, App
5	117	100.0	117	9 US-09-989-279-268	Sequence 268, App
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ALIGNMENTS

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; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
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; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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; Patent NO. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: 251g33-like peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
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RESULT 3
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; Sequence 268, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Garber, Hanspeter
; APPLICANT: Gertszen, Mary E.
; APPLICANT: Goddard, Audrey
;

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Garber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurnee, Austin L.

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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zenin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 117; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 7.5e-104; Mismatches 0; Indels 0; Gaps 0;

Matches 117; Conservative 0;

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RESULT 5

US-09-989-279-268

; Sequence 268, Application US/09989279

; Patent No. US20020072496A1

GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
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; PRIOR FILING DATE: 1998-06-10

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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
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 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
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 ; APPLICANT: Nepier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC70
 ; CURRENT APPLICATION NUMBER: US/09/989.731
 ; CURRENT FILING DATE: 2001-11-20
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Query Match 100.0%; Score 117; DB 10; Length 117;
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Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
US-09-989-732-268
; Sequence 268, Application US/09989732
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match          100.0%; Score 117; DB 10; Length 117;
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Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      61  DGGQAGGADELEVRNPFVDGVIKLSGVQYQOHSOALGKFQDIIWEEAKEAPADK 117
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RESULT 10
US-09-990-442-268
; Sequence 268, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
;
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

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; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
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Query Match 100.0%; Score 117; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 7.5e-104; Indels 0; Gaps 0;
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RESULT 11

US-09-991-163-268
; Sequence 268, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT FILING DATE: 2001-11-14
; CURRENT APPLICATION NUMBER: US/09/991,163
; PRIOR FILING DATE: 1997-06-16
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RESULT 12
US-09-993-604-268
;; Sequence 268, Application US/09993604
;; Patent No. US20020137075A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
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;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730PIC25
;; CURRENT APPLICATION NUMBER: US/09/993,604
;; CURRENT FILING DATE: 2001-11-14
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59	PRIOR FILING DATE: 1998-06-25	59
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61	PRIOR FILING DATE: 1998-06-25	61
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73	PRIOR FILING DATE: 1998-07-02	73

; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 117; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 7.5e-104;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPGTVCSLLGLMLDLAMAGSFLSPHORVORKEKPPAKLOPRALAGWLRE 60

Db 1 MSPGTVCSLLGLMLDLAMAGSFLSPHORVORKEKPPAKLOPRALAGWLRE 60

QY 61 DGGQAGAEDELEVRNPFVDYGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

Db 61 DGGQAGAEDELEVRNPFVDYGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 13

US-09-990-456-268

; Sequence 268, Application US/09990456

; Patent No. US20020137890A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730PIC22

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 117; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.5e-104;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSTLLLLGMLWLDLDMAGSSFLSPHQRVQQRKSKKPPAKLOPRALAGWLKPE 60
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Db 1 MPSPGTVCSTLLLLGMLWLDLDMAGSSFLSPHQRVQQRKSKKPPAKLOPRALAGWLKPE 60
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Qy 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117
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Db 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117
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RESULT 14
US-09-989-721-268
; Sequence 268, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PLC55
; CURRENT APPLICATION NUMBER: US/09/989,721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/065770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

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9	PRIOR FILING DATE:	1998-06-18
10	PRIOR APPLICATION NUMBER:	60/089908
11	PRIOR FILING DATE:	1998-06-18
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18	PRIOR APPLICATION NUMBER:	60/090246
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22	PRIOR APPLICATION NUMBER:	60/090254
23	PRIOR FILING DATE:	1998-06-22
24	PRIOR APPLICATION NUMBER:	60/090349
25	PRIOR FILING DATE:	1998-06-23
26	PRIOR APPLICATION NUMBER:	60/090355
27	PRIOR FILING DATE:	1998-06-23
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29	PRIOR FILING DATE:	1998-06-24
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33	PRIOR FILING DATE:	1998-06-24
34	PRIOR APPLICATION NUMBER:	60/090444
35	PRIOR FILING DATE:	1998-06-24
36	PRIOR APPLICATION NUMBER:	60/090445
37	PRIOR FILING DATE:	1998-06-24
38	PRIOR APPLICATION NUMBER:	60/090472
39	PRIOR FILING DATE:	1998-06-24
40	PRIOR APPLICATION NUMBER:	60/090535
41	PRIOR FILING DATE:	1998-06-24
42	PRIOR APPLICATION NUMBER:	60/090540
43	PRIOR FILING DATE:	1998-06-24
44	PRIOR APPLICATION NUMBER:	60/090542
45	PRIOR FILING DATE:	1998-06-24
46	PRIOR APPLICATION NUMBER:	60/090557
47	PRIOR FILING DATE:	1998-06-24
48	PRIOR APPLICATION NUMBER:	60/090676
49	PRIOR FILING DATE:	1998-06-25
50	PRIOR APPLICATION NUMBER:	60/090678
51	PRIOR FILING DATE:	1998-06-25
52	PRIOR APPLICATION NUMBER:	60/090690
53	PRIOR FILING DATE:	1998-06-25
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55	PRIOR FILING DATE:	1998-06-25
56	PRIOR APPLICATION NUMBER:	60/090862
57	PRIOR FILING DATE:	1998-06-26
58	PRIOR APPLICATION NUMBER:	60/090863
59	PRIOR FILING DATE:	1998-06-26
60	PRIOR APPLICATION NUMBER:	60/091360
61	PRIOR FILING DATE:	1998-07-01
62	PRIOR APPLICATION NUMBER:	60/091478
63	PRIOR FILING DATE:	1998-07-02
64	PRIOR APPLICATION NUMBER:	60/091544
65	PRIOR FILING DATE:	1998-07-01
66	PRIOR APPLICATION NUMBER:	60/091519
67	PRIOR FILING DATE:	1998-07-02
68	PRIOR APPLICATION NUMBER:	60/091626
69	PRIOR FILING DATE:	1998-07-02

; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 117; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.5e-104; Indels 0; Gaps 0;
Matches 117; Conservative 0; Mismatches 0;
QY 1 MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVRQQRKESKPKLQPRALAGWL RPE 60
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DB 1 MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVRQQRKESKPKLQPRALAGWL RPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117
|||||
DB 61 DGGQAGAEDELEVRNAPFDVGKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 15

US-09-992-598-268
; Sequence 268, Application US/09992598
; Patent No. US20020160384A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
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;; PRIOR APPLICATION NUMBER: 60/090444
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;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
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;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978

;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 117; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.5e-104;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSSLLLLGLMLWLDLWAGSSFLSPFHQRVQQRKESKPPAKLQPRALAGWLRPE 60
|||||
Db 1 MPSPGTVCSSLLLLGLMLWLDLWAGSSFLSPFHQRVQQRKESKPPAKLQPRALAGWLRPE 60
|||||

Qy 61 DGGQAEAGAELEVRNAPFDVGIKLSGVQYQOHSOALGKFLQDILWEEAKEAPADK 117
|||||
Db 61 DGGQAEAGAELEVRNAPFDVGIKLSGVQYQOHSOALGKFLQDILWEEAKEAPADK 117
|||||

Search completed: September 11, 2003, 18:16:17
Job time : 72.9519 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:37 ; Search time 44.4225 Seconds
(without alignments)
253.289 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 117

Sequence: 1 MSPSGTVCSSLLGLMLWLDL.....LCKFLQDILWEAKEAPADK 117

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	117	100.0	117	1 A59316	ghrelin precursor
2	18	15.4	117	1 B59316	ghrelin precursor
3	8	6.8	23	2 A49221	14K aggregative ad
4	8	6.8	302	2 JH0572	hypothetical prote
5	8	6.8	344	2 A48990	transcription regu
6	8	6.8	483	2 T04453	hypothetical prote
7	7	6.0	22	2 PH1333	ig heavy chain DJ
8	7	6.0	138	2 F83841	hypothetical prote
9	7	6.0	207	2 B83523	hypothetical prote
10	7	6.0	216	2 B73469	hypothetical prote
11	7	6.0	247	2 F82101	DNA polymerase III
12	7	6.0	256	2 B64050	DNA-directed DNA p
13	7	6.0	406	2 AG0548	probable ABC-trans
14	7	6.0	435	2 A86195	hypothetical prote
15	7	6.0	443	2 F87488	prolyl-trNA synth
16	7	6.0	444	2 D87296	multidrug resist
17	7	6.0	464	2 A47655	spliceosome-assoc
18	7	6.0	493	2 S77612	amidophosphoribos
19	7	6.0	502	2 A53444	activin receptor-1
20	7	6.0	502	2 JC2491	serine/threonine k
21	7	6.0	562	2 T34319	hypothetical prote
22	7	6.0	633	2 G71026	hypothetical prote
23	7	6.0	662	2 E82991	probable O-antigen
24	7	6.0	698	2 D90541	atp synthase beta
25	7	6.0	809	2 A12747	conserved hypothet
26	7	6.0	873	2 H97528	hypothetical prote
27	7	6.0	904	2 D90772	sensor protein tor
28	7	6.0	904	2 H85634	sensor protein tor
29	7	6.0	904	2 G64840	protein-histidine

ALIGNMENTS

RESULT 1

A59316

ghrelin precursor - human

N:Alternate names: preproghrelin

C:Species: Homo sapiens (man)

C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000

C:Accession: A59316

R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A:Reference number: A59316; MUID:20067959; PMID:10604470

A:Accession: A59316

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-117 <KOJ>

A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BAA89371.1; PID:g6691572

A:Experimental source: tissue stomach endocrine cells

A:Note: submitted to GenBank, June 1999

C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone releasing hormone) from the hypothalamus.

C:Superfamily: motilin

C:Keywords: hormone; lipoprotein; stomach

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-51/Product: ghrelin #status predicted <MAT>

F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 117; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.2e-109;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSGTVCSSLLGLMLWLDLWLAGSSFLSPHQVQVRKESKPPAKLQPRALAGWL RPE 60

DB 1 MSPSGTVCSSLLGLMLWLDLWLAGSSFLSPHQVQVRKESKPPAKLQPRALAGWL RPE 60

QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQHSOALGKFLQDILWEAKEAPADK 117

DB 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQHSOALGKFLQDILWEAKEAPADK 117

RESULT 2

B59316

ghrelin precursor - rat

N:Alternate names: preproghrelin

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000

C:Accession: B59316

R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A:Reference number: A59316; MUID:20067959; PMID:10604470

A:Accession: B59316

A:Status: not compared with conceptual translation

30 7 6.0 910 2 B83451
31 7 6.0 1239 1 Q0BE10
32 7 6.0 1970 2 T03284
33 7 6.0 3165 2 S1010
34 6 5.1 52 2 C83241
35 6 5.1 59 2 G97930
36 6 5.1 69 2 C87574
37 6 5.1 72 2 S48790
38 6 5.1 80 1 PCCG
39 6 5.1 84 2 AH3402
40 6 5.1 89 2 E83141
41 6 5.1 103 2 F82266
42 6 5.1 104 2 T48688
43 6 5.1 106 2 A71193
44 6 5.1 106 2 AE2124
45 6 5.1 108 2 T04117

aconitate hydratase
BOLFI protein - hu
myoblast city prote
hypothetical prote
hypothetical prote
hypothetical prote
cold-shock domain
troponin T, cardia
pancreatic hormone
hypothetical cytos
hypothetical prote
conserved hypothet
hypothetical prote
hypothetical prote
hypothetical prote
SEC18 protein homo

A:Molecule type: mRNA; protein
A:Residues: 1-117 <KO>
A:Cross-references: GB:AB029433; NID:g6691569; PIDN:BA089370.1; PID:g6691570
A:Experimental source: strain SD; tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone) from the pituitary gland.
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 15.4%; Score 18; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 QQRKSKPPAKLQPRAL 53
|||||
DB 36 QQRKSKPPAKLQPRAL 53

RESULT 3
A49221
14k aggregative adherence fimbriae I protein - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
C:Accession: A49221
R:Nataro, J.P.; Yikang, D.; Giron, J.A.; Savarino, S.J.; Kothary, M.H.; Hall, R.
Infect. Immun. 61, 1126-1131, 1993
A:Title: Aggregative adherence fimbria I expression in enteroaggregative Escherichia coli
A:Reference number: A49221; MUID:93162805; PMID:8094379
A:Accession: A49221
A:Contents: 17-2, serotype O3:H2
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <NAT>
A:Note: sequence extracted from NCBI backbone (NCBIP:125179)

Query Match 6.8%; Score 8; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 IKLSGVQY 91
|||||
DB 16 IKLSGVQY 23

RESULT 4
JH0572
hypothetical protein - Streptomyces lividans (fragment)
C:Species: Streptomyces lividans
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-1999
C:Accession: JH0572
R:Lichenstein, H.S.; Busse, L.A.; Smith, G.A.; Narhi, L.O.; McGinley, M.O.; Rohde, M.F.; Gene 111, 125-130, 1992
A:Title: Cloning and characterization of a gene encoding extracellular metalloprotease from Streptomyces lividans
A:Reference number: JH0571; MUID:92192468; PMID:1547948
A:Accession: JH0572
A:Molecule type: DNA
A:Residues: 1-302 <LIC>
A:Cross-references: GB:M09476; NID:g153411; PIDN:AAA26804.1; PID:g153412
A:Experimental source: strain TK24
A:Note: the authors translated the codon GTA for residue 260 as Asp
A:Note: this protein has a strong similarity to LysR family of transcriptional regulators
C:Superfamily: Pseudomonas putida regulatory protein catR

Query Match 6.8%; Score 8; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RALAGWLR 58
|||||

Db 99 RALAGWLR 106

RESULT 5
A48990
transcription regulator LysR family homolog SnpR - Streptomyces lividans
C:Species: Streptomyces lividans
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C:Accession: A48990
R:Butler, M.J.; Davey, C.C.; Krygsman, P.; Walczyk, E.; Malek, L.T.
Can. J. Microbiol. 38, 912-920, 1992
A:Title: Cloning of genetic loci involved in endoprotease activity in Streptomyces lividans
A:Reference number: A48990; MUID:93099553; PMID:1464066
A:Contents: 66
A:Accession: A48990
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-344 <BUT>
A:Note: sequence extracted from NCBI backbone (NCBIN:121210, NCBIP:121213)
C:Superfamily: Pseudomonas putida regulatory protein catR

Query Match 6.8%; Score 8; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RALAGWLR 58
|||||
DB 103 RALAGWLR 110

RESULT 6
T04453
hypothetical protein F4D11.80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04453
R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Hohelsel, J.; Mewes, S.
Submitted to the Protein Sequence Database, April 1998
A:Reference number: 215360
A:Accession: T04453
A:Molecule type: DNA
A:Residues: 1-483 <BEV>
A:Cross-references: EMBL:AL022537
A:Experimental source: cultivar Columbia; BAC clone F4D11
C:Genetics:
A:Map position: 4
A:Introns: 17/3; 44/1; 94/1; 141/3; 206/2; 247/2; 345/3; 395/1; 434/2
A:Note: F4D11.80

Query Match 6.8%; Score 8; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 QAEGAED 71
|||||
DB 302 QAEGAED 309

RESULT 7
PH1333
Ig heavy chain DJ region (clone C238-133) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1333
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1333
A:Molecule type: DNA
A:Residues: 1-22 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 6.0%; Score 7; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VCSLLLL 13
DB 6 VCSLLLL 12

RESULT 8
F83841
hypothetical protein BH1534 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: F83841
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: F83841
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <STO>
A:Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA05253.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1534
C:Superfamily: Bacillus subtilis hypothetical protein yndB

Query Match 6.0%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 EVRFNAP 79
DB 10 EVRFNAP 16

RESULT 9
B83523
hypothetical protein PA0981 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83523
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <STO>
A:Cross-references: GB:AE004531; GB:AE004091; NID:g9946882; PIDN:AAG04370.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0981

Query Match 6.0%; Score 7; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPGTV 7
DB 84 MPSPGTV 90

RESULT 10
B75469
hypothetical protein - Deinococcus radiodurans (strain RL)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: B75469
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RL
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: B75469
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-216 <WHI>
A:Cross-references: GB:AE001938; GB:AE000513; NID:g6458553; PIDN:AAF10422.1; PID:9645
A:Experimental source: strain RL
C:Genetics:
A:Gene: DR0838
A:Map position: 1

Query Match 6.0%; Score 7; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 LDLAMAG 24
DB 50 LDLAMAG 56

RESULT 11
F82101
DNA polymerase III, epsilon chain VC2233 [imported] - Vibrio cholerae (strain N16961)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82101
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
; chardson, D.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: F82101
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <HEI>
A:Cross-references: GB:AE004295; GB:AE003852; NID:g9656789; PIDN:AAF95377.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2233
A:Map position: 1
C:Superfamily: dnaQ protein

Query Match 6.0%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 NAPFDVG 83
DB 104 NAPFDVG 110

RESULT 12
B64050
DNA-directed DNA polymerase (EC 2.7.7.7) III epsilon chain - Haemophilus influenzae (s
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 21-Jul-2000
C:Accession: B64050
R:Feischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: B64050
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-256 <TIGR>

A:Cross-references: GB:U32699; GB:L42023; NID:g3212180; PIDN:AAC21808.1; PID:g1573090; T

C:Genetics:

A:Gene: dnaQ

C:Function:

A:Pathway: DNA biosynthesis

C:Superfamily: dnaQ protein

C:Keywords: DNA biosynthesis; DNA replication initiation; nucleotidyltransferase

Query Match 6.0%; Score 7; DB 2; Length 256;

Best Local Similarity 100.0%; Pred. No. 36;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 NAPPDVG 83

Db 98 NAPPDVG 104

RESULT 13

AG0548

probable ABC-transporter inner membrane protein SbmA sbmA [imported] - Salmonella enteri

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: This species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AG0548

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AG0548

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-406 <PAR>

A:Cross-references: GB:AL51382; PIDN:CAD08831.1; PID:g16501645; GSPDB:GN00176

C:Genetics:

A:Gene: sbmA

C:Superfamily: probable inner membrane transport protein bacA

Query Match 6.0%; Score 7; DB 2; Length 406;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 VGKLSG 88

Db 261 VGKLSG 267

RESULT 14

A86195

hypothetical protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A86195

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A86195

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-435 <STO>

A:Cross-references: GB:AE005172; NID:g8810462; PIDN:AAF80123.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

C:Superfamily: flavonol O3-glucosyltransferase

Query Match 6.0%; Score 7; DB 2; Length 435;

Best Local Similarity 100.0%; Pred. No. 56;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GSSFLSP 30

Db 123 GSSFLSP 129

RESULT 15

F87488

prolyl-tRNA synthetase [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002

C:Accession: F87488

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,

n, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A>Title: Complete genome sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: F87488

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-443 <STO>

A:Cross-references: GB:AE005673; NID:gl3423386; PIDN:AAK23906.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC1931

C:Superfamily: proline-tRNA ligase pros

Query Match 6.0%; Score 7; DB 2; Length 443;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 APFDVGI 84

Db 344 APFDVGI 350

Search completed: September 11, 2003, 17:57:03

Job time : 47.4225 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:30:37 : Search time 22.5241 Seconds
(without alignments)
244.278 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 117

Sequence: 1 MPSPGTGCSLLLLGLMLDL.....LCKFLQDILWEEAKEAPADK 117

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	100.0	117	1	GHRL_HUMAN
2	18	15.4	117	1	GHRL_CANFA
3	18	15.4	117	1	GHRL_MOUSE
4	18	15.4	117	1	GHRL_RAT
5	15	12.8	116	1	GHRL_BOVIN
6	15	12.8	118	1	GHRL_PIG
7	8	6.8	328	1	MPR2_STRCO
8	8	6.8	344	1	MPRR_STRLI
9	7	6.0	253	1	DP3E_PASMU
10	7	6.0	256	1	DP3E_HAEIN
11	7	6.0	286	1	CHM1_BRARE
12	7	6.0	327	1	NAS1_HORVU
13	7	6.0	464	1	S3A2_HUMAN
14	7	6.0	475	1	S3A2_MOUSE
15	7	6.0	493	1	PUR1_SYNP7
16	7	6.0	502	1	BMRB_HUMAN
17	7	6.0	502	1	BMRB_MOUSE
18	7	6.0	914	1	TORS_ECO57
19	7	6.0	914	1	TORS_ECOLI
20	7	6.0	1142	1	SPK_HUMAN
21	7	6.0	1239	1	V120_EBV
22	6	5.1	80	1	PAHO_CHICK
23	6	5.1	105	1	RL36_TRIHM
24	6	5.1	112	1	RBFA_MYCPU
25	6	5.1	112	1	SVS4_RAT
26	6	5.1	112	1	SY27_HUMAN
27	6	5.1	116	1	CART_HUMAN
28	6	5.1	117	1	NUSM_PROWI
29	6	5.1	125	1	MSP1_GLORO
30	6	5.1	125	1	MSP2_GLORO
31	6	5.1	125	1	MSP3_GLORO
32	6	5.1	127	1	ACPS_SHEON
33	6	5.1	129	1	CART_MOUSE

34	6	5.1	129	1	CART_RAT
35	6	5.1	140	1	LCA_MACEU
36	6	5.1	144	1	CSF2_HUMAN
37	6	5.1	149	1	TTHY_MONDO
38	6	5.1	154	1	PFDA_HALNI
39	6	5.1	154	1	RNS6_BOVIN
40	6	5.1	156	1	PSPN_MOUSE
41	6	5.1	162	1	MUG_SERMA
42	6	5.1	165	1	SSPB_ECOLI
43	6	5.1	168	1	IAO3_WHEAT
44	6	5.1	170	1	NU6M_XENLA
45	6	5.1	178	1	EFAB_CHICK

ALIGNMENTS

RESULT 1
GHRL_HUMAN
ID GHRL_HUMAN STANDARD; PRT; 117 AA.
AC Q9UBU3: Q8TAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRL OR WTLRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach.";
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Stomach;
RT Tomasetto C., Karam S.M., Rio M.-C.;
RA "Identification of a novel gastric protein m46.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wajratch M.P., Ten I.S., Gertner J.M., Leibell R.L.;
RT "Genomic organization of the human Ghrelin gene.";
RL J. Endocrinol. Genet. 1:231-233(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Hellton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [6]
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RL hormone: the motilin-related peptide.";
 RN Gastroenterology 119:395-405(2000).
 RP [7]
 RP REVIEW.
 RA MEDLINE=21203998; PubMed=11306336;
 RX Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RL hormone secretagogue receptor.";
 CC Trends Endocrinol. Metab. 12:118-122(2001).
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -!- PTM: O-n-octanoylation is essential for activity.
 CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobogen.fr/services/chromocancer/Genes/GhrelinID327.html".
 CC -----
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 CC -----
 CC EMBL; AB029434; BAA89371.1; -
 CC EMBL; AB035700; BAB19045.1; -
 CC EMBL; AJ252278; CAB5733.1; -
 CC EMBL; AF296538; AAG10300.1; -
 CC EMBL; BC025791; AAH25791.1; -
 CC PIR; A59316; A59316.
 CC MIM; 605353; -
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0005111; P:growth hormone receptor ligand activity; TAS.
 CC GO; GO:0007287; P:cell-cell signaling; TAS.
 CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
 CC InterPro; IPR006737; motilin_assoc.
 CC InterPro; IPR005441; Preproghrelin.
 CC Pfam; PF04643; motilin_assoc; 1.
 CC Pfam; PF04644; motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD332162; Preproghrelin; 1.
 CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing 23
 FT SIGNAL 1 23
 FT PEPTIDE 24 51
 FT PROPEP 52 117
 FT LIPID 26 26
 FT VARSPLIC 37 37
 FT Missing (in Isoform 2).
 FT /FTId=VSP_003245.
 FT L -> M (IN REF. 5).
 FT CONFLICT 72 72

SQ SEQUENCE 117 AA; 12911 MW; 39C0572EBECA2755 CRC64;
 Query Match 100.0%; Score 117; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8e-111;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 1 MPSPTGCSLLGLMLDLAMAGSSFLSPHQRVQQRKSKPKPKLQPRALAGWLRLPE 60
 Db 1 MPSPTGCSLLGLMLDLAMAGSSFLSPHQRVQQRKSKPKPKLQPRALAGWLRLPE 60
 QY 61 DGGQAEAGAEDELEVRFNAPFDVGKLSGVQVQHQISQALGKFLQDILWEEAEAPDK 117
 Db 61 DGGQAEAGAEDELEVRFNAPFDVGKLSGVQVQHQISQALGKFLQDILWEEAEAPDK 117
 RESULT 2
 GHRL_CANFA
 ID GHRL_CANFA STANDARD; PRT; 117 AA.
 AC Q9BEF8; Q9BEF7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide) (Motilin-related peptide).
 GN GHRL OR MTLRP.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Gastric fundus;
 RA Tomasetto C., Wendling C., Rio M.-C., Poltras P.;
 RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
 RT fundus.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation (by similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9BEF8-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9BEF8-2; Sequence=VSP_003244;
 CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ298295; CAC29155.1; -
 CC EMBL; AJ298296; CAC29156.1; -
 CC InterPro; IPR006737; motilin_assoc.
 CC InterPro; IPR006738; motilin_ghrelin.
 CC InterPro; IPR005441; Preproghrelin.
 CC Pfam; PF04643; motilin_assoc; 1.
 CC Pfam; PF04644; motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD332162; Preproghrelin; 1.
 CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing 23
 FT SIGNAL 1 23
 FT PEPTIDE 24 51
 FT PROPEP 52 117
 FT LIPID 26 26
 FT VARSPLIC 37 37
 FT Missing (in Isoform 2).
 FT /FTId=VSP_003245.
 FT L -> M (IN REF. 5).
 FT CONFLICT 72 72

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FT LIPID          26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC      37 37 Missing (in isoform 2).
FT FTID-VSP_003244
SQ SEQUENCE      117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Query Match      15.4%; Score 18; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 QQRKSKPPAKLPAL 53
Db 36 QQRKSKPPAKLPAL 53

RESULT 3
GHRM_MOUSE
ID GHRM_MOUSE STANDARD; PRT; 117 AA.
AC Q9EQX0; Q9WU21;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRM OR MTLRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
RC TISSUE=Stomach;
RX MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Kazem S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT Identification and characterization of a novel gastric peptide
RT hormone: the motilin-related peptide.;
RL Gastroenterology 119:395-405(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Kojima M.;
RT "Mouse mRNA for preproghrelin.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336;

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RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
receptor type 1 (GHSR) inducing the release of growth hormone from
the pituitary. Has an appetite-stimulating effect, induces
adiposity and stimulates gastric acid secretion. Involved in
growth regulation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC -!- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
with higher levels in the stomach, medium levels in the duodenum,
jejunum, ileum and colon. Low expression in the testis and brain.
CC Not detected in the salivary gland, pancreas, liver and lung.
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
CC EMBL; AJ243503; CAB46500.1; -
CC EMBL; AB035701; BAB19046.1; -
CC EMBL; AB060078; BAB69857.1; -
CC EMBL; AK008658; BAB25814.1; -
CC EMBL; AK008860; BAB25934.1; -
CC MGD; MGI:1930008; Ghrl.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005576; C:extracellular; IDA.
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC Pfam; PF04643; motilin_assoc. 1.
CC Pfam; PF04644; motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN
CC ProDom; PD332162; Preproghrelin; 1.
CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
KW SIGNAL
FT SIGNAL 1 23 GHRELIN.
FT PEPTIDE 24 51 REMOVED IN MATURE FORM (BY SIMILARITY).
FT PROPEP 52 117 N-OCTANOATE (BY SIMILARITY).
FT LIPID 26 26 MISSING (in isoform 2).
FT VARSPLIC 37 37 /FTID-VSP_003246.
FT FT SEQUENCE 117 AA; 13207 MW; EACB49D2E3CA7203 CRC64;
SQ
Query Match 15.4%; Score 18; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 QQRKSKPPAKLPAL 53
Db 36 QQRKSKPPAKLPAL 53

RESULT 4
GHRM_RAT
ID GHRM_RAT STANDARD; PRT; 117 AA.
AC Q9QYH7; Q9ET69;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone

```

DE releasing peptide).

GN GHRL.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,

RP AND ACYLATION OF SER-26.

PC STRAIN-Sprague-Dawley; TISSUE=Stomach;

RX MEDLINE=20067959; PubMed=10604470;

RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;

RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach.";

RL Nature 402:656-660(1999).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS

RP SPECTROMETRY, AND ACYLATION OF SER-26.

RC STRAIN-Sprague-Dawley; TISSUE=Stomach;

RX MEDLINE=20357315; PubMed=10801861;

RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;

RT "Purification and characterization of rat des-Gln14-ghrelin, a second

RT endogenous ligand for the growth hormone secretagogue receptor.";

RL J. Biol. Chem. 275:21995-22000(2000).

RN [3]

RP CHARACTERIZATION.

RP MEDLINE=21092536; PubMed=11162448;

RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;

RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide

RT in gastrointestinal tissue.";

RL Biochem. Biophys. Res. Commun. 279:909-913(2000).

RN [4]

RP STRUCTURE-ACTIVITY RELATIONSHIP.

RP MEDLINE=21433488; PubMed=11549267;

RA Matsunoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,

RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;

RT "Structure-activity relationship of ghrelin: pharmacological study of

RT ghrelin peptides.";

RL Biochem. Biophys. Res. Commun. 287:142-146(2001).

RN [5]

RP REVIEW.

RP MEDLINE=21203998; PubMed=11306336;

RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;

RT "Ghrelin: discovery of the natural endogenous ligand for the growth

RT hormone secretagogue receptor.";

RL Trends Endocrinol. Metab. 12:118-122(2001).

CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue

CC receptor type 1 (GHSR) inducing the release of growth hormone from

CC the pituitary. Has an appetite-stimulating effect, induces

CC adiposity and stimulates gastric acid secretion. Involved in

CC growth regulation.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=1; Synonyms=Ghrelin;

CC IsoId=Q9QYH7-1; Sequence=Displayed;

CC Name=2; Synonyms=del-Gln14-ghrelin;

CC IsoId=Q9QYH7-2; Sequence=VSP_003248;

CC -1- TISSUE SPECIFICITY: Broadly expressed with higher expression in

CC the stomach. Very low levels are detected in the hypothalamus,

CC heart, lung, pancreas, intestine and adipose tissue.

CC -1- PTM: O-n-octanoylation is essential for activity. The replacement

CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.

CC -1- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;

CC RANGE=24-51.

CC -1- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;

CC RANGE=24-36, 38-51.

CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.

CC -----

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CC -----

CC EMBL; AB029433; BAA89370.1; -;

DR EMBL; AB035699; BAB11956.1; -;

DR PIR; B59316; B59316.

DR InterPro; IPR006737; motilin_assoc.

DR InterPro; IPR006738; motilin-ghrelin.

DR InterPro; IPR005441; Preproghrelin.

DR Pfam; PF04643; motilin_assoc; 1.

DR Pfam; PF04644; motilin-ghrelin; 1.

DR PRINTS; PR01624; GHRELIN.

DR ProDom; PD332162; Preproghrelin; 1.

DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;

KW Alternative splicing.

KW SIGNAL 1 23

FT PEPTIDE 24 51 GHRELIN.

FT PROPEP 52 117 REMOVED IN MATURE FORM.

FT LIPID 26 26 N-OCTANOATE.

FT VARSPLIC 37 37 Missing (in isoform 2).

FT /FTID=VSP_003248.

SO SEQUENCE 117 AA; 13176 MW; 8857546FE51A7691 CRC64;

Query Match 15.4%; Score 18; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.3e-11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 QQRKESKPPAKLPQPRAL 53

Db 36 QQRKESKPPAKLPQPRAL 53

|||||

RESULT 5

GHRL_BOVIN

ID GHRL_BOVIN STANDARD; PRT; 116 AA.

AC Q9BDJ6; Q9GKY6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ghrelin precursor (growth hormone secretagogue) (Growth hormone

DE releasing peptide).

GN GHRL.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RA Kita K., Harada K., Yokota H.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 24-99 FROM N.A.

RA Kojima M.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue

CC receptor type 1 (GHSR) inducing the release of growth hormone from

CC the pituitary. Has an appetite-stimulating effect, induces

CC adiposity and stimulates gastric acid secretion. Involved in

CC growth regulation (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).

CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.

CC -----

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```
DR EMBL; AL939131; CAB76352.1; -.
DR InterPro; IPR000847; HTH_LYSR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; Protease; Transcription regulation; Complete proteome.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL)
SQ SEQUENCE 328 AA; 35885 MW; 2BA97730AE4FA16B CRC64;

Query Match 6.8%; Score 8; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 RALAGWLR 58
DB 103 RALAGWLR 110
|||||

RESULT 8
MPRR_STRLI STANDARD; PRT; 344 AA.
ID MPRR_STRLI STANDARD; PRT; 344 AA.
AC P43163;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Small neutral protease regulatory protein.
GN MPRR OR SNPR.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=66 / 1326;
RX MEDLINE=93099553; PubMed=1464066;
RA Butler M.J., Davey C.C., Krygsman P., Walczyk E., Malek L.T.;
RT "Cloning of genetic loci involved in endoprotease activity in
RT Streptomyces lividans 66: a novel neutral protease gene with an
RT adjacent divergent putative regulatory gene.";
RL Can. J. Microbiol. 38:912-920(1992).
RN [2]
RP SEQUENCE OF 1-305 FROM N.A.
RC STRAIN=TK24;
RX MEDLINE=92192468; PubMed=1547948;
RA Lichenstein H.S., Busse L.A., Smith G.A., Narhi L.O.,
RA McGinley M.O., Rohde M.F., Katowitz J.L., Zukowski M.M.;
RT "Cloning and characterization of a gene encoding extracellular
RT metalloprotease from Streptomyces lividans.";
RL Gene 111:125-130(1992).
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE GENE (SNPA) FOR THE
CC SMALL NEUTRAL PROTEASE.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----
DR EMBL; M81703; AAA26739.1; -.
DR EMBL; M89476; AAA26804.1; ALT_INIT.
DR InterPro; IPR000847; HTH_LYSR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW Transcription regulation; DNA-binding; Activator.
FT DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
```

```
FT CONFLICT 270 270 G -> AR (IN REF. 2).
SQ SEQUENCE 344 AA; 37415 MW; 485C82C813B52312 CRC64;

Query Match 6.8%; Score 8; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 RALAGWLR 58
DB 103 RALAGWLR 110
|||||

RESULT 9
DP3E_PASMU STANDARD; PRT; 253 AA.
ID DP3E_PASMU STANDARD; PRT; 253 AA.
AC Q9CPE0;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE DNA polymerase III, epsilon chain (EC 2.7.7.7).
GN DNAO OR PM0106.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THE EPSILON SUBUNIT CONTAIN THE EDITING FUNCTION AND IS A
CC PROOFREADING 3'-5' EXONUCLEASE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC + [DNA](N).
CC -!- SUBUNIT: DNA polymerase III contains a core (composed of alpha,
CC epsilon and theta chains) that associates with a tau subunit. This
CC core dimerizes to form the POLIII' complex. POLIII' associates
CC with the gamma complex (composed of gamma, delta, delta', psi and
CC chi chains) and with the beta chain to form the complete DNA
CC polymerase III complex (By similarity).
CC -----
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CC -----
DR EMBL; AE006046; AAK02190.1; -.
DR InterPro; IPR006054; DnaQ.
DR InterPro; IPR006309; DnaQ_proteo.
DR Pfam; IPR006055; Exonuclease.
DR Pfam; PF00929; Exonuclease; 1.
DR SMART; SM00479; EXOIII; 1.
DR TIGRFAMS; TIGR00573; dnaq; 1.
DR TIGRFAMS; TIGR01406; dnaq_proteo; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
KW Exonuclease; Complete proteome.
SQ SEQUENCE 253 AA; 28559 MW; AEF3C48030D4B64C CRC64;

Query Match 6.0%; Score 7; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 77 NAFPDVG 83
DB 101 NAFPDVG 107
|||||
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RESULT 10
DP3E_HAEIN          STANDARD;          PRT;      256 AA.
AC  P43745;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  DNA polymerase III, epsilon chain (EC 2.7.7.7).
GN  DNAQ OR HI0137
OS  Haemophilus influenzae.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC  Pasteurellaceae; Haemophilus.
OX  NCBI_TaxID=727;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Rd / KW20 / ATCC 51907;
RX  MEDLINE=95350630; PubMed=7542800;
RA  Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA  Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA  McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA  Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA  Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA  Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA  Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA  Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA  Venter J.C.;
RT  "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT  Rd.";
RL  Science 269:496-512(1995).
CC  -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC  RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC  THE EPSILON SUBUNIT CONTAIN THE EDITING FUNCTION AND IS A
CC  PROOFREADING 3'-5' EXONUCLEASE (BY SIMILARITY).
CC  -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC  + [DNA]([N]).
CC  -1- SUBUNIT: DNA polymerase III contains a core (composed of alpha,
CC  epsilon and theta chains) that associates with a tau subunit. This
CC  core dimerizes to form the POLIII' complex. POLIII' associates
CC  with the gamma complex (composed of gamma, delta, delta', psi and
CC  chi chains) and with the beta chain to form the complete DNA
CC  polymerase III complex (by similarity).
-----
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-----
EMBL: U32699; AAC21808.1;
DR  PIR: B64050; B64050.
DR  TIGR: HT0137;
DR  InterPro: IPR006054; DnaQ.
DR  InterPro: IPR006309; DnaQ_proteo.
DR  Pfam: PF00929; Exonuclease.
DR  SMART: SM00479; EXOIII; 1.
DR  TIGRFAMs: TIGR00573; dnaQ; 1.
DR  TIGRFAMs: TIGR01406; dnaQ_proteo; 1.
KW  Transferase: DNA-directed DNA polymerase; DNA replication; Hydrolase;
KW  Exonuclease; Complete proteome.
SQ  SEQUENCE 256 AA; 29131 MW; 694C9273AD4438D1 CRC64;

Query Match          6.0%; Score 7; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  77 NAPFDVG 83
Db  98 NAPFDVG 104

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RESULT 11
CHM1_BRARE          STANDARD;          PRT;      286 AA.
ID  CHM1_BRARE
AC  P58239;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Chondromodulin-I precursor (Chm-I) (Leukocyte cell-derived chemotaxin
DE  1) [Contains: Chondrosurfactant protein (CH-SP)].
GN  LECT1 OR CHM1 OR CHM1.
OS  Brachydanio rerio (zebrafish) (Danio rerio).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC  Cyprinidae; Danio.
OX  NCBI_TaxID=7955;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21322690; PubMed=11429291;
RA  Sachdev S.W., Dietz U.H., Oshima Y., Lang M.R., Knapik E.W.,
RA  Hiraki Y., Shukunami C.;
RT  "Sequence analysis of zebrafish chondromodulin-1 and expression
RT  profile in the notochord and chondrogenic regions during cartilage
RT  morphogenesis.";
RL  Mech. Dev. 105:157-162(2001).
CC  -1- FUNCTION: Bifunctional growth regulator. May contribute to the
CC  rapid growth of cartilage and vascular invasion prior to the
CC  replacement of cartilage by bone during endochondral bone
CC  development (By similarity).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
CC  inter-territorial matrix of cartilage (By similarity).
CC  -1- PTM: After cleavage, the post-translationally modified Chm-I is
CC  secreted as a glycoprotein (By similarity).
CC  -1- SIMILARITY: BELONGS TO THE CHONDROMODULIN-I FAMILY.
-----
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-----
EMBL: AF323374; AAK77023.1;
DR  ZFIN: ZDB-GENE-010713-1; lect1.
DR  Pfam: PF04089; BRICHOS; 1.
KW  Cartilage; Glycoprotein; Transmembrane;
KW  Cleavage on pair of basic residues.
FT  CHAIN 1 165
FT  CHONDROSURFACTANT PROTEIN
FT  (BY SIMILARITY).
FT  PROPEP 166 169
FT  CHAIN 170 286
FT  TRANSMEM 29 49
FT  CARBOHYD 191 191
FT  N-LINKED (GLCNAC...) (POTENTIAL).
SQ  SEQUENCE 286 AA; 32235 MW; 21B377E0348EDDB3 CRC64;

Query Match          6.0%; Score 7; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  25 SSFLSPE 31
Db  138 SSFLSPE 144

RESULT 12
NAS1_HORVU          STANDARD;          PRT;      327 AA.
ID  NAS1_HORVU
AC  Q9ZOV9;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Nicotianamine synthase 1 (EC 2.5.1.43) (S-adenosyl-L-methionine:S-

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DE adenosyl-L-methionine:S-adenosyl-methionine 3-amino-3-
GN carboxypropyltransferase 1) (HVNAS1).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Tricaceae; Hordeum.
OX NCBI_TaxID=4513;
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-19; 63-69; 181-243 AND 247-266.
RC STRAIN=cv. Ehimehata No.1; TISSUE=Root;
RX MEDLINE=99137899; PubMed=9952442;
RA Higuchi K., Suzuki K., Nakanishi H., Yamaguchi H., Nishizawa N.-K.,
RA Mori S.;
RT "Cloning of nicotianamine synthase genes, novel genes involved in the
RT biosynthesis of phytosiderophores."
RT Plant Physiol. 119:471-480(1999).
CC -1- FUNCTION: Synthesizes nicotianamine, a polyamine that is the first
CC intermediate in the synthesis of the phytosiderophores of the
CC mugineic acid type found in gramineae which serves as a sensor for
CC the physiological iron status within the plant, and/or might be
CC involved in the transport of iron (By similarity).
CC -1- CATALYTIC ACTIVITY: 3 S-adenosyl-L-methionine -> 3 5'-S-methyl-5'-
CC thioadenosine + nicotianamine.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- TISSUE SPECIFICITY: In roots but not in leaves.
CC -1- INDUCTION: By iron deficiency.
CC -1- SIMILARITY: Contains 1 NAS domain.
CC -----
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CC -----
DR EMBL; AB010086; BAA74580.1; -
DR InterPro; IPR004298; Nicotian_synth.
DR Pfam; PF03059; NAS; 1.
KW Transferase; Pyridoxal phosphate; Multigene family.
FT INT_MET 0
FT DOMAIN 2 281 NAS.
SQ SEQUENCE 327 AA; 35015 MW; C476B9622E76816 CRC64;
-----
Query Match 6.0%; Score 7; DB 1; Length 327;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 28 LSPQHQR 34
DB 55 LSPQHQR 61
-----
RESULT 13
S3A2_HUMAN
ID S3A2_HUMAN STANDARD; PRT; 464 AA.
AC Q15428; O75245;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Splicing factor 3A subunit 2 (Spliceosome associated protein 62) (SAP
DE 62) (SF3a66).
GN SF3A2 OR SAP62.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC MEDLINE=94023929; PubMed=8211113;
RA Bennett M., Reed R.;
RA "Correspondence between a mammalian spliceosome component and an

```

essential yeast splicing factor.";

Science 262:105-108(1993).

[2]

SEQUENCE FROM N.A.

LAmerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhardt-Schultz K.J., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Carnes J.,
Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
Cosfield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
Kobayashi A., Olsen A.S., Carrano A.V.;
"Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a
serine protease gene cluster.";
Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

[3]

SEQUENCE FROM N.A.

TISSUE=Lung, and Lymph;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J.J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
Rodriguez A.C., Grilwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Scherer A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[4]

CHARACTERIZATION OF THE SPLICEOSOME.

MEDLINE=20337962; PubMed=10882114;

Das R., Zhou Z., Reed R.;

"Functional association of U2 snRNP with the ATP-independent

spliceosomal complex E.";

Mol. Cell 5:779-787(2000).

-1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'

COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE

BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT

BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS

ESSENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE

INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.

-1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF

THREE SUBUNITS: SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A

ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO

FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).

-1- SUBCELLULAR LOCATION: Nuclear (By similarity).

-1- SIMILARITY: BELONGS TO THE SF3A2 FAMILY.

-1- SIMILARITY: Contains 1 matrix-type zinc finger.

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EMBL; L21990; AAA60301.1; -

EMBL; AC005263; AAC25613.1; -

EMBL; BC004434; AAH04434.1; -

EMBL; BC009903; AAH09903.1; -

PIR; A47655; A47655.


```

DR Genew; HGNC:10766; SF3A2.
DR GK; Q15428; -.
DR MIM; 600796; -.
DR GO; GO:0005681; C:spliceosome complex; TAS.
DR GO; GO:0003734; F:small nuclear nucleoprotein; TAS.
DR GO; GO:0006371; P:mRNA splicing; TAS.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR000690; Znf_matrin.
DR InterPro; IPR003604; Znf_U1.
DR SMART; SM00355; Znf_C2H2; 1.
DR SMART; SM00451; Znf_U1; 1.
DR SMART; SM00451; Znf_U1; 1.
DR PROSITE; PS50171; ZF_MATRIN; 1.
DR Spliceosome; mRNA processing; Nuclear protein;
KW Zinc-finger; Repeat.
FT ZN_FING 54 84 MATRIN-TYPE.
FT DOMAIN 233 236 POLY-PRO.
FT DOMAIN 252 256 POLY-PRO.
FT DOMAIN 458 462 POLY-PRO.
FT CONFLICT 29 29 R -> P (IN REF. 1).
SQ SEQUENCE 464 AA; 49255 MW; FA46F064A55EA2CE CRC64;

Query Match 6.0%; Score 7; DB 1; Length 464;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 EAKEAPA 115
DB 89 EAKEAPA 95

RESULT 14
S3A2_MOUSE STANDARD; PRT; 475 AA.
AC Q62703.
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Splicing factor 3A subunit 2 (Spliceosome associated protein 62) (SAP
DE 62) (SF3a66).
OS SF3A2 OR SAP62.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=96081226; PubMed=8541848;
RA Dresser D.W., Hacker A., Lovell-Badge R., Guerrier D.;
RT "The genes for a spliceosome protein (SAP62) and the anti-Mullerian
RT hormone (AMH) are contiguous."
RL Hum. Mol. Genet. 4:1613-1618(1995).
RN [2]
RP REVISIONS TO 101 AND 195-196.
RC STRAIN=129;
RA Dresser D.W., Atkins C.J., Guerrier D.;
RT "A GNP-like gene shares a bidirectional promoter with SAP62
RT immediately upstream of AMH."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE
CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT
CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS
CC ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE
CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.
CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF
CC THREE SUBUNITS; SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A
CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO
CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED.
CC -1- SIMILARITY: BELONGS TO THE SF3A2 FINGER.
CC -1- SIMILARITY: Contains 1 matrin-type zinc finger.

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EMBL; X83733; CAC10449.1; -.
DR MGD; MGI:104912; Sf3a2.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR000690; Znf_matrin.
DR InterPro; IPR003604; Znf_U1.
DR SMART; SM00355; Znf_C2H2; 1.
DR SMART; SM00451; Znf_U1; 1.
DR PROSITE; PS50171; ZF_MATRIN; 1.
DR Spliceosome; mRNA processing; Nuclear protein;
KW Zinc-finger; Repeat.
FT ZN_FING 54 84 MATRIN-TYPE.
FT DOMAIN 233 236 POLY-PRO.
FT DOMAIN 242 246 POLY-PRO.
FT DOMAIN 469 473 POLY-PRO.
SQ SEQUENCE 475 AA; 49911 MW; E8651DC3B0E29C7C CRC64;

Query Match 6.0%; Score 7; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 EAKEAPA 115
DB 89 EAKEAPA 95

RESULT 15
PURL_SYNP7 STANDARD; PRT; 493 AA.
AC Q55038;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amidophosphoribosyltransferase precursor (EC 2.4.2.14) (Glutamine
DE phosphoribosylpyrophosphate amidotransferase) (ATASE) (GPATase).
GN PURF.
OS Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96405630; PubMed=8809759;
RA Liu Y., Tsinoiremas N.F., Golden S., Kondo T., Johnson C.H.;
RT "Circadian expression of genes involved in the purine biosynthetic
RT pathway of the cyanobacterium Synecococcus sp. strain PCC 7942."
RL Mol. Microbiol. 20:1071-1081(1996).
CC -1- CATALYTIC ACTIVITY: 5-phospho-beta-D-ribose-5-phosphate +
CC L-glutamate -> L-glutamine + 5-phospho-alpha-D-ribose 1-diphosphate
CC + H(2)O.
CC -1- PATHWAY: De novo purine biosynthesis; first step.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE
CC PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC -1- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
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EMBL; U33211; AAA75107.1; -.
DR PIR; S77612; S77612.
DR HSP; P00497; 1A00.

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DR MEROPS: C44.001; ..
DR InterPro: IPR005854; Amd_phospho_trans.
DR InterPro: IPR00583; GATase_2.
DR InterPro: IPR002375; Pt/py_ip_transf.
DR InterPro: IPR000836; PRtransferase.
DR Pfam: PF00310; GATase_2; 1.
DR Pfam: PF00156; Ribosyltran; 1.
DR TIGRFAMs: TIGR01134; purF; 1.
DR PROSITE: PS00103; PUR_PVR_PR_TRANSFER; FALSE_NEG.
DR PROSITE: PS00443; GATASE_TYPE_II; FALSE_NEG.
KW Purine biosynthesis; Transferase; Glycosyltransferase;
KW Glutamine amidotransferase.
FT PROPEP 1 26 BY SIMILARITY.
FT CHAIN 27 493 AMIDOPHOSPHORIBOSYLTRANSFERASE.
FT ACT_SITE 27 27 GATASE (BY SIMILARITY).
SQ SEQUENCE 493 AA; 53809 MW; E03508F8A922910C CRC64;

Query Match 6.0%; Score 7; DB 1; Length 493;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 AKEAPAD 116
| | | | |
Db 299 AKEAPAD 305

Search completed: September 11, 2003, 17:52:38
Job time : 24.5241 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:02 : Search time 111.995 Seconds
(without alignments)
269.586 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 117

Sequence: 1 MPSPGTVCVSLLLGLMLDL.....LGKFLQDILWEEAKEAPADK 117

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	60.7	117	4	Q8TAT9
2	18	15.4	117	11	Q8CH53
3	8	6.8	23	2	Q9R5D1
4	8	6.8	111	13	Q8JFY4
5	8	6.8	116	13	Q8AV73
6	8	6.8	313	2	Q8VP52
7	8	6.8	433	10	Q93ZV7
8	8	6.8	433	10	Q8L7E4
9	8	6.8	483	10	Q65529
10	7	6.0	103	16	Q9L063
11	7	6.0	114	16	Q8FF03
12	7	6.0	138	16	Q9KCN5
13	7	6.0	140	6	Q8HXR4
14	7	6.0	143	5	Q9VDP0
15	7	6.0	152	5	Q9XZC4
16	7	6.0	207	16	Q9I4Y8

17	7	6.0	216	16	Q9RW31
18	7	6.0	235	5	Q9U2L3
19	7	6.0	243	16	Q8DBD4
20	7	6.0	247	16	Q8KPA9
21	7	6.0	253	16	Q9CPE0
22	7	6.0	267	16	Q9L1R0
23	7	6.0	280	6	Q95JM5
24	7	6.0	289	16	Q8EVS8
25	7	6.0	365	11	Q8BW62
26	7	6.0	371	6	Q8SPU3
27	7	6.0	405	13	Q8AVV0
28	7	6.0	406	16	Q8Z8Z8
29	7	6.0	428	10	Q94IO8
30	7	6.0	428	11	Q8C1F2
31	7	6.0	433	16	Q8CNV4
32	7	6.0	435	10	Q8LGD9
33	7	6.0	435	10	Q9LNE6
34	7	6.0	438	11	Q8BL56
35	7	6.0	443	16	Q9A6Z5
36	7	6.0	444	16	Q9AB53
37	7	6.0	452	2	Q9XCK2
38	7	6.0	495	11	Q8K124
39	7	6.0	497	16	Q9A0P2
40	7	6.0	497	16	Q8NZR7
41	7	6.0	502	6	Q9BDI4
42	7	6.0	502	6	Q95L23
43	7	6.0	502	11	Q9QV77
44	7	6.0	562	11	Q9CZT0
45	7	6.0	562	11	Q8C3S5

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY: PRT; 117 AA.
AC Q8TAT9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025791; AAH25791.1; -;
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
SQ SEQUENCE 117 AA; 12929 MW; 2580572EBECB7610 CRC64;

Query Match 60.7%; Score 71; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.5e-65;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPGTVCVSLLLGLMLDLAMAGSFLSPHQVQORVKESKPPAKLPQPRALAGWLRLPE 60
|||||
DB 1 MPSPGTVCVSLLLGLMLDLAMAGSFLSPHQVQORVKESKPPAKLPQPRALAGWLRLPE 60
|||||

QY 61 DGGQAEAGDE 71
|||||

DB 61 DGGQAEAGDE 71
|||||

RESULT 2

Q8CH53

```

ID Q8CH53 PRELIMINARY; PRT; 117 AA.
AC Q8CH53;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AAO06965.1; -.
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 15.4%; Score 18; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 QQRKSKPPAKLPQRL 53
Db 36 QQRKSKPPAKLPQRL 53

RESULT 3
ID Q9R5D1 PRELIMINARY; PRT; 23 AA.
AC Q9R5D1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 14 kDa aggregative adherence fimbriae I protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.
RA MEDLINE=93162805; PubMed=8094379;
RA Nataro J.P., Yikang D., Giron J.A., Savarino S.J., Kothary M.H.,
RA Hall R.;
RT "Aggregative adherence fimbria I expression in enteroaggregative
RT Escherichia coli requires two unlinked plasmid regions.";
RL Infect. Immun. 61:1126-1131(1993).
SQ SEQUENCE 23 AA; 2403 MW; 688113EAC484CE1E CRC64;

Query Match 6.8%; Score 8; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 IKLSGVQY 91
Db 16 IKLSGVQY 23

RESULT 4
ID Q8JFY4 PRELIMINARY; PRT; 111 AA.
AC Q8JFY4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Prepro-ghrelin precursor.
GN GHRELIN.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
```

```

OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Kalya H., Kojima M., Hosoda H., Riley L.G., Hirano T., Grau G.E.,
RA Kangawa K.;
RT "Identification of eel ghrelin.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062427; BAB96565.1; -.
KW Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 111 PROGHRELIN.
FT CHAIN 27 48 GHRELIN-21.
SQ SEQUENCE 111 AA; 12831 MW; 7AF95E04DD22DE7B CRC64;

Query Match 6.8%; Score 8; DB 13; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AGSSFSLSP 30
Db 26 AGSSFSLSP 33

RESULT 5
ID Q8AV73 PRELIMINARY; PRT; 116 AA.
AC Q8AV73;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin precursor.
GN GHR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=22181232; PubMed=12193558;
RA Kalya H., Van der Geyten S., Kojima M., Hosoda H., Kitajima Y.,
RA Matsumoto M., Geelissen S., Darras V.M., Kangawa K.;
RT "Chicken ghrelin: purification, cDNA cloning, and biological
RT activity.";
RL Endocrinology 143:3454-3463(2002).
DR EMBL; AB075215; BAC24980.1; -.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 49 GHRELIN-26.
SQ SEQUENCE 116 AA; 13227 MW; F5C5FA038F187DE9 CRC64;

Query Match 6.8%; Score 8; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AGSSFSLSP 30
Db 23 AGSSFSLSP 30

RESULT 6
ID Q8VP52 PRELIMINARY; PRT; 313 AA.
AC Q8VP52;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE LysR-like transcriptional activator SnpR.
OS Streptomyces sp. C5.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomyces.
```

```

OX NCBI_TaxID=45212;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C5;
RA DeSanti C.L., Strohl W.R.;
RT "Characterization of the Streptomyces sp. strain C5 snp locus and
   development of an snp-derived expression vector family.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
   REGULATORS.
CC EMBL: AY072041; AAL61992.1; -.
DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR005119; LysR_subst.
DR Pfam: PF00126; HTH_1; 1.
DR Pfam: PF03466; LysR_substrate; 1.
DR PRINTS: PR00039; HTHLYSR.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; transcription; Transcription regulation.
SQ SEQUENCE 313 AA; 34258 MW; C907C8AF51C3FA13 CRC64;

Query Match 6.8%; Score 8; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RALAGWLR 58
DB 102 RALAGWLR 109

RESULT 7
Q932V7 PRELIMINARY; PRT; 433 AA.
AC Q932V7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative RNA-binding protein LAH1.
GN AT4632720.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene AT4g32720 (GI:7270219).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AY056237; AAL07086.1; -.
DR InterPro: IPR002344; Lupus_La.
DR InterPro: IPR006630; Lupus_La_dom.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00076; rrm; 1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA; 1.
DR PROSITE: PS50102; RRM; 1.
SQ SEQUENCE 433 AA; 48095 MW; E58EBAF51C35A8F7 CRC64;

Query Match 6.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 QAEGAED 71
DB 287 QAEGAED 294

RESULT 8
Q932V7 PRELIMINARY; PRT; 433 AA.
AC Q932V7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative RNA-binding protein LAH1.
GN AT4632720.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AY136302; AAM96968.1; -.
DR EMBL: BT000396; AAN15715.1; -.
DR InterPro: IPR002344; Lupus_La.
DR InterPro: IPR006630; Lupus_La_dom.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00076; rrm; 1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA; 1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 433 AA; 48126 MW; CFF611A29AA0318 CRC64;

Query Match 6.8%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 QAEGAED 71
DB 287 QAEGAED 294

RESULT 9
O65529 PRELIMINARY; PRT; 483 AA.
AC O65529;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 54.1 kDa protein.
GN F4D11.80 OR AT4G32720.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

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RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoerge W., Hoheisel J.,
RA Meves H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoerge W., Meves H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022537; CAAL18589.1; -.
DR EMBL; AL161582; CAB79989.1; -.
DR InterPro; IPR002344; Lupus.La.
DR InterPro; IPR006630; Lupus.La.dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;
Query Match 6.8%; Score 8; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 QAEGAED 71
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DB 302 QAEGAED 309

RESULT 10
Q9L063 PRELIMINARY; PRT; 103 AA.
AC Q9L063;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SC02791.
GN SC02791 OR SC0105.22C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939114; CAB87228.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;

Query Match 6.0%; Score 7; DB 16; Length 103;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 DGGQAG 67
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DB 48 DGGQAG 54

RESULT 11
Q8FF03 PRELIMINARY; PRT; 114 AA.
AC Q8FF03;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein yfim.
GN YFIM OR C3111.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=2238234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Maynew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016764; AAN81560.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 114 AA; 12611 MW; 8FECSA91285FA0A8 CRC64;

Query Match 6.0%; Score 7; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VCSLLLL 13
| | | | |
DB 13 VCSLLLL 19

RESULT 12
Q9KCN5 PRELIMINARY; PRT; 138 AA.
AC Q9KCN5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BHI534.
GN BHI534.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001512; BAB05253.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 138 AA; 15918 MW; C75E1FDFE5F972FF CRC64;

Query Match 6.0%; Score 7; DB 16; Length 138;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 EVRENAP 79
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DB 10 EVRENAP 16

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RESULT 13
Q8HXR4
ID Q8HXR4 PRELIMINARY; PRT; 140 AA.
AC Q8HXR4
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Bone morphogenetic protein receptor 1B (Fragment).
GN BMP1B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Cumulus oocyte complex;
RA Einspanier R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Cumulus oocyte complex;
RA Schoenfelder M.;
RT "Expression of ovarian growth factors.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ534389; CAD59880.1; -.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 16076 MW; 0DC51D1517C1A4A6 CRC64;

Query Match 6.0%; Score 7; DB 6; Length 140;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVCSLL 12
DB 47 TVCSLL 53

RESULT 14
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ID Q9VDP0 PRELIMINARY; PRT; 143 AA.
AC Q9VDP0
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE CG10883 protein.
GN CG10883.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananthites P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Gaig N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003729; AAF55750.1; -.
DR FlyBase: FBgn0038781; CG10883.
SQ SEQUENCE 143 AA; 14645 MW; 09FE17B83214692B CRC64;

Query Match 6.0%; Score 7; DB 5; Length 143;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLGL 16
DB 98 LLLGL 104

RESULT 15
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AC Q9XZC4
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Serine proteinase (Fragment).
GN T684.
OS Helicoverpa armigera (Cotton bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=29058;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IARI;
RA Mazumdar-Leighton S., Babu C.R., Bennett J.;
RT "Identification of novel serine proteinase gene transcripts in the
RT midguts of two tropical agricultural pests, Scirpophaga incertulas
RT (WK.) and Helicoverpa armigera (Hb.).";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF134490; AAD31713.1; -.
DR HSSP: P00761; IAKS.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR SMART: SM00020; tryp_Spc; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1 1
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 16933 MW; 1AB9F5115392A319 CRC64;

Query Match 6.0%; Score 7; DB 5; Length 152;

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Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PSPGTV 8
Db 89 PSPGTV 95

Search completed: September 11, 2003, 17:55:45
Job time : 114.995 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 122.005 Seconds
(without alignments)
152.215 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 611

Sequence: 1 MSPGTCVCSLLGLGLDL.....LGKFLQDILWEAKEAPADK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611	100.0	117	AAW87991	Protein designated
2	611	100.0	117	AA1987236	Human signal pepti
3	611	100.0	117	AA1987236	Human polypeptide
4	611	100.0	117	AA1987236	Human zsig33 poly
5	611	100.0	117	AA1987236	Human zsig33 protein
6	611	100.0	117	AA1987236	Human ghrelin prep
7	611	100.0	117	AA1987236	Amino acid sequenc
8	611	100.0	117	AA1987236	Human zsig33 prote
9	611	100.0	117	AA1987236	Human zsig33 prote

10	611	100.0	117	24	ABU66790	Human PRO polypept
11	611	100.0	117	24	ABU67066	Human secreted/tra
12	611	100.0	117	24	ABU59871	Novel secreted and
13	611	100.0	117	24	ABU59124	Novel human secret
14	611	100.0	117	24	ABU59271	Human secreted/tra
15	611	100.0	117	24	ABU59420	Novel human secret
16	611	100.0	117	24	ABU60555	Human secreted/tra
17	611	100.0	117	24	ABU58046	Human PRO polypept
18	611	100.0	117	24	ABU58977	Human secreted/tr
19	611	100.0	117	24	AAE33409	Human preproghrell
20	611	100.0	117	24	ABU13937	Human PRO1066 poly
21	611	100.0	117	24	ABU10892	Human PRO polypept
22	611	100.0	118	21	AAV66708	Membrane-bound pro
23	611	100.0	118	22	AAU12392	Human PRO1066 poly
24	611	100.0	118	22	AAE65231	Human PRO1066 (UNQ
25	611	100.0	126	22	AAW40676	Human polypeptide
26	595.5	97.5	116	22	AAE60517	Human des-Gln14-gh
27	518	84.8	117	22	AAE60510	Rat ghrelin prepro
28	502.5	82.2	116	22	AAE60516	Rat des-Gln14-ghre
29	472.5	77.3	118	22	AAE60520	Porcine ghrelin pr
30	457	74.8	117	22	AAE60521	Porcine des-Gln14-
31	392	64.2	90	23	ABP08375	Human ORFX protein
32	392	64.2	91	24	AAE33410	Human exon 3-delet
33	315.5	51.6	89	22	AAE60523	Bovine ghrelin pre
34	146	23.9	108	22	AAE60531	Eel ghrelin-like G
35	145	23.7	28	22	AAE60509	Human ghrelin, SQ
36	145	23.7	28	23	ABE09532	Human ghrelin, Ho
37	145	23.7	28	23	AAE19032	Human ghrelin pept
38	141	23.1	28	23	AAE19021	Human ghrelin pept
39	141	23.1	28	23	AAE19027	Human ghrelin pept
40	141	23.1	28	23	AAE19028	Human ghrelin pept
41	141	23.1	28	23	AAE19029	Human ghrelin pept
42	141	23.1	28	23	AAE19030	Human ghrelin pept
43	141	23.1	28	23	AAE19031	Human ghrelin pept
44	141	23.1	28	23	AAE19033	Human ghrelin pept
45	141	23.1	28	23	AAE19034	Human ghrelin pept

ALIGNMENTS

RESULT 1
AAW87991
ID AAW87991 standard; Protein; 117 AA.
AC AAW87991;
XX
XX
DT 07-APR-1999 (first entry)
DE Protein designated zsig33.
KW zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
KW nutrient absorption regulation; obesity; metabolic disorder.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..23
FT /note= "signal peptide"
FT Protein 24..117
FT /note= "mature protein"
XX
XX
PN WO9842840-A1.
XX
PD 01-OCT-1998.
XX
XX
PF 23-MAR-1998; 98WO-US05620.
XX
PR 24-MAR-1997; 97US-0822897.
PR 24-MAR-1997; 97US-0041102.
XX
XX
(ZYMO) ZYMOGENETICS INC.

PI Delsner TA, Sheppard PO;
 XX WPI: 1999-070071/06.
 DR N-PSDB; AAX04550.
 XX Human polypeptide having homology to motilin, zsig33 - useful e.g.
 PT to treat gastrointestinal motility disorders, obesity etc. and to
 PT identify antagonists to treat gastrointestinal hypermotility
 XX
 PS Claim 13; Page 55-56; 69pp; English.
 XX
 CC The present sequence represents a protein designated zsig33. The nucleic
 CC acids are strongly expressed in stomach tissue. The polypeptide (or
 CC allelic variants/orthologs) can be used to stimulate gastric motility,
 CC measured as increased transit time or gastric emptying of an ingested
 CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. zsig33 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC and CNS functions. They may therefore be used e.g. to regulate satiety
 CC or treat obesity and other metabolic disorders where neurological
 CC feedback modulates nutritional absorption. They are useful to identify
 CC zsig33 agonists, antagonists and ligands and to produce antibodies.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 611; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQQRKSKPPAKLPQALAGWLRPE 60
 DB 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQQRKSKPPAKLPQALAGWLRPE 60
 QY 61 DGGQAEAGAEDELEVRNAPFDVGKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAEAGAEDELEVRNAPFDVGKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 RESULT 2
 AAY87236
 ID AAY87236 standard; Protein: 117 AA.
 XX
 AC AAY87236;
 XX
 DT 11-MAY-2000 (first entry)
 DE
 DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
 XX
 KW Human: signal peptide-containing protein; HSPP: diagnosis: cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
 KW antischismatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 PN WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-US14484.
 PF
 PF 26-JUN-1998; 98US-0090762.
 PR
 PR 31-JUL-1998; 98US-0094983.
 PR
 PR 01-OCT-1998; 98US-0102686.

PR 11-DEC-1998; 98US-0112129.
 XX (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX WPI: 2000-160673/14.
 DR N-PSDB; AAZ98121.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease
 XX
 PS Claim 1; Page 168-169; 327pp; English.
 XX
 CC AAY98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antischismatic activities, and can
 CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPP
 CC from natural sources.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 611; DB 21; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQQRKSKPPAKLPQALAGWLRPE 60
 DB 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQQRKSKPPAKLPQALAGWLRPE 60
 QY 61 DGGQAEAGAEDELEVRNAPFDVGKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAEAGAEDELEVRNAPFDVGKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 RESULT 3
 AAM38890
 ID AAM38890 standard; Protein: 117 AA.
 XX
 AC AAM38890;
 XX
 DT 22-OCT-2001 (first entry)
 DE
 DE Human polypeptide SEQ ID NO 2035.
 XX
 KW Human: neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.
 OS WO200153312-A1.
 XX 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-US34263.
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX WPI: 2001-442253/47.
 DR N-PSDB; AAI58046.
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX Example 3; SEQ ID NO 2035; 10078pp; English.
 PS The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAI38642-AAI42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Actin/thymidin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 611; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPGTVCSLLLLGLMLWLDLAMAGSSFLSPFHQRVQQRKESKPPAKLQPRALAGWLRLPE 60
 DB 1 MPSPGTVCSLLLLGLMLWLDLAMAGSSFLSPFHQRVQQRKESKPPAKLQPRALAGWLRLPE 60
 QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117
 RESULT 4
 AAB62649
 ID AAB62649 standard; Protein; 117 AA.
 XX AAB62649;
 AC AAB62649;
 XX 23-JUL-2001 (first entry)
 DT Human zsig33 polypeptide.
 XX

XX zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
 KW G-protein coupled receptor.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT Peptide 24..37
 FT /note= "specifically claimed fragment that binds to
 FT the GHS-R"
 XX WO200138355-A2.
 XX 31-MAY-2001.
 XX 22-NOV-2000; 2000WO-US32074.
 XX 22-NOV-1999; 99US-0166765.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 XX WPI: 2001-355879/37.
 DR N-PSDB; AAF83678.
 XX Forming reversible peptide receptor complex for purifying cell and
 PT peptides, stimulating signal transduction and modulating hormone
 PT secretion, involves contacting a receptor with zsig33 polypeptide -
 XX Claim 1; Page 93-94; 111pp; English.
 XX The invention relates to a method of forming a reversible peptide-
 CC receptor complex that involves providing an immobilized receptor, and
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
 CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
 CC is useful for purifying cells, purifying a peptide, stimulating signal
 CC transduction in a cell expressing a receptor. It is also useful for
 CC modulating secretion of hormones, neural development and/or utilization,
 CC gastric contractility, nutrient uptake, secretion of digestive and
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
 CC hormone secretion in a mammal having a disease associated with abnormal
 CC levels of growth hormone, such as osteoporosis, bone repair, bone
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,
 CC protein catabolic responses after surgery, cachexia, protein loss,
 CC dwarfism, wound healing and ovulation induction, treating a mammal having
 CC a metabolic disorder requiring neurological feedback, such as satiety
 CC regulation, glucose absorption and metabolism and neuropathy-associated
 CC gastrointestinal disorders, and stimulating glucose-induced insulin
 CC release in a mammal. The present sequence represents the human zsig33
 CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 611; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPGTVCSLLLLGLMLWLDLAMAGSSFLSPFHQRVQQRKESKPPAKLQPRALAGWLRLPE 60
 DB 1 MPSPGTVCSLLLLGLMLWLDLAMAGSSFLSPFHQRVQQRKESKPPAKLQPRALAGWLRLPE 60
 QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117
 RESULT 5

AAB20101
ID AAB20101 standard; Protein; 117 AA.
XX AAB20101;
AC AAB20101;
XX 23-APR-2001 (first entry)
DT 23-APR-2001 (first entry)
XX Zsig33 protein.
DE Zsig33 protein.
XX SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
KW nutritional absorption modulator; growth hormone secretagogue;
KW therapy; human.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH 1..23 /label= Signal_peptide
FT 24..117 /label= Mature_protein
FT 24..34 /label= SGIP_peptide
FT /note= "this peptide is claimed in Claim 1"
XX WO200100830-A1.
XX PD 04-JAN-2001.
XX PF 30-JUN-2000; 2000WO-US18306.
XX PR 30-JUN-1999; 99US-0345157.
XX PA (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX WPI; 2001-123010/13.
XX DR N-PSDB; AAF30033.
XX Novel variants of SGIP peptides for modulating contractility in
PT duodenum or jejunum tissue, pancreatic secretion of hormones and
PT digestive enzymes, inducing growth hormone secretion or modulating
PT gastric emptying -
XX Disclosure; 54; 61pp; English.
PS The present sequence is that of zsig33, a secreted protein with
CC homology to motilin (see AAB20102). zsig33 is expressed at high
CC levels in the stomach, and at lower levels in the small intestine
CC and pancreas. A novel peptide fragment of zsig33, termed SGIP (see
CC AAB20100), is claimed. SGIP is a ligand for growth hormone
CC secretagogue receptor, and is therefore useful for modulating
CC secretion of growth hormone and insulin like growth factor 1.
CC SGIP, and variant SGIP peptides, are used in claimed methods for
CC stimulating contractility in duodenum or jejunum tissue,
CC modulating pancreatic secretion of hormones and digestive enzymes,
CC inducing growth hormone secretion, and modulating gastric emptying.
XX SQ Sequence 117 AA;
Query Match 100.0%; Score 611; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.6e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MPSPTVCSLLGLMGLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRLPE 60
DB 1 MPSPTVCSLLGLMGLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRLPE 60
OY 61 DGGQAEAGDELEVRNAPFDVGIKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117
DB 61 DGGQAEAGDELEVRNAPFDVGIKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 6
AAB60511
ID AAB60511 standard; Protein; 117 AA.
XX AAB60511;
AC AAB60511;
XX 24-APR-2001 (first entry)
DT 24-APR-2001 (first entry)
XX Human ghrelin preproprotein, SEQ ID NO:5.
DE Human ghrelin preproprotein, SEQ ID NO:5.
XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
KW calcium concentration elevation; infant growth disorder;
KW growth hormone deficiency.
XX Homo sapiens.
OS Homo sapiens.
XX WO200107475-A1.
XX PD 01-FEB-2001.
XX PF 24-JUL-2000; 2000WO-JP04907.
XX PR 23-JUL-1999; 99JP-0210002.
XX PR 29-NOV-1999; 99JP-0338841.
XX PR 26-APR-2000; 2000JP-0136623.
XX PA (KANG/) KANGAWA K.
XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
PI WPI; 2001-159704/16.
XX DR N-PSDB; AAF59645.
XX New peptide compounds which induce growth hormone secretion and
FT elevate cell calcium concentrations, useful in treatment and diagnosis
PT of infant growth disorders -
XX Claim 3; Page 182; 210pp; Japanese.
XX The invention relates to a novel peptide compound or its salt which
CC induces the secretion of growth hormone and/or elevates calcium ion
CC concentration in cells. The peptides are ghrelin homologues and are
CC characterised in that at least one amino acid has been substituted by
CC a modified amino acid and/or a non-amino acid compound. The invention
CC also encompasses the unmodified peptides; the DNA encoding the peptides;
CC vectors and host cells comprising such DNA; a method of producing the
CC peptides comprising recombinant production, optionally followed by
CC chemical modification; an antibody specific for a peptide of the
CC invention; and an assay and kit for detecting the peptides. The peptides
CC of the invention are useful for treating and/or diagnosing diseases
CC caused by a deficiency in growth hormone expression or activity. In
CC particular, they are useful for promoting infant growth due to growth
CC hormone deficiency. The compounds of the invention are safe with
CC no accompanying side effects. The present sequence represents a
CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
CC of the invention.
XX SQ Sequence 117 AA;
Query Match 100.0%; Score 611; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.6e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MPSPTVCSLLGLMGLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRLPE 60
DB 1 MPSPTVCSLLGLMGLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRLPE 60
OY 61 DGGQAEAGDELEVRNAPFDVGIKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117
DB 61 DGGQAEAGDELEVRNAPFDVGIKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117
RESULT 7

ABB78319
ID ABB78319 standard; Protein; 117 AA.

XX AC ABB78319;

XX DT 05-DEC-2002 (first entry)

XX DE Amino acid sequence of a human zsig33.

XX KW Short gastrointestinal peptide; SGIP; zsig33; motilin.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..23

FT FT /note= "signal peptide"

FT Protein 24..119

FT FT /note= "mature protein"

XX US6420521-B1.

XX PN 16-JUL-2002.

XX PD 30-JUN-2000; 2000US-0608810.

XX PF 30-JUN-1999; 99US-141592P.

XX PR (ZYMO) ZYMOGENETICS INC.

XX PA Sheppard PO, Jaspers SR, Delsher TA, Bishop PD;

XX PI WPI; 2002-634794/68.

XX DR N-PSDB; ABV72214.

XX PT New Short Gastrointestinal Peptide, which has homology to motilin,

PT useful for preventing, diagnosing and treating gastrointestinal

PT disorders -

XX Disclosure; Columns 39-40; 23pp; English.

XX CC The present sequence represents human zsig33. The specification describes

CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.

CC SGIP has homology to motilin. The SGIP peptide may be used in the

CC prevention, diagnosis and treatment of diseases associated with

CC inappropriate SGIP expression. For example, SGIP may be used to treat

CC disorders associated with decreased expression by rectifying mutations

CC or deletions in a patient's genome that affect the activity of SGIP by

CC expressing inactive proteins or to supplement the patients own production

CC of SGIP. SGIP may also be used as an antigen in the production of

CC antibodies against SGIP and in assays to identify modulators of SGIP

CC expression and activity. The anti-SGIP antibodies, agonists and

CC antagonists may also be used to regulate expression and activity. The

CC anti-SGIP antibodies may also be used as diagnostic agents for detecting

XX the presence of SGIP in samples.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 23; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.6e-59;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPGTVCVCSLLLLGLMLWDLAMAGSSFLSPHQVQQRKESKPPAKLPALAGWLRPE 60

DB 1 MPSPGTVCVCSLLLLGLMLWDLAMAGSSFLSPHQVQQRKESKPPAKLPALAGWLRPE 60

QY 61 DGGQAGAEDELEVRNAPFDVGICKLSGVQYQOHSOALGKFLQDILWEAKEAPADK 117

DB 61 DGGQAGAEDELEVRNAPFDVGICKLSGVQYQOHSOALGKFLQDILWEAKEAPADK 117

XX AAE23838;

XX AC 10-SEP-2002 (first entry)

XX DT Human zsig33 protein.

XX DE Human; zsig33-like peptide; gastric contractility; nutrient uptake;

XX KW growth hormone; digestive enzyme; restorative therapy; gene therapy;

XX KW protein therapy; gastrointestinal; endocrine; anabolic.

XX OS Homo sapiens.

XX US2002055156-A1.

XX PN 09-MAY-2002.

XX PD 10-MAY-2001; 2001US-0853253.

XX PF 11-MAY-2000; 2000US-203300P.

XX PR (JASP/) JASPERS S R.

XX PA (SHEP/) SHEPPARD P O.

XX PA (DEIS/) DEISHER T A.

XX PA (BISH/) BISHOP P D.

XX PI Jaspers SR, Sheppard PO, Delsher TA, Bishop PD;

XX WPI; 2002-443750/47.

XX DR N-PSDB; AAD38238.

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

PT contractility, nutrient uptake, growth hormones and/or secretion Of

PT digestive/pancreatic enzymes and hormones -

XX Disclosure; Page 27; 34pp; English.

XX CC The invention relates to zsig33-like peptides and their corresponding

CC nucleic acids and methods for modulating gastric contractility, nutrient

CC uptake, growth hormones, secretion of digestive enzymes and hormones.

CC The sequences of the invention are used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate ZSIG33 expression.

CC The nucleic acids of the invention and their complements are used as

CC DNA probes in diagnostic assays to detect and quantitate the presence

CC of similar nucleic acids in samples, and therefore which patients may be

CC in need of restorative therapy. The ZSIG33 peptides are used as antigens

CC in the production of antibodies against ZSIG33 and in assays to identify

CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies

CC and antagonists are used to down regulate expression and activity. The

CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting

CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent

CC assay (ELISA)). The peptides and nucleic acids of the invention are used

CC to modulate gastric contractility, nutrient uptake, growth hormones, the

CC secretion of digestive enzymes and hormones, and/or secretion of enzymes

CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy

CC and zsig33-like peptide is used in protein therapy. The present sequence

XX is human zsig33 protein.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 23; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.6e-59;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPGTVCVCSLLLLGLMLWDLAMAGSSFLSPHQVQQRKESKPPAKLPALAGWLRPE 60

DB 1 MPSPGTVCVCSLLLLGLMLWDLAMAGSSFLSPHQVQQRKESKPPAKLPALAGWLRPE 60

QY 61 DGGQAGAEDELEVRNAPFDVGICKLSGVQYQOHSOALGKFLQDILWEAKEAPADK 117

DB 61 DGGQAGAEDELEVRNAPFDVGICKLSGVQYQOHSOALGKFLQDILWEAKEAPADK 117

RESULT 9
AAE15883
ID AAE15883 standard; Protein; 117 AA.
XX
AC AAE15883;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human zsig33 protein.
XX
KW Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33 protein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Signal_peptide
FT Protein 24..117
FT /note= "Human mature zsig33 protein"
XX
PN WO200187933-A2.
XX
PD 22-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-US15091.
XX
PR 11-MAY-2000; 2000US-0569271.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Jaspers SR, Sheppard PO, Delisher TA, Bishop PD;
XX
DR WPI; 2002-082982/11.
XX
DR N-P5DB; AAD25759.
XX
PT New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and
PT treating gastrointestinal and growth related diseases, comprises
PT zsig33-like peptides -
XX
PS Disclosure; Page 80-81; 89pp; English.
XX
CC The invention relates to zsig33-like peptides (ZS33LP) including
CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and
CC zsig33-epsilon peptides and nucleic acid molecules encoding such
CC zsig33-like peptides. ZS33LP peptides activate the immune system
CC in boosting immunity to infectious diseases, treating immunocompromised
CC patients such as human immunodeficiency virus (HIV) patients, in
CC improving vaccines and in treatment of bacterial, viral, protozoal and
CC fungal infections. Peptides of the invention are used to identify and
CC isolate receptors involved in growth regulation in the liver, blood
CC vessel formation and other developmental processes. They are useful for
CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
CC growth and/or differentiation of tumour cells, as additives to anti-
CC hypoglycaemic preparations containing glucose and as adsorption
CC enhancers for oral drugs which require fast nutrient action and to
CC stimulate glucose-induced insulin release. They are also useful as
CC research reagents for the expansion, differentiation, growth factor and
CC hormone secretion and/or cell-cell interactions of tissues associated
CC with gastrointestinal system, brain and central nervous system. These
CC molecules are useful for treating dysfunction associated with contractile
CC tissues or to suppress or enhance contractility in vivo and to treat
CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
CC acids and/or antibodies are useful for treating disorders associated
CC with gastrointestinal contractility, secretion of digestive enzymes,
CC hormone and acids, secretion of hormones in the pancreas and/or brain,
CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
CC and regulation of nutrient absorption. Sequences of the invention are
CC useful in gene therapy. The present sequence is human zsig33 protein.

XX
SQ Sequence 117 AA;
Query Match 100.0%; Score 611; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.6e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPSPTVCSSLLLLGMLWLDLWLAGSSFLSPESHQVQQRKESKPPAKLQPRALAGWLRPE 60
|||||
Db 1 MPSPTVCSSLLLLGMLWLDLWLAGSSFLSPESHQVQQRKESKPPAKLQPRALAGWLRPE 60
|||||
Qy 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
|||||
Db 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
|||||
RESULT 10
ABU66790
ID ABU66790 standard; Protein; 117 AA.
XX
AC ABU66790;
XX
DT 23-MAY-2003 (first entry)
XX
DE Human PRO polypeptide #221.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytostatic.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-0143114.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX

(GETH) GENENTECH INC.

PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-332040/31.
 DR

DR N-PSDB; ACA03823.
 XX New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification
 XX Claim 12; Fig 442; 660pp; English.
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating the
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. ABU66570-ABU66844 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsideEntry.html.
 XX Sequence 117 AA:
 SQ
 Query Match 100.0%; Score 611; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred No. 4, 6e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPGTVCSSLLLGLMLDLAMAGSFLSPHEHQVQQRKESKPPAKLQPRALAGWL RPE 60
 Db 1 MPSPGTVCSSLLLGLMLDLAMAGSFLSPHEHQVQQRKESKPPAKLQPRALAGWL RPE 60
 QY 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
 Db 61 DGGQAEAGDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
 RESULT 11
 ABU67066
 ID ABU67066 standard; Protein; 117 AA.
 XX ABU67066;
 AC
 DT 27-MAY-2003 (first entry)
 XX
 DE Human secreted/transmembrane, PRO, protein SEQ ID 442.
 XX Human; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioreactor; tumour.
 XX Homo sapiens.
 XX US2003032155-A1.
 PN
 XX 13-FEB-2003.
 PD
 XX 03-MAY-2002; 2002US-0137865.
 XX
 PF 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.

PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 98WO-US00106.
PR 08-MAR-1999; 98WO-US05028.
PR 10-MAR-1999; 98WO-US05190.
PR 20-APR-1999; 98WO-US08615.
PR 14-MAY-1999; 98WO-US10733.
PR 02-JUN-1999; 98WO-US12252.
PR 01-SEP-1999; 98WO-US20111.
PR 08-SEP-1999; 98WO-US20594.
PR 13-SEP-1999; 98WO-US20944.
PR 15-SEP-1999; 98WO-US21090.
PR 15-SEP-1999; 98WO-US21547.
PR 05-OCT-1999; 98WO-US23089.
PR 29-NOV-1999; 98WO-US28214.
PR 30-NOV-1999; 98WO-US28313.
PR 30-NOV-1999; 98WO-US28409.
PR 01-DEC-1999; 98WO-US28301.
PR 01-DEC-1999; 98WO-US28634.
PR 02-DEC-1999; 98WO-US28551.
PR 02-DEC-1999; 98WO-US28564.
PR 02-DEC-1999; 98WO-US28585.
PR 16-DEC-1999; 98WO-US30095.
PR 20-DEC-1999; 98WO-US30911.
PR 20-DEC-1999; 98WO-US30999.
PR 22-DEC-1999; 98WO-US30720.
PR 30-DEC-1999; 98WO-US31243.
PR 30-DEC-1999; 98WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04114.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 10-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23528.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.

PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0806689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-331925/31.
DR N-PSDB; ACA04244.

XX New secreted and transmembrane nucleic acids and polypeptides,
designated as PRO, useful for treating inflammation, organ failure,
atherosclerosis, cardiac injury, infertility, birth defects, premature
aging, AIDS, or cancer

Claim 12; Fig 442; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is
at least 80% identical to, or the full-length coding sequence of, any of
the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
(one of 275 secreted or transmembrane proteins). The nucleic acid
further comprises the full-length coding sequence of the DNA deposited
under American Type Culture Collection (ATCC) accession number in a list
given in the specification. Also included are vectors and host
cells for producing PRO proteins, PRO fusion proteins, anti-PRO
antibodies, PRO extracellular domains and mature sequences, methods
of detecting PRO proteins, methods for stimulating the release of
TNF-alpha (tumour necrosis factor alpha) from human blood,
(and the proliferation of differentiation of chondrocyte cells, the
proliferation of, or gene expression in pericyte cells, the release or
proteoglycans from cartilage, proliferation of inner ear utricular
supporting cells, the proliferation of T-lymphocyte cells, the release
of a cytokine from peripheral blood mononuclear cells (PBMC), or the
proliferation of endothelial cells), a method for modulating the uptake
of glucose or free fatty acid (FFA) by skeletal muscle cells,
a method for inhibiting the binding of A-peptide to factor VIIA,
or the differentiation of adipocyte cells, a peptide to factor VIIA,
presence of a tumour in a mammal and an oligonucleotide probe derived
from any of the nucleotide sequences cited above. The nucleic acids and
polypeptides are useful for treating inflammatory diseases, organ
failure, atherosclerosis, cardiac injury, infertility, birth defects,
premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
diabetic complications. The nucleic acids are useful as hybridisation
probes, in chromosome and gene mapping, and in generating antisense RNA
or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
biosensors or bioreactors. Both are useful in tissue typing.
CC The present sequence represents a PRO protein of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 611; DB 24; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.6e-59;

Matches 117: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQQRKSKPKAKLPQALAGWLPE 60
|||||
Db 1 MPSPTVCSLLGLMLDLAMAGSSFLSPHQVQQRKSKPKAKLPQALAGWLPE 60
|||||

QY 61 DGGQAGAEDELEVRFNAPFDVGKLSGVQYQHSQALGKFLQDILWEAKEAPADK 117
|||||
Db 61 DGGQAGAEDELEVRFNAPFDVGKLSGVQYQHSQALGKFLQDILWEAKEAPADK 117
|||||

RESULT 12
ABU59871
ID ABU59871 standard; Protein: 117 AA.
XX
AC ABU59871;
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO1066.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; Herpetiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-0140808.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12450.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24853.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 22-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Wood WI, Zhang Z;
XX

DR WPI; 2003-148238/14.
 DR N-PSDB; ABX89361.
 XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments -
 XX
 XX
 PS Claim 12; Fig 442; 659pp; English.
 PS
 XX
 CC The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of
 CC retinal neurons cells (PRO132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO130, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC is the amino acid sequence of a novel human PRO protein.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 611; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.6e-59;
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 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosum; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
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KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
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; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc. East
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
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Best Local Similarity 100.0%; Pred. No. 4.1e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPSPGVC	SLLILG	MLDL	ANAG	SSFL	SPHQ	RVOQ	RESK	KKPA	KI	QPRAL	AGWL	RPE	60
Db	1	MPSPGVC	SLLILG	MLDL	ANAG	SSFL	SPHQ	RVOQ	RESK	KKPA	KI	QPRAL	AGWL	RPE	60
Qy	61	DGQAGAE	DELEV	RNAP	FDV	GIKL	SGVQ	YQOH	SOAL	GKFL	QDIL	WEAE	APAD	K	117
Db	61	DGQAGAE	DELEV	RNAP	FDV	GIKL	SGVQ	YQOH	SOAL	GKFL	QDIL	WEAE	APAD	K	117

RESULT 2

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US-08-822-897C-2
; Sequence 2, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,897C
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
US-08-822-897C-2

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RESULT 3

US-09-608-810A-4
; Sequence 4, Application US/09508810A
; Patent No. 6420521
; GENERAL INFORMATION:


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; 1CCEA:
;
; INFORMATION FOR SEQ ID NO: 4:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 119 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;

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[illegible]

QY 26 SFLSPHQHVQRKESKPAPKLQPRLALAGWLRPDGGQAEGAEDELEVRNAPPDVGIK 85
|| || : | : | : | : | : | : | : | : | :
Dd 29 STFYGLQMQRKNKGOKKSLSVQQASEELGPLDPSEPTKEEBRVVIKLLAPVDIGIR 88
| : | : | : | : | : | : | : | : | :
QY 86 LSGVQYQHSHSQALGRPL 102
; : | : | :

Db 89 MDSRQLEKYRATLERLL 105

RESULT 7

US-09-029-213B-25

Sequence 5, Application US/090608810A

Patent No. 6420521

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Jaspers, Stephen R.

APPLICANT: Deisher, Theresa A.

APPLICANT: Bishop, Paul D.

TITLE OF INVENTION: SGIP PEPTIDES

FILE REFERENCE: 99-51

CURRENT APPLICATION NUMBER: US/09/608,810A

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: 60/141,592

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 119

TYPE: PRT

ORGANISM: Sus scrofa

US-09-608-810A-5

Query Match 14.1%; Score 86; DB 4; Length 119;

Best Local Similarity 26.0%; Pred. No. 0.0067;

Matches 20; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

QY 26 SFLSPHQRVQQRKSKPPAKLPQPRALAGWLRPEDGGQAGAEDELEVRFNAPFDVGIK 85

Db 29 SFTYGLQRMQEKRNKGKQKSLVSQQAEEGLDPSPTKEERVRVKKLLAPVDIGIR 88

QY 86 LSGVQYQOHSQALGKFL 102

Db 89 MDSRQLEKYRATLERLL 105

RESULT 8

US-09-029-213B-25

Sequence 25, Application US/09029213B

Patent No. 6180098

GENERAL INFORMATION:

APPLICANT: CHRISTIAN, Peter D.

TITLE OF INVENTION: RECOMBINANT HELICOVERPA BACULOVIRUSES

TITLE OF INVENTION: EXPRESSING HETEROLOGOUS DNA

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDermott, Will & Emery

STREET: 600 13th Street, NW

CITY: Washington

STATE: District of Columbia

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/029,213B

FILING DATE: 31-AUG-1998

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Joseph Hyosuk Kim

REGISTRATION NUMBER: 41,425

REFERENCE/DOCKET NUMBER: 50179-048

TELEPHONE: 202-756-8000

TELEFAX: 202-756-8087

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 119; Score 72.5; DB 1; Length 244;

Best Local Similarity 24.4%; Pred. No. 0.78;

Matches 30; Conservative 23; Mismatches 43; Indels 27; Gaps 5;

QY 2 PSPGTVCSSLLGLMLDLAMAGSSPL---SPEHQRVQQRKSKPPAKLPQPRALAGWLR 58

LENGTH: 323 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLSCULE TYPE: protein

US-09-029-213B-25

Query Match 11.9%; Score 73; DB 3; Length 323;

Best Local Similarity 27.9%; Pred. No. 0.99;

Matches 31; Conservative 14; Mismatches 36; Indels 30; Gaps 5;

QY 34 RVQQRKSKPPAKLPQPRALAGWLRPEDGGQAGAEDELE--VR--FNAPFD----- 81

Db 144 KVLQRIAVQSPVSVSESENGW---TDDEQQQRASSELKQVRSLYNITLSDSSWIKNYP 200

QY 82 -----VGIK-----LSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117

Db 201 LSTEADQTLISIKNQLNQLNSAQIQVSAKLIQFIEDNLIOETDYNPLDK 251

RESULT 9

US-08-696-827-1

Sequence 1, Application US/08696827

Patent No. 5798213

GENERAL INFORMATION:

APPLICANT: MIYADERA Kazutaka

APPLICANT: YAMADA, Yuji

APPLICANT: TAKEBAYASHI, Yuji

APPLICANT: AKIYAMA, Shinichi

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUB, MION, ZINN, MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W., Suite 800

CITY: Washington, D.C.

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/696,827

FILING DATE: 21-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/USJP/02661

FILING DATE: 25-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 327328/1994

FILING DATE: 28-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: KIT, Gordon

REGISTRATION NUMBER: 30,764

REFERENCE/DOCKET NUMBER: Q-42514

TELEPHONE: (202) 293-7060

TELEFAX: (202) 293-7860

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-696-827-1

Query Match 11.9%; Score 72.5; DB 1; Length 244;

Best Local Similarity 24.4%; Pred. No. 0.78;

Matches 30; Conservative 23; Mismatches 43; Indels 27; Gaps 5;

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Db      7 PAPG-----DFSGGSOGLPDPSPKQLPELIRMKRDGRLSEADIRGVA 53
      59 PEDGQGAEGAEDEVRENAFDVGIKLSGVYQOHS---QALGKFLQDILWEEA-KEAP 114
      54 AVVNGAAGAOIGAML-----MAIRLURGMDLEETSVLTQALAQSGOQLEWPEAWROOL 106
Qy      115 ADK 117
      107 VDK 109
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RESULT 10
US-09-252-991A-23192
; Sequence 23192, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23192
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23192
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Query Match      11.9%; Score 72.5; DB 4; Length 773;
Best Local Similarity 28.7%; Pred. No. 3.7;
Matches 25; Conservative 8; Mismatches 29; Indels 25; Gaps 3;

Qy      3 SPGTVCVCSLL-LGMLWLDLAMAGSSFLSPHERVQQRKESKPPAKLPQALAGWLRPD 61
      421 SPALICRYTADLVLTYNRFADSLATSPE-----RLVGRLDLWLAED 465
Qy      62 -----GQAGAEDELEVRNAP 79
      466 ASALRARLLGSPREGASEVPELRFNLP 492
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RESULT 11
US-08-761-248B-4
; Sequence 4, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761.248B
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 60/008,348
; FILING DATE: 07-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 34012.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-761-248B-4

Query Match      11.5%; Score 70; DB 2; Length 220;
Best Local Similarity 32.7%; Pred. No. 1.4;
Matches 37; Conservative 10; Mismatches 36; Indels 30; Gaps 7;

Qy      30 PEHQ-----VQQRKESKPPAKL-----QPRALA--GWL--RPEDGGQAE----- 66
      90 PHRRCCYNGCAYACLEAVPPVLDLWLPKPRWLGGWLDGPPEVLQAEACSTTED 149
Qy      67 GADEL-----EVRFNAPFDV--GIKLSGVYQOHSQALGKFLQDILWEEAKE 112
      150 GAEPLLCPSGYEHILSPGDVAEGIPNRGOCVKORROADGRILRHLYKEYPE 202
Db
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RESULT 12

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US-09-252-991A-27419
; Sequence 27419, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27419
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27419
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Query Match      11.4%; Score 69.5; DB 4; Length 247;
Best Local Similarity 24.1%; Pred. No. 1.8;
Matches 20; Conservative 8; Mismatches 10; Indels 45; Gaps 2;

Qy      62 GGQAGAEDE-----LEVR-----F 76
      43 GGOSQGAEDQPGRTGDRDRDTCQRRHPRRLDHRHRRRQOQPPHPLNIRGRRVRRTF 102
Db      77 NAFPDVGIKLSGVYQOHSQALG 99
      103 NRPARAGLFVCGVRHGHSQPF 125
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RESULT 13

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US-09-252-991A-27327
; Sequence 27327, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
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RESULT 15
US-09-130-242-2
; Sequence 2, Application US/09130242B
; Patent No. 6194558
; GENERAL INFORMATION:

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Job time : 33.2834 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2003, 17:26:32 ; Search time 71.3262 Seconds
(without alignments)
239.348 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 611

Sequence: 1 MPSPTVCSLLLLGLMLDL.....LGKFLQILWEEAKEAPADK 117

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Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	611	100.0	117	9	US-09-853-253-2
3	611	100.0	117	9	US-09-989-722-268
4	611	100.0	117	9	US-09-989-723-268
5	611	100.0	117	9	US-09-989-279-268
6	611	100.0	117	9	US-09-989-727-268
7	611	100.0	117	10	US-09-989-731-268
8	611	100.0	117	10	US-09-989-732-268
9	611	100.0	117	10	US-09-991-073-268
10	611	100.0	117	10	US-09-990-442-268
11	611	100.0	117	10	US-09-991-163-268
12	611	100.0	117	10	US-09-993-604-268
13	611	100.0	117	10	US-09-990-456-268
14	611	100.0	117	10	US-09-989-721-268
15	611	100.0	117	10	US-09-992-598-268

16	611	100.0	117	10	US-09-989-293A-268
17	611	100.0	117	10	US-09-989-735-268
18	611	100.0	117	10	US-09-990-444-268
19	611	100.0	117	10	US-09-991-181-268
20	611	100.0	117	10	US-09-989-730-268
21	611	100.0	117	10	US-09-990-436-268
22	611	100.0	117	10	US-09-993-687-268
23	611	100.0	117	11	US-09-989-734-268
24	611	100.0	117	11	US-09-997-653-268
25	611	100.0	117	11	US-09-993-667-268
26	611	100.0	117	11	US-09-997-428-268
27	611	100.0	117	11	US-09-997-666-268
28	611	100.0	117	11	US-09-990-438-268
29	611	100.0	117	11	US-09-990-562-268
30	611	100.0	117	11	US-09-990-711-268
31	611	100.0	117	11	US-09-989-726-268
32	611	100.0	117	11	US-09-998-156-268
33	611	100.0	117	11	US-09-990-437-268
34	611	100.0	117	11	US-09-991-157-268
35	611	100.0	117	11	US-09-997-514-268
36	611	100.0	117	11	US-09-997-573-268
37	611	100.0	117	11	US-09-991-172-268
38	611	100.0	117	11	US-09-990-726-268
39	611	100.0	117	11	US-09-997-559-268
40	611	100.0	117	11	US-09-997-601-268
41	611	100.0	117	11	US-09-990-443-268
42	611	100.0	117	11	US-09-991-854-268
43	611	100.0	117	11	US-09-997-628-268
44	611	100.0	117	11	US-09-997-683-268
45	611	100.0	117	11	US-09-989-729A-268

ALIGNMENTS

RESULT 1

US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; DELSHER, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELE: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Query Match          100.0%; Score 611; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRPE 60
Db 1 MPSPGTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRPE 60

Qy 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117

RESULT 2
US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-2

Query Match          100.0%; Score 611; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRPE 60
Db 1 MPSPGTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRPE 60

Qy 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQQHSGALGKFLQDILWEEAKEAPADK 117

RESULT 3
US-09-989-722-268
; Sequence 268, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
```

```
;
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730FIC83
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.7e-60;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-989-723-268
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PICG2
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RESULT 5

US-09-989-279-268

; Sequence 268, Application US/09989279

; Patent No. US20020072496A1

; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSSLLLLGMLWLDLAMAGSSFLSPHQRVQQRKSKPPAKLQPRALAGWURPE 60
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Qy 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQHQSHQALGFLODILWEEAKEAPADK 117
Db 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQHQSHQALGFLODILWEEAKEAPADK 117

RESULT 6

US-09-989-727-268
; Sequence 268, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC65
CURRENT FILING DATE: 2001-11-19
CURRENT FILING DATE: 2001-11-19
PRIORITY APPLICATION NUMBER: US/09/989,727
PRIORITY FILING DATE: 1997-06-16
PRIORITY APPLICATION NUMBER: 60/049787
PRIORITY FILING DATE: 1997-06-16
PRIORITY APPLICATION NUMBER: 60/062250
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/065186
PRIORITY FILING DATE: 1997-11-12
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PRIORITY FILING DATE: 1998-02-25
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.7e-60; Mismatches 0; Indels 0; Gaps 0;

Matches 117; Conservative 0;

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Db 1 MPSPGTVCSSLLGLMLDLAMAGSFLSPSPHQRVQQRKSKPPAKLQPRALAGWL RPE 60

Oy 61 DGGQAGAEDELEVRFNAPDVGILKSGVOYQHQSHQALGXFLQDILWEEAKEAPDK 117

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Db 61 DGGQAGAEDELEVRFNAPDVGILKSGVOYQHQSHQALGXFLQDILWEEAKEAPDK 117

RESULT 7

US-09-989-731-268

; Sequence 268, Application US/09989731

; Patent No. US20020103125A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730FIC70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1997-11-24
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;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690

;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPGTVCSSLLGLMLWLDLAMAGSSFLSPHQRVQORRESKPPAKLOPRALAGWL RPE 60
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DB 1 MPSPGTVCSSLLGLMLWLDLAMAGSSFLSPHQRVQORRESKPPAKLOPRALAGWL RPE 60
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RESULT 8
US-09-989-732-268
; Sequence 268, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

	TITLE OF INVENTION:	Acids Encoding the Same
	FILE REFERENCE:	P2730PIC57
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	CURRENT FILING DATE:	2001-11-19
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Query Match 100.0%; Score 611; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9

US-09-991-073-268
; Sequence 268, Application US/09991073
; Patent No. US2002012756A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC15
;; CURRENT APPLICATION NUMBER: US/09/991,073

;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 611; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 6,7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61  D G G Q A E G A D E L E V R N A P F D V G I K L S G V Q O O H S Q A L K G F L Q D I L W E A K E A P A D K 117
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RESULT 10
US-09-990-442-268
; Sequence 268, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

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; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 611; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 6,7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MPSPGTVCSSLLLGLMLWLDLAMAGSSFLSPFHQVQQRKESKPPAKLQPRALAGWL RPE 60
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Db      1 MPSPGTVCSSLLLGLMLWLDLAMAGSSFLSPFHQVQQRKESKPPAKLQPRALAGWL RPE 60
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QY      61 DGGQAGAEDELEVRENFAPFDVGIKLSGVQYQHQHSLGKFLQDILWEEAKEAPADK 117
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RESULT 12
US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1997-11-13

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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.7e-60;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 DGGQAGABDELEVRNPFVDGKILSGVQYQHQHQAQKFLQDILWEEAKEAPADK 117

RESULT 13

US-09-990-456-268
 ; Sequence 268, Application US/09990456

Patent No. US20020137890A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC22
 ; CURRENT APPLICATION NUMBER: US/09/990,456
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 611; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHQVQQRKESKPKLQPRALAGWLRP 60
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Db 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHQVQQRKESKPKLQPRALAGWLRP 60
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Qy 61 DGGQAEAELEVRFNAPFDVGIKLSGVQVQHSQALGKFLQDILWEEAKEAPDK 117
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RESULT 15

US-09-992-598-268
; Sequence 268, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
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; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978

;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPGTVCSSLLLLGMLWLDLDMAGSSFLSPHQRVQQRKESKPPAKLQPRALAGWLRPE 60
|||||
Db 1 MPSPGTVCSSLLLLGMLWLDLDMAGSSFLSPHQRVQQRKESKPPAKLQPRALAGWLRPE 60
|||||
QY 61 DGGQAGGADELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
|||||
Db 61 DGGQAGGADELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
|||||

Search completed: September 11, 2003, 17:48:31
Job time : 74.3262 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 111.369 Seconds
(without alignments)
271.100 Million cell updates/sec

Title: US-09-853-253-2

Perfect score: 611

Sequence: 1 MPSPTVCSLLLLGLMLDL.....LGKFLQDILWEAKEAPADK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	609	99.7	117	4 Q8TAT9	Q8tat9 homo sapien
2	515	84.3	117	11 Q8CH53	Q8ch53 meriones un
3	229.5	37.6	116	13 Q8AV73	Q8av73 gallus gall
4	146	23.9	111	13 Q8JFY4	Q8jfy4 anguilla ja
5	97.5	16.0	103	13 Q8AUU1	Q8auu1 cerassius a
6	87	14.2	114	13 Q9W422	Q9w422 rana catesb
7	79	12.9	1239	5 O01505	O01505 caenorhabdi
8	78.5	12.8	119	16 Q8PFF9	Q8pff9 xanthomonas
9	75.5	12.4	410	17 Q9HS01	Q9hs01 halobacteri
10	75	12.3	158	16 Q8XW90	Q8xw90 ralstonia s
11	73.5	12.0	709	16 Q9PGM1	Q9pgm1 xylella fas
12	73	11.9	359	5 Q9VQX3	Q9vqx3 drosophila
13	73	11.9	534	2 Q9RPV9	Q9rpv9 bacillus me
14	73	11.9	961	10 Q9SXN6	Q9sxn6 nicotiana t
15	73	11.9	1035	10 Q9M7J0	Q9m7j0 populus tre
16	72.5	11.9	482	4 Q8WVB7	Q8wvb7 homo sapien

17	72.5	11.9	922	16 Q9HWA7	Q9hwa7 pseudomonas
18	71.5	11.7	820	10 Q8H911	Q8h911 oryza sativ
19	71	11.6	81	15 Q9LJT7	Q9ljt7 human immun
20	71	11.6	299	2 Q03087	Q03087 escherichia
21	71	11.6	783	5 Q9VF04	Q9vf04 drosophila
22	71	11.6	1947	2 Q9RFK7	Q9rfk7 stigmatella
23	70.5	11.5	392	10 Q8LS32	Q8ls32 blepharandr
24	70.5	11.5	392	10 Q8LS31	Q8ls31 blepharandr
25	70.5	11.5	392	10 Q8LS30	Q8ls30 blepharandr
26	70	11.5	104	8 Q37609	Q37609 pontia prot
27	70	11.5	220	4 Q8NC27	Q8nc27 homo sapien
28	70	11.5	317	5 Q9N9B9	Q9n9b9 leishmania
29	70	11.5	454	11 Q8C381	Q8c381 mus musculu
30	70	11.5	479	10 Q9LSD7	Q9lsd7 arabidopsis
31	70	11.5	510	10 Q8W4X3	Q8w4x3 sorghum bic
32	70	11.5	619	4 Q9H5Y6	Q9h5y6 homo sapien
33	70	11.5	637	11 Q8CBD5	Q8cbd5 mus musculu
34	70	11.5	822	4 Q9UGT4	Q9ugt4 homo sapien
35	70	11.5	840	16 Q8XAP8	Q8xap8 escherichia
36	69.5	11.4	727	11 Q8R319	Q8r319 mus musculu
37	69.5	11.4	1218	5 Q9W201	Q9w201 drosophila
38	69.5	11.4	3892	5 Q9VU08	Q9vu08 drosophila
39	69	11.3	181	4 Q9H884	Q9h884 homo sapien
40	69	11.3	264	2 Q8GD25	Q8gd25 bordetella
41	69	11.3	298	16 Q8RAL0	Q8ral0 thermoanaer
42	69	11.3	311	16 Q8DV82	Q8dv82 streptococc
43	69	11.3	314	4 Q8NC15	Q8nc15 homo sapien
44	69	11.3	411	5 Q26766	Q26766 trypanosoma
45	69	11.3	412	12 O10610	O10610 helicoverpa

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY; PRT; 117 AA.
AC Q8TAT9;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025791; AAH25791.1; -
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
SQ SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;

Query Match 99.7%; Score 609; DB 4; Length 117;
Best Local Similarity 99.1%; Pred. No. 3.1e-58;
Matches 116; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPHEQVQQRKESKPPAKLPALACWLRPE 60

DB 1 MPSPTVCSLLLLGLMLDLAMAGSFLSPHEQVQQRKESKPPAKLPALACWLRPE 60

QY 61 DGGQAGEADELEVRFNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEAKEAPADK 117

DB 61 DGGQAGEADELEVRFNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEAKEAPADK 117

RESULT 2

Q8CH53

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ID Q8CH53 PRELIMINARY; PRT; 117 AA.
AC Q8CH53;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AA006965.1; -
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 84.3%; Score 515; DB 11; Length 117;
Best Local Similarity 82.1%; Pred. No. 4.8e-48;
Matches 96; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 MPSPGVTCVSLLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPQALAGLWLRPE 60
DB 1 MMSSGTCVSLLLGLVMDVAMAGSFLSPHQVQQRKESKPPAKLPQALAGLWLRPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117
DB 61 GRCQAGAEDELEVRNAPFDVGIKLSGVQYQHSQALGKFLQDILWEEVKEATDK 117

RESULT 3
Q8AV73 PRELIMINARY; PRT; 116 AA.
AC Q8AV73;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Ghrelin precursor.
GN GHR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=22181232; PubMed=12193558;
RA Kaiya H., Van der Geyten S., Kojima M., Hosoda H., Kitajima Y.,
RA Matsumoto M., Geelissen S., Darras V.M., Kangawa K.;
RT "Chicken ghrelin: purification, cDNA cloning, and biological
RT activity.";
RL Endocrinology 143:3454-3463(2002).
DR EMBL; AB075215; BAC24980.1; -
KW Signal.
FT SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT CHAIN 24 49 GHRELIN-26.
SQ SEQUENCE 116 AA; 13227 MW; F5C5FA038F187DE9 CRC64;

Query Match 37.6%; Score 229.5; DB 13; Length 116;
Best Local Similarity 43.4%; Pred. No. 4.1e-17;
Matches 46; Conservative 27; Mismatches 26; Indels 7; Gaps 3;

QY 10 LLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPQALAGLWLRPEGGQAGEA 68
DB 10 ILLSLGTETALAGSFLSPYKNIQQQDKTRKPTARLHRRGTSFV---DTDETEGE 65

QY 69 ED--ELEVNRNAPFDVGIKLSGVQYQHSQALGKFLQDILWEEAKE 112
DB 66 DDNSVDIKFNPVFEIGVITEREYQYGOALEKMLQDILAEENAE 111

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RESULT 4

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Q8JFY4 PRELIMINARY; PRT; 111 AA.
AC Q8JFY4;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Prepro-ghrelin precursor.
GN GHRELIN.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Kaiya H., Kojima M., Hosoda H., Riley L.G., Hirano T., Grau G.E.,
RA Kangawa K.;
RT "Identification of eel ghrelin.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062427; BAB96565.1; -
KW Signal.
FT SIGNAL.
FT CHAIN 1 26 POTENTIAL.
FT CHAIN 27 111 PROGHRELIN.
FT CHAIN 27 48 GHRELIN-21.
SQ SEQUENCE 111 AA; 12831 MW; 7AF95E04DD22DE7B CRC64;

Query Match 23.9%; Score 146; DB 13; Length 111;
Best Local Similarity 38.1%; Pred. No. 4.4e-08;
Matches 43; Conservative 19; Mismatches 29; Indels 22; Gaps 8;

QY 7 VCSLLGLMLDLAMAGSFLSPHQVQQRKESKPPAKLPQALAGLWLRPE--E 60
DB 14 VCVL----ALMDSVQAGSFLSPS-QRQCK--DKKPP-RVGRDRSDGLDLFMRPLQ 65
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQHSQALGKFLQDILWE-EAKE 112
DB 66 D-----EDIRHITNTPEIGITWTTELFQQYGEVMQIMQDLMDDTPAKE 111

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RESULT 5

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Q8AUU1 PRELIMINARY; PRT; 103 AA.
AC Q8AUU1;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Preproghrelin.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22224486; PubMed=12239128;
RA Unniappan S., Lin X., Cervini L., Rivier J., Kaiya H., Kangawa K.,
RA Peter R.E.;
RT "Goldfish ghrelin: molecular characterization of the complementary
RT deoxyribonucleic acid, partial gene structure and evidence for its
RT stimulatory role in food intake.";
RL Endocrinology 143:4143-4146(2002).
DR EMBL; AF454389; AAN16215.1; -
DR EMBL; AF454390; AAN16216.1; -
SQ SEQUENCE 103 AA; 11520 MW; 0881343BDC0C012 CRC64;

Query Match 16.0%; Score 97.5; DB 13; Length 103;
Best Local Similarity 25.7%; Pred. No. 0.0072;
Matches 29; Conservative 22; Mismatches 31; Indels 31; Gaps 4;

```

AN
[4]
RP SEQUENCE FROM N. A.

Matches 31; Conservative 19; Mismatches 48; Indels 15; Caps 4

QY 6 TVCSLLILGLMLDLAMAGSFFLSPEHQVRQKESKKPPAKLQPRALAGWLR---PEDG 62

Qy 6 TVCSLLLLGLMLWLDLAWAGSSFFUSPEHQVRQQRKESKKPPAKLQPRALACWLR---PEDG 62

[illegible]


```
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 709 AA; 79163 MW; 0EAA922E4B463318 CRC64;

Query Match 12.0%; Score 73.5; DB 16; Length 709;
Best Local Similarity 23.5%; Pred. No. 28;
Matches 36; Conservative 14; Mismatches 52; Indels 51; Gaps 6;

Oy 5 GTVCSL-----LLGLMLDLAMAGSSF----- 27
Db 422 GALASLGFARLYLGAHWLSDVGLGMLFGIFWLLVLGYATRRRLTHELOVNPLSWLYGT 481
Oy 28 -----LSPHORVQQRKESKPPAKLQPRALA--GWLRPEDGGQAGBADELEVRFA 78
Db 482 FSIAIVMAPRHLEQKLTFFPPPPS---PRAIAEGWKK-NDWRQLPARNEFDRAERW 537
Oy 79 PFDVGIKLSGVQYQHQSHQALGKFLQ-DILWEEA 110
Db 538 PLNVQVAGSLVPLQOHLETCGWRROPQTGMKEA 570

RESULT 12
Q9VQX3 SEQUENCE FROM N.A.
ID Q9VQX3 PRELIMINARY; PRT; 359 AA.
AC Q9VQX3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG2958 protein (HL05328P) (LP02926P).
GN LECTIN-24DB OR CG2958.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA Sutton G.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler K.A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kelush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Minkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Retnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleeb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuncio J., Pacleeb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003577; AAF51038.1; -.
DR EMBL; AY061025; AAL28573.1; -.
DR EMBL; AY119000; AAM50860.1; -.
DR HSSP; P22897; 1EGG.
DR FlyBase; FBgn0040102; lectin-24Db.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 359 AA; 41546 MW; 1895E525594584C4 CRC64;

Query Match 11.9%; Score 73; DB 5; Length 359;
Best Local Similarity 28.1%; Pred. No. 14;
Matches 27; Conservative 16; Mismatches 33; Indels 20; Gaps 4;

Oy 31 EHQRVQQRKESKPPAKL-----QPRALAGLRPEDGGQAGBADELEVRFA-PF 80
Db 111 EHLQTLQESLKKMPAELDLARLKMENQOKTLQDLENQINLTRESQDQLEALKNPMPI 170
Oy 81 DVGKLSGVQYQHQSHQALGKFLQDILWEEAKEAPAD 116
Db 171 NFEMRLAQIEQQ-----KLLQETL-----RKIPED 196

RESULT 13
Q9RPV9 SEQUENCE FROM N.A.
ID Q9RPV9 PRELIMINARY; PRT; 534 AA.
AC Q9RPV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 60.1 kDa protein.
OS Bacillus megaterium.
OX Plasmid pBM400.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=QM B1551;
RX MEDLINE=21150449; PubMed=11251820;
RA Kuninimalaiyan M., Stevenson D.M., Zhou Y., Vary P.S.;
RT on pBM400 of Bacillus megaterium and identification of an rRNA operon
RL Mol. Microbiol. 39:1010-1021(2001).
DR EMBL; AF142677; AAF0594.1; -.
KW Hypothetical protein; plasmid.
SQ SEQUENCE 534 AA; 60110 MW; 816057052FA159DC CRC64;

Query Match 11.9%; Score 73; DB 2; Length 534;
Best Local Similarity 22.3%; Pred. No. 22;
Matches 33; Conservative 19; Mismatches 46; Indels 50; Gaps 5;
```

QY 6 TVCSLLGLLGLWLDLWAGSSFLSPHQH----- 34
 Db 349 TTWGLLLAKLIFIMLVAGVIGILIREHLKNDSPSLFKFLMSDVSEFMLIIVLIVGTIAHL 408
 QY 35 --VQOR-----KESKK-----PPAKLPQALAGWLR---PEDGGQAGAEDELEVRFN- 77
 Db 409 NPVPQNEPLVWKENKDIEFLVKTSTLSPGKASLWKLKASLPQDGGSSIQSIEIALSPKNKG 468
 QY 78 --APFDVGIKLSGVQYQOQHQAALCKFLQ 103
 Db 469 ELAPIDVPLAVNKDESOEQVQYKMYE 496

RESULT 14

Q9SXN6 PRELIMINARY; PRT; 961 AA.
 ID Q9SXN6
 AC Q9SXN6
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE NTRB1 protein.
 GN NTRB1.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sekine M.;
 RT "Tumor suppressor gene.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB015221; BAA76477.1; -
 DR HSSP; P06400; IGUX.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR002720; RB_A.
 DR InterPro; IPR002719; RB_B.
 DR Pfam; PF01858; RB_A; 1.
 DR Pfam; PF01857; RB_B; 1.
 DR SMART; SM00385; CYCLIN; 1.
 SQ SEQUENCE 961 AA; 106602 MW; 0138DE06FC89ED2C CRC64;

Query Match 11.9%; Score 73; DB 10; Length 961;
 Best Local Similarity 33.3%; Pred. No. 45;
 Matches 30; Conservative 8; Mismatches 40; Indels 12; Gaps 4;
 QY 3 SPCTVCSLLGLLGLWLDLWAGSSFLSPHQH--VQORRESKPPAKLPQALAGWLRPE 60
 Db 666 SPKKVCS-----EYRSVLVERNSFTSPVKDRFLALNNIKSKFPFPALQ-SAFASPTRPN 718
 QY 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQ 90
 Db 719 PGG--GGETCAETAINVFEKIVKLAVR 745

RESULT 15

Q9M7J0 PRELIMINARY; PRT; 1035 AA.
 ID Q9M7J0
 AC Q9M7J0
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Retinoblastoma-related protein 1.
 GN RB1.
 OS Populus tremula x Populus tremuloides.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosidids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=47664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bhalarao R.P., Sivertson M., Sterky F., Lundeborg J., Sandberg G.;
 RT "The role of Rb-related protein from hybrid aspen in wood formation.";

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF133675; AAF61377.1; -
 DR HSSP; P06400; IGUX.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR002720; RB_A.
 DR InterPro; IPR002719; RB_B.
 DR Pfam; PF01858; RB_A; 1.
 DR Pfam; PF01857; RB_B; 1.
 DR SMART; SM00385; CYCLIN; 1.
 SQ SEQUENCE 1035 AA; 114608 MW; F66191BF50BAAAA5 CRC64;
 Query Match 11.9%; Score 73; DB 10; Length 1035;
 Best Local Similarity 35.0%; Pred. No. 49;
 Matches 28; Conservative 5; Mismatches 33; Indels 14; Gaps 3;
 QY 25 SSFLSPEHQHVQQRKESKPPAKLPQALAGWLRPEGGQAGAEDELEVRFNAPFDVGI 84
 Db 709 NSFTSPVKDRLLGNLKSLLPPPLQ-SAFASPTRPNPGG---GGETCAETGINVFFTKIN 764
 QY 85 KLSGVQY-----QQH 94
 Db 765 KLAAYRINGMIEKLQPSQQH 784

Search completed: September 11, 2003, 17:30:24
 Job time : 115.369 secs

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:48:42 ; Search time 8.2139 seconds
(without alignments)
123.627 Million cell updates/sec

Title: US-09-853-253-4

Perfect score: 24

Sequence: 1 ALAGWLPRPDGQAEGBAELEVR 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	117	3 US-09-046-479-2	Sequence 2, Appl
2	24	100.0	117	4 US-08-822-897C-2	Sequence 2, Appl
3	24	100.0	117	4 US-09-608-810A-4	Sequence 4, Appl
4	24	100.0	117	4 US-09-996-243-268	Sequence 268, App
5	7	29.2	442	4 US-09-134-001C-3033	Sequence 3033, Ap
6	7	29.2	552	4 US-09-252-991A-27032	Sequence 27032, A
7	7	29.2	599	4 US-09-252-991A-20368	Sequence 20368, A
8	7	29.2	981	4 US-09-252-991A-16798	Sequence 16798, A
9	6	25.0	39	1 US-08-428-488-13	Sequence 13, Appl
10	6	25.0	97	2 US-08-403-852D-31	Sequence 31, Appl
11	6	25.0	97	3 US-08-510-646B-32	Sequence 32, Appl
12	6	25.0	97	3 US-09-231-818-31	Sequence 31, Appl
13	6	25.0	129	3 US-09-135-994-12	Sequence 12, Appl
14	6	25.0	129	4 US-09-684-843A-12	Sequence 12, Appl
15	6	25.0	183	4 US-09-198-452A-612	Sequence 612, App
16	6	25.0	199	4 US-09-252-991A-32089	Sequence 32089, A
17	6	25.0	202	4 US-09-252-991A-26333	Sequence 26333, A
18	6	25.0	259	4 US-09-252-991A-17300	Sequence 17300, A
19	6	25.0	288	1 US-08-396-650-1	Sequence 1, Appl
20	6	25.0	288	1 US-08-768-626-1	Sequence 1, Appl
21	6	25.0	292	4 US-09-252-991A-18951	Sequence 18951, A
22	6	25.0	292	4 US-09-252-991A-30162	Sequence 30162, A
23	6	25.0	305	4 US-09-328-352-6794	Sequence 6794, Ap
24	6	25.0	326	4 US-09-252-991A-33000	Sequence 33000, A
25	6	25.0	329	4 US-09-843-297-2	Sequence 2, Appl
26	6	25.0	359	4 US-09-266-965-120	Sequence 120, App
27	6	25.0	366	4 US-09-252-991A-29569	Sequence 29569, A

Sequence 158, App
Sequence 25687, A
Sequence 4, Appl
Sequence 4, Appl
Sequence 32421, A
Sequence 22896, A
Sequence 19, Appl
Sequence 17695, A
Sequence 2, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 23, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 21, Appl

6 25.0 378 4 US-09-325-932A-158
6 25.0 399 4 US-09-252-991A-25687
6 25.0 402 3 US-09-464-483-4
6 25.0 402 3 US-09-414-664-4
6 25.0 461 4 US-09-252-991A-32421
6 25.0 489 4 US-09-252-991A-22896
6 25.0 502 4 US-09-207-388-19
6 25.0 510 4 US-09-252-991A-17695
6 25.0 529 3 US-09-464-483-2
6 25.0 529 3 US-09-414-664-2
6 25.0 531 1 US-08-531-601-1
6 25.0 531 2 US-08-859-032-1
6 25.0 535 1 US-08-737-597-10
6 25.0 548 4 US-09-207-388-23
6 25.0 550 4 US-09-207-388-20
6 25.0 568 4 US-09-207-388-22
6 25.0 568 4 US-09-207-388-24
6 25.0 570 4 US-09-207-388-21

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291553
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
US-09-046-479-2

Query Match 100.0%; Score 24; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQGAEGAEDELEVR 24
|||||
Db 52 ALAGWLRPEDGGQGAEGAEDELEVR 75

RESULT 2

US-08-822-897C-2
; Sequence 2, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,897C
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-822-897C-2

Query Match 100.0%; Score 24; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQGAEGAEDELEVR 24
|||||
Db 52 ALAGWLRPEDGGQGAEGAEDELEVR 75

RESULT 3

US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608,810A
; CURRENT FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4

Query Match 100.0%; Score 24; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQGAEGAEDELEVR 24
|||||
Db 52 ALAGWLRPEDGGQGAEGAEDELEVR 75

RESULT 4

US-09-996-243-268
; Sequence 268, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2;le-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLPEDGGQGAEGAEDELEVR 24
Db 52 ALAGWLPEDGGQGAEGAEDELEVR 75

RESULT 5

US-09-134-001C-3033
; Sequence 3033, Application US/09134001C
; Patent No. 6380370

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3033
; LENGTH: 442
; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3033

Query Match 29.2%; Score 7; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAG 16
Db 189 DGGQAG 195

RESULT 6

US-09-252-991A-27032
; Sequence 27032, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27032
; LENGTH: 552
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27032

Query Match 29.2%; Score 7; DB 4; Length 552;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAG 16

Db 22 DGGQAG 28

RESULT 7

US-09-252-991A-20368
; Sequence 20368, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20368
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20368

Query Match 29.2%; Score 7; DB 4; Length 599;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGOAEGA 17
Db 383 GGOAEGA 389

RESULT 8

US-09-252-991A-16798
; Sequence 16798, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16798
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16798

Query Match 29.2%; Score 7; DB 4; Length 981;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
Db 136 ALAGWLR 142

RESULT 9

US-08-428-488-13
; Sequence 13, Application US/08428488
; Patent No. 5624894

GENERAL INFORMATION:

; APPLICANT: BOBOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE

;; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
;; NUMBER OF SEQUENCES: 107
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/428,488
;; FILING DATE: 27-APR-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Baumeister, Mary Katherine
;; REGISTRATION NUMBER: 26,254
;; REFERENCE/DOCKET NUMBER: 028724-087
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 39 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /note= "Position 1 - H-Ser."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 39
;; OTHER INFORMATION: /note= "Position 39 - Phe-OH."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 30
;; OTHER INFORMATION: /note= "Position 30 - Glu-NH2."
US-08-428-488-13

Query Match 25.0%; Score 6; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GAEDEL 21
| | | | |
Db 26 GAEDEL 31

RESULT 10
US-08-403-852D-31
; Sequence 31, Application US/08403852D
; Patent No. 5891695

;; GENERAL INFORMATION:
;; APPLICANT: Blanc, Veronique
;; APPLICANT: Blanche, Francis
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Jacques, Nathalie
;; APPLICANT: Lacroix, Patricia
;; APPLICANT: Thibaut, Denis
;; APPLICANT: Zagorec, Monique
;; APPLICANT: Debussche, Laurent
;; APPLICANT: De Crecy Lagard, Valerie
;; TITLE OF INVENTION: Polypeptides Involved In The
;; Biosynthesis Of Streptogramins, Nucleotide Sequences
;; AND Their Use
;; NUMBER OF SEQUENCES: 43

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/403,852D
;; FILING DATE: 10-MAY-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR 93/00923
;; FILING DATE: 25-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 92/11441
;; FILING DATE: 25-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03806.0054-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 97 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-403-852D-31

Query Match 25.0%; Score 6; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAE 18
| | | | |
Db 2 QAEGAE 7

RESULT 11
US-08-510-646B-32
; Sequence 32, Application US/08510646B
; Patent No. 6077699

;; GENERAL INFORMATION:
;; APPLICANT: Blanc, Veronique
;; APPLICANT: Blanche, Francis
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Jacques, Nathalie
;; APPLICANT: Lacroix, Patricia
;; APPLICANT: Thibaut, Denis
;; APPLICANT: Zagorec, Monique
;; APPLICANT: Debussche, Laurent
;; APPLICANT: De Crecy Lagard, Valerie
;; TITLE OF INVENTION: Polypeptides Involved In The
;; Biosynthesis Of Streptogramins, Nucleotide Sequences
;; AND Their Use
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,646B
; FILING DATE: 03-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-510-646B-32

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Query Match          25.0%; Score 6; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 13 QAEGAE 18
Db 2 QAEGAE 7

```

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RESULT 12
US-09-231-818-31
; Sequence 31, Application US/09231818
; Patent No. 6171846
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanc, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,818
; FILING DATE:
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/08/403,852
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-231-818-31

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Query Match          25.0%; Score 6; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 13 QAEGAE 18
Db 2 QAEGAE 7

```

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RESULT 13
US-09-135-994-12
; Sequence 12, Application US/09135994A
; Patent No. 6280938
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/135,994A
; CURRENT FILING DATE: 1998-08-18
; EARLIER APPLICATION NUMBER: 60/056,170
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-135-994-12

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Query Match          25.0%; Score 6; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 RPEDGG 12
Db 57 RPEDGG 62

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RESULT 14
US-09-684-843A-12
; Sequence 12, Application US/09684843A
; Patent No. 6514755
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/684,843A
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994

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; PRIOR FILING DATE: 1998-08-18
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 129
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-684-843A-12

Query Match 25.0%; Score 6; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RPEDGG 12
 |||||
 Db 57 RPEDGG 62

RESULT 15
 US-09-198-452A-612
 ; Sequence 612, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffiths, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 612
 ; LENGTH: 183
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 US-09-198-452A-612

Query Match 25.0%; Score 6; DB 4; Length 183;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AEGAEED 19
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 Db 155 AEGAEED 160

Search completed: September 11, 2003, 17:58:13
 Job time : 9.2139 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: September 11, 2003, 17:27:22 ; Search time 25.2834 Seconds
(without alignments)
150.669 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 24
Sequence: 1 ALAGWLRPEDGGGAEGAELEVR 24

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0
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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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- 13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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- 19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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- 23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	AAE23839	Human zsig33-linker
2	24	100.0	24	AAE15884	Human zsig33-linker
3	24	100.0	91	AAE33410	Human exon 3-delet
4	24	100.0	116	AAE60517	Human des-Gln14-gh
5	24	100.0	117	AAW87991	Protein designated
6	24	100.0	117	AAW87236	Human signal pepti
7	24	100.0	117	AAW36890	Human polypeptide
8	24	100.0	117	AAE62649	Human zsig33 polyp
9	24	100.0	117	AAE20101	Zsig33 protein. H

10	24	100.0	117	22	AAE60511	Human ghrelin prep
11	24	100.0	117	23	ABW78319	Amino acid sequenc
12	24	100.0	117	23	AAE23838	Human zsig33 prote
13	24	100.0	117	23	AAE15883	Human PRO polypept
14	24	100.0	117	24	ABU66790	Human secreted/tra
15	24	100.0	117	24	ABU67066	Human secreted and
16	24	100.0	117	24	ABU59871	Novel human secret
17	24	100.0	117	24	ABU59124	Human secreted/tra
18	24	100.0	117	24	ABU59271	Novel human secret
19	24	100.0	117	24	ABU59420	Human secreted/tra
20	24	100.0	117	24	ABU60555	Human PRO polypept
21	24	100.0	117	24	ABU58046	Human secreted/tr
22	24	100.0	117	24	ABU58977	Human preproghreli
23	24	100.0	117	24	AAE33409	Human PRO1066 poly
24	24	100.0	117	24	ABU13937	Human PRO1066 poly
25	24	100.0	117	24	ABU10892	Human PRO polypept
26	24	100.0	118	21	AAE66708	Membrane-bound pro
27	24	100.0	118	22	AAU12392	Human PRO1066 poly
28	24	100.0	118	22	AAE65231	Human PRO1066 (UNQ
29	24	100.0	126	22	AAE40676	Human polypeptide
30	23	95.8	23	23	AAE23840	Human zsig33-linker
31	23	95.8	23	23	AAE23841	Human zsig33-linker
32	23	95.8	23	23	AAE15885	Human zsig33-linker
33	23	95.8	23	23	AAE15886	Human zsig33-linker
34	10	41.7	89	22	AAE60523	Bovine ghrelin pre
35	8	33.3	334	21	AAG29677	Arabidopsis thalia
36	8	33.3	428	21	AAG29676	Arabidopsis thalia
37	8	33.3	483	21	AAG29675	Arabidopsis thalia
38	7	29.2	311	19	AAW36129	Snpr activator pro
39	7	29.2	311	21	AAE30494	Amino acid sequenc
40	7	29.2	442	23	ABP38188	Staphylococcus epi
41	7	29.2	1931	22	ABE66948	Drosophila melanog
42	6	25.0	14	22	AAE66948	Human peptide #168
43	6	25.0	26	24	AAE33406	PD-1-related peptid
44	6	25.0	26	24	ABJ18534	Neutrophil-activat
45	6	25.0	39	20	AAE50239	

ALIGNMENTS

RESULT 1	AAE23839	standard; peptide; 24 AA.
ID	AAE23839	standard; peptide; 24 AA.
XX	AAE23839	
AC	AAE23839	
XX	10-SEP-2002	(first entry)
DT	Human zsig33-linker peptide #1.	
XX	Human; zsig33-like peptide; gastric contractility; nutrient uptake;	
KW	growth hormone; digestive enzyme; restorative therapy; gene therapy;	
KW	protein therapy; gastrointestinal; endocrine; anabolic.	
XX	Homo sapiens.	
OS		
XX	Key	Location/Qualifiers
FT	Region	7..18
FT		/note= "Hydrophilic region"
XX	US2002055156-A1.	
XX	09-MAY-2002.	
XX	10-MAY-2001; 2001US-0853253.	
XX	11-MAY-2000; 2000US-203300P.	
XX	(JASP/) JASPERS S R.	
PA	(SHEP/) SHEPPARD P O.	
PA	(DEIS/) DEISHER T A.	
PA	(BISH/) BISHOP P D.	

PN WO200290387-A1.
 XX 14-NOV-2002.
 PD
 XX 10-MAY-2002; 2002WO-AU00582.
 XX
 PF 10-MAY-2001; 2001AU-0004919.
 PR 17-DEC-2001; 2001AU-0009567.
 PR
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 PA
 XX Choplin LK, Jeffery PL, Herington AC;
 PI
 XX WPI; 2003-111957/10.
 DR N-PSDB; AAD50726.
 DR
 XX Identifying a cancer cell or tissue for treating prostate, ovarian,
 PT breast cancer, or benign prostatic hyperplasia, by detecting the
 PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
 PT 1b proteins or nucleic acids -
 XX
 XX Claim 14; Page 34; 50pp; English.
 PS
 XX The invention relates to a method for identifying a cancer cell or
 CC tissue of the reproductive system by detecting expression of a ghrelin,
 CC an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic
 CC acids. The antibodies, exon 3-deleted form of preproghrelin and
 CC antagonists are useful for treating cancer of the reproductive system
 CC such as prostate, ovarian, breast, cervical or uterine cancer,
 CC choriocarcinoma or benign prostatic hyperplasia. The present sequence
 CC is human exon 3-deleted ghrelin protein.
 XX
 XX Sequence 91 AA;
 SQ
 Query Match 100.0%; Score 24; DB 24; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.1e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGGADELEVR 24
 Db 52 ALAGWLRPEDGGQAGGADELEVR 75
 RESULT 4
 AAB60517
 ID AAB60517 standard; Protein; 116 AA.
 XX
 AC AAB60517;
 XX
 XX 24-APR-2001 (first entry)
 DT
 XX
 DE Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
 XX
 KW Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX
 XX WO200107475-A1.
 PN
 XX 01-FEB-2001.
 PD
 XX 24-JUL-2000; 2000WO-JP04907.
 PF
 XX 23-JUL-1999; 99JP-0210002.
 PR 29-NOV-1999; 99JP-0338841.
 PR 26-APR-2000; 2000JP-0126623.
 PR
 XX (KANG/) KANGAWA K.
 PA
 XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 PI
 XX WPI; 1999-070071/06.
 XX

DR WPI; 2001-159704/16.
 DR N-PSDB; AAF59647.
 XX
 XX New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 XX
 XX Claim 3; Page 186-187; 210pp; Japanese.
 PS
 XX The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 XX Sequence 116 AA;
 SQ
 Query Match 100.0%; Score 24; DB 22; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGGADELEVR 24
 Db 51 ALAGWLRPEDGGQAGGADELEVR 74
 RESULT 5
 AAW87991
 ID AAW87991 standard; Protein; 117 AA.
 XX
 AC AAW87991;
 XX
 XX 07-APR-1999 (first entry)
 DT
 XX Protein designated zsig33.
 DE
 XX
 KW Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
 KW nutrient absorption regulation; obesity; metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1..23
 FT Peptide /note= "signal peptide"
 FT Protein 24..117
 FT /note= "mature protein"
 XX
 XX WO9842840-A1.
 PN
 XX 01-OCT-1998.
 PD
 XX 23-MAR-1998; 98WO-US05620.
 XX
 XX 24-MAR-1997; 97US-0822897.
 PR 24-MAR-1997; 97US-0041102.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Deisher TA, Sheppard PO;
 PI
 XX WPI; 1999-070071/06.
 XX

DR N-PSDB; AAX04550.

XX Human polypeptide having homology to motilin, zsig33 - useful e.g.

PT to treat gastrointestinal motility disorders, obesity etc. and to

PT identify antagonists to treat gastrointestinal hypermotility

XX

PS Claim 13; Page 55-56; 69pp; English.

XX

CC The present sequence represents a protein designated Zsig33. The nucleic

CC acids are strongly expressed in stomach tissue. The polypeptide (or

CC allelic variants/orthologs) can be used to stimulate gastric motility,

CC measured as increased transit time or gastric emptying of an ingested

CC substance in mammals. The products are used to treat disorders associated

CC with gastrointestinal cell contractility, secretion of digestive

CC enzymes/acids, gastrointestinal motility, recruitment of digestive

CC enzymes, gastrointestinal inflammation, reflux disease and nutrient

CC absorption regulation. Zsig33 polypeptides may also be important

CC neurologically, since the family of gut-brain peptides to which the

CC homologous protein motilin belongs has been associated with neurological

CC and CNS functions. They may therefore be used e.g. to regulate satiety

CC or treat obesity and other metabolic disorders where neurological

CC feedback modulates nutritional absorption. They are useful to identify

CC zsig33 agonists, antagonists and ligands and to produce antibodies.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 24; DB 20; Length 117;

Best Local Similarity 100.0%; Pred. NO. 2.6e-15;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24

DB 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 6

AAY87236

ID AAY87236 standard; Protein; 117 AA.

XX

AC AAY87236;

XX

DT 11-MAY-2000 (first entry)

XX

DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.

XX

KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;

KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;

KW antimicrobial; nontropic; neuroprotective; cardiovascular; hepatotropic;

KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;

KW reproductive disorder; developmental disorder; arteriosclerosis;

KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;

KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;

KW Parkinson's disease; Huntington's diseases; ovulatory defect;

KW muscular dystrophy.

XX

OS Homo sapiens.

XX

PN WO200000610-A2.

XX

PD 06-JAN-2000.

XX

PF 25-JUN-1999; 99WO-US14484.

XX

PF 26-JUN-1998; 98US-0090762.

PR 31-JUL-1998; 98US-0094983.

PR 01-OCT-1998; 98US-0102686.

PR 11-DEC-1998; 98US-0112129.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Lai P. Tang YT, Gorgone GA, Corley NC, Guegler KT, Baughn MR;

PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;

PI Bandman O;

XX WPI; 2000-160673/14.

DR N-PSDB; AAZ98121.

XX

PT New human signal peptide-containing proteins useful in treatment,

PT prevention and diagnosis of e.g. cancer, inflammation and

PT cardiovascular disease

XX

PS Claim 1; Page 168-169; 327pp; English.

XX

CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the

CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have

CC anticancer, anti-inflammatory, antimicrobial, nontropic, hepatotropic,

CC neuroprotective, cardiovascular and antiasthmatic activities, and can

CC be used in gene therapy. HSPPs can be used to treat or prevent disorders

CC associated with decreased activity or function of HSPP. Antagonists of

CC HSPP are used to treat or prevent disorders associated with increased

CC activity or function of HSPP. Such diseases include cell proliferation

CC (including cancer), inflammation, cardiovascular, neurological,

CC reproductive or developmental disorders, (e.g. arteriosclerosis,

CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,

CC asthma, Crohn's disease, microbial or other infections, congestive or

CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's

CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP

CC nucleic acids can be used for the recombinant production of HSPP, for

CC detecting HSPP in standard hybridisation and amplification assays (for

CC diagnosis and monitoring), in gene therapy, as antisense,

CC triplex-forming or ribozyme therapeutics, for detecting related sequences

CC or genetic variations (Ab) and to screen for agonists and

CC raise specific antibodies (Ab) and to screen for agonists and

CC antagonists (potential therapeutic agents). Ab are used to diagnose, or

CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic

CC antagonists, in competitive drug screens, and for purification of HSPP

CC from natural sources.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 24; DB 21; Length 117;

Best Local Similarity 100.0%; Pred. NO. 2.6e-15;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24

DB 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 7

AAM38890

ID AAM38890 standard; Protein; 117 AA.

XX

AC AAM38890;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 2035.

XX

DE Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

PD 26-JUL-2001.

XX

PF 26-DEC-2000; 2000WO-US34263.

XX

XX 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AAI58046.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 3: SEQ ID NO 2035; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAI38642-AAI42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 24; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRLPEDGGQAGAEDELEVR 24
 DB 52 ALAGWLRLPEDGGQAGAEDELEVR 75
 RESULT 8
 AAB62649
 ID AAB62649 standard; Protein; 117 AA.
 AC AAB62649;
 XX
 XX 23-JUL-2001 (first entry)
 DT Human zsig33 polypeptide.
 DE
 DE zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R;
 KW G-protein coupled receptor.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 24..37
 FT /note= "specifically claimed fragment that binds to
 FT the GHS-R"
 XX
 PN WO200138355-A2.

XX 31-MAY-2001.
 PD
 XX 22-NOV-2000; 2000WO-US32074.
 PF
 XX 22-NOV-1999; 99US-0166765.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 PI WPI: 2001-355879/37.
 DR N-PSDB: AAF83678.
 DR
 XX Forming reversible peptide receptor complex for purifying cell and
 XX peptides, stimulating signal transduction and modulating hormone
 PT secretion, involves contacting a receptor with zsig33 polypeptide -
 PT
 XX Claim 1; Page 93-94; 111pp; English.
 XX
 CC The invention relates to a method of forming a reversible peptide-
 CC receptor complex that involves providing an immobilized receptor, and
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
 CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
 CC is useful for purifying cells, purifying a peptide, stimulating signal
 CC transduction in a cell expressing a receptor. It is also useful for
 CC modulating secretion of hormones, neural development and/or utilization,
 CC gastric contractility, nutrient uptake, secretion of digestive and
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
 CC hormone secretion in a mammal having a disease associated with abnormal
 CC levels of growth hormone, such as osteoporosis, bone repair, bone
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,
 CC protein catabolic responses after surgery, cachexia, protein loss,
 CC dwarfism, wound healing and ovulation induction, treating a mammal having
 CC a metabolic disorder requiring neurological feedback, such as satiety
 CC regulation, glucose absorption and metabolism and neuropathy-associated
 CC gastrointestinal disorders, and stimulating glucose-induced insulin
 CC release in a mammal. The present sequence represents the human zsig33
 CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 24; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRLPEDGGQAGAEDELEVR 24
 DB 52 ALAGWLRLPEDGGQAGAEDELEVR 75
 RESULT 9
 AAB20101
 ID AAB20101 standard; Protein; 117 AA.
 AC AAB20101;
 XX
 XX 23-APR-2001 (first entry)
 DT Zsig33 protein.
 DE
 DE zsig33 protein.
 KW SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
 KW nutritional absorption modulator; growth hormone secretagogue;
 KW therapy; human.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= signal_peptide
 FT Protein 24..117

FT Peptide /label- Mature_protein
FT 24..34
FT /label- SGIP_peptide
FT /note- "this peptide is claimed in Claim 1"
XX
XX
XX WO200100830-A1.
XX
XX 04-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-US18306.
XX
XX 30-JUN-1999; 99US-0345157.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
XX WPI; 2001-123010/13.
XX
XX N-PSDB; AAF30033.
XX
XX Novel variants of SGIP peptides for modulating contractility in
XX duodenum or jejunal tissue, pancreatic secretion of hormones and
XX digestive enzymes, inducing growth hormone secretion or modulating
XX gastric emptying -
XX
XX Disclosure: 54; 61pp; English.
XX
XX The present sequence is that of zsig33, a secreted protein with
XX homology to motilin (see AAB20102). Zsig33 is expressed at high
XX levels in the stomach, and at lower levels in the small intestine
XX and pancreas. A novel peptide fragment of zsig33, termed SGIP (see
XX AAB20100), is claimed. SGIP is a ligand for growth hormone
XX secretagogue receptor, and is therefore useful for modulating
XX secretion of growth hormone and insulin like growth factor 1.
XX SGIP, and variant SGIP peptides, are used in claimed methods for
XX stimulating contractility in duodenum or jejunal tissue,
XX modulating pancreatic secretion of hormones and digestive enzymes,
XX inducing growth hormone secretion, and modulating gastric emptying.
XX
XX Sequence 117 AA;
XX
XX Query Match 100.0%; Score 24; DB 22; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-15;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
XX
XX Db 52 ALAGWLRPEDGGQAGAEDELEVR 75
XX
XX
XX RESULT 10
XX AAB60511
XX ID AAB60511 standard; Protein; 117 AA.
XX
XX AC AAB60511;
XX
XX DT 24-APR-2001 (first entry)
XX
XX DE Human ghrelin preproprotein, SEQ ID NO:5.
XX
XX KW Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
XX calcium concentration elevation; infant growth disorder;
XX growth hormone deficiency.
XX
XX OS Homo sapiens.
XX
XX PN WO200107475-A1.
XX
XX PD 01-FEB-2001.
XX
XX PF 24-JUL-2000; 2000WO-JP04907.
XX
XX PR 23-JUL-1999; 99JP-0210002.
XX

PR 29-NOV-1999; 99JP-0338841.
XX 26-APR-2000; 2000JP-0126623.
XX
XX PA (KANG/) KANGAWA K.
XX
XX PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
XX
XX DR WPI; 2001-159704/16.
XX
XX DR N-PSDB; AAF59645.
XX
XX PT New peptide compounds which induce growth hormone secretion and
XX elevate cell calcium concentrations, useful in treatment and diagnosis
XX of infant growth disorders -
XX
XX PS Claim 3; Page 182; 210pp; Japanese.
XX
XX CC The invention relates to a novel peptide compound or its salt which
XX induces the secretion of growth hormone and/or elevates calcium ion
XX concentration in cells. The peptides are ghrelin homologues and are
XX characterised in that at least one amino acid has been substituted by
XX a modified amino acid and/or a non-amino acid compound. The invention
XX also encompasses the unmodified peptides; the DNA encoding the peptides;
XX vectors and host cells comprising such DNA; a method of producing the
XX peptides comprising recombinant production, optionally followed by
XX chemical modification; an antibody specific for a peptide of the
XX invention; and an assay and kit for detecting the peptides. The peptides
XX of the invention are useful for treating and/or diagnosing diseases
XX caused by a deficiency in growth hormone expression or activity. In
XX particular, they are useful for promoting infant growth due to growth
XX hormone deficiency. The compounds of the invention are safe with
XX no accompanying side effects. The present sequence represents a
XX ghrelin-type growth hormone secretagogue (GHS) precursor protein
XX of the invention.
XX
XX SQ Sequence 117 AA;
XX
XX Query Match 100.0%; Score 24; DB 22; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-15;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
XX
XX Db 52 ALAGWLRPEDGGQAGAEDELEVR 75
XX
XX
XX RESULT 11
XX ABB78319
XX ID ABB78319 standard; Protein; 117 AA.
XX
XX AC ABB78319;
XX
XX DT 05-DEC-2002 (first entry)
XX
XX DE Amino acid sequence of a human zsig33.
XX
XX KW Short gastrointestinal peptide; SGIP; zsig33; motilin.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..23
XX FT /note= "signal peptide"
XX FT Protein 24..119
XX FT /note= "mature protein"
XX
XX PN US6420521-B1.
XX
XX PD 16-JUL-2002.
XX
XX PF 30-JUN-2000; 2000US-0608810.
XX
XX PR 30-JUN-1999; 99US-141592P.
XX

PA (ZYMO) ZYMOGENETICS INC.
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 PI
 DR WPI: 2002-634794/68.
 DR N-PSDB; ABV72214.
 XX
 XX New Short Gastrointestinal Peptide, which has homology to motilin,
 PT useful for preventing, diagnosing and treating gastrointestinal
 PT disorders -
 XX
 XX Disclosure: Columns 39-40; 23pp; English.
 PS
 XX The present sequence represents human zsig33. The specification describes
 CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.
 CC SGIP has homology to motilin. The SGIP peptide may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate SGIP expression. For example, SGIP may be used to treat
 CC disorders associated with decreased expression by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of SGIP by
 CC expressing inactive proteins or to supplement the patients own production
 CC of SGIP. SGIP may also be used as an antigen in the production of
 CC antibodies against SGIP and in assays to identify modulators of SGIP
 CC expression and activity. The anti-SGIP antibodies, agonists and
 CC antagonists may also be used to regulate expression and activity. The
 CC anti-SGIP antibodies may also be used as diagnostic agents for detecting
 CC the presence of SGIP in samples.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 24; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24
 DB 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 12
 AAE23838
 ID AAE23838 standard; Protein; 117 AA.
 XX
 AC AAE23838;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human zsig33 protein.
 XX
 KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
 KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
 KW protein therapy; gastrointestinal; endocrine; anabolic.
 XX
 OS Homo sapiens.
 XX
 PN US2002055156-A1.
 XX
 PD 09-MAY-2002.
 XX
 PF 10-MAY-2001; 2001US-0853253.
 XX
 PR 11-MAY-2000; 2000US-203300P.
 XX
 XX (JASP/) JASPERS S R.
 PA (SHEP/) SHEPPARD P O.
 PA (DEIS/) DEISHER T A.
 PA (BISH/) BISHOP P D.
 XX
 XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 PI
 XX WPI: 2002-443750/47.
 DR N-PSDB; AAD38238.
 XX

PT zsig33-Like peptides and polynucleotides, useful for modulating gastric
 PT contractility, nutrient uptake, growth hormones and/or secretion of
 PT digestive/pancreatic enzymes and hormones -
 XX
 PS Disclosure: Page 27; 34pp; English.
 XX
 CC The invention relates to zsig33-like peptides and their corresponding
 CC nucleic acids and methods for modulating gastric contractility, nutrient
 CC uptake, growth hormones, secretion of digestive enzymes and hormones.
 CC The sequences of the invention are used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate zsig33 expression.
 CC The nucleic acids of the invention and their complements are used as
 CC DNA probes in diagnostic assays to detect and quantitate the presence
 CC of similar nucleic acids in samples, and therefore which patients may be
 CC in need of restorative therapy. The zsig33 peptides are used as antigens
 CC in the production of antibodies against zsig33 and in assays to identify
 CC modulators of zsig33 expression and activity. The anti-zsig33 antibodies
 CC and antagonists are used to down regulate expression and activity. The
 CC anti-zsig33 antibodies are also used as diagnostic agents for detecting
 CC the presence of zsig33 in samples (e.g. by enzyme linked immunosorbent
 CC assay (ELISA)). The peptides and nucleic acids of the invention are used
 CC to modulate gastric contractility, nutrient uptake, growth hormones, the
 CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
 CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
 CC and zsig33-like peptide is used in protein therapy. The present sequence
 CC is human zsig33 protein.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 24; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24
 DB 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 13
 AAE15883
 ID AAE15883 standard; Protein; 117 AA.
 XX
 AC AAE15883;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human zsig33 protein.
 XX
 KW Human; zsig33-like peptide; zsig33LP; immunity; developmental process;
 KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
 KW adsorption enhancer; gastrointestinal disease; growth related disease;
 KW inflammation; gene therapy; growth regulation; blood vessel formation;
 KW HIV; zsig33 protein.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide 1..23
 FT /label= Signal_peptide
 FT Protein 24..117
 FT /note= "Human mature zsig33 protein"
 XX
 PN WO200187933-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-US15091.
 XX
 PR 11-MAY-2000; 2000US-0569271.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 PI

XX WPI; 2002-082982/11.
 DR N-PSDB; AAD25759.
 XX
 PT New polypeptides, useful for modulating gastric contractility, nutrient
 PT uptake, pancreatic secretion of hormones, digestive enzymes and
 PT treating gastrointestinal and growth related diseases, comprises
 PT zsig33-like peptides -
 XX
 PS Disclosure; Page 80-81; 89pp; English.
 XX
 CC The invention relates to zsig33-like peptides (ZS33LP) including
 CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and
 CC zsig33-epsilon peptides and nucleic acid molecules encoding such
 CC zsig33-like peptides. ZS33LP peptides activate the immune system
 CC in boosting immunity to infectious diseases, treating immunocompromised
 CC patients such as human immunodeficiency virus (HIV) patients, in
 CC improving vaccines and in treatment of bacterial, viral, protozoal and
 CC fungal infections. Peptides of the invention are used to identify and
 CC isolate receptors involved in growth regulation in the liver, blood
 CC vessel formation and other developmental processes. They are useful for
 CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
 CC growth and/or differentiation of tumour cells, as additives to anti-
 CC hypoglycaemic preparations containing glucose and as adsorption
 CC enhancers for oral drugs which require fast nutrient action and to
 CC stimulate glucose-induced insulin release. They are also useful as
 CC research reagents for the expansion, differentiation, growth factor and
 CC hormone secretion and/or cell-cell interactions of tissues associated
 CC with gastrointestinal system, brain and central nervous system. These
 CC molecules are useful for treating dysfunction associated with contractile
 CC tissues or to suppress or enhance contractility in vivo and to treat
 CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
 CC acids and/or antibodies are useful for treating disorders associated
 CC with gastrointestinal contractility, secretion of digestive enzymes,
 CC hormone and acids, secretion of hormones in the pancreas and/or brain,
 CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
 CC and regulation of nutrient absorption. Sequences of the invention are
 CC useful in gene therapy. The present sequence is human zsig33 protein.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 24; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQGADELEVR 24
 DQ 52 ALAGWLRPEDGGQGADELEVR 75

RESULT 14
 ABU66790
 ID ABU66790 standard; Protein; 117 AA.

XX AC ABU66790;
 XX
 XX 23-MAY-2003 (first entry)
 XX
 XX Human PRO polypeptide #221.

XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KW differentiation; chondrocyte; tumour; genetic disorder;
 KW cytosolic.
 XX
 XX Homo sapiens.

OS
 XX US2003036180-A1.
 FN

XX 20-FEB-2003.
 PD

XX 09-MAY-2002; 2002US-0143114.
 PF

XX

PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 98WO-US00106.
 PR 08-MAR-1999; 98WO-US05028.
 PR 10-MAR-1999; 98WO-US05190.
 PR 20-APR-1999; 98WO-US08615.
 PR 14-MAY-1999; 98WO-US10733.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-SEP-1999; 98WO-US20111.
 PR 08-SEP-1999; 98WO-US20594.
 PR 13-SEP-1999; 98WO-US20944.
 PR 15-SEP-1999; 98WO-US21090.
 PR 15-SEP-1999; 98WO-US21547.
 PR 05-OCT-1999; 98WO-US23089.
 PR 29-NOV-1999; 98WO-US28214.
 PR 30-NOV-1999; 98WO-US28313.
 PR 30-NOV-1999; 98WO-US28409.
 PR 01-DEC-1999; 98WO-US28301.
 PR 01-DEC-1999; 98WO-US28634.
 PR 02-DEC-1999; 98WO-US28551.
 PR 02-DEC-1999; 98WO-US28584.
 PR 02-DEC-1999; 98WO-US28585.
 PR 16-DEC-1999; 98WO-US30095.
 PR 20-DEC-1999; 98WO-US30911.
 PR 20-DEC-1999; 98WO-US30999.
 PR 22-DEC-1999; 98WO-US30720.
 PR 30-DEC-1999; 98WO-US31243.
 PR 30-DEC-1999; 98WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.

PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 30-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 01-JUN-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI: 2003-332040/31.
 DR N-PSDB; ACA03823.

XX
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification -
 XX
 PS Claim 12; Fig 442; 660pp; English.

CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. AB066570-AB066844 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsdIDentry.html.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 24; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24
 ||||||||||||||||||||
 DB 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 15
 AB067066
 ID AB067066 standard; Protein; 117 AA.
 XX
 AC AB067066;
 XX
 DT 27-MAY-2003 (first entry)
 XX
 DE Human secreted/transmembrane, PRO, protein SEQ ID 442.
 XX
 KW Human; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioreactor; tumour.
 XX
 OS Homo sapiens.
 XX
 PN US2003032155-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 03-MAY-2002; 2002US-0137865.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17886.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
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 PR 29-OCT-1998; 98WO-US22992.
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 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
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 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
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 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
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 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
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 PR 30-DEC-1999; 99WO-US31274.
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 PR 06-JAN-2000; 2000WO-US00277.
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 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21086.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 01-JUN-2001; 2001US-0866034.
 PR 05-JUN-2001; 2001US-0872035.
 PR 14-JUN-2001; 2001US-0874503.
 PR 19-JUN-2001; 2001US-0882636.
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 PR 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI: 2003-331925/31.
 N-PSDB; ACA04244.

New secreted and transmembrane nucleic acids and polypeptides,
 designated as PRO, useful for treating inflammation, organ failure,
 atherosclerosis, cardiac injury, infertility, birth defects, premature
 aging, AIDS, or cancer

Claim 12: Fig 442: 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is
 at least 80% identical to, or the full-length coding sequence of, any of
 the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 (one of 275 secreted or transmembrane proteins). The nucleic acid
 further comprises the full-length coding sequence of the DNA deposited

CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 24; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.6e-15;
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Db 52 ALAGWLRPEDGGGAGAEDELEVR 75

Search completed: September 11, 2003, 17:51:54
 Job time : 26.2834 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:55:57 ; Search time 14.7594 Seconds
(without alignments)
237.266 Million cell updates/sec

Title: US-09-853-253-4

Perfect score: 24

Sequence: 1 ALAGWLRPEDGGGAEGAEDELEVR 24

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Minimum DB seq length: 0

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	24	100.0	117	9 US-09-794-987-2	Sequence 2, Appl1
3	24	100.0	117	9 US-09-853-253-2	Sequence 2, Appl1
4	24	100.0	117	9 US-09-989-722-268	Sequence 268, App
5	24	100.0	117	9 US-09-989-723-268	Sequence 268, App
6	24	100.0	117	9 US-09-989-279-268	Sequence 268, App
7	24	100.0	117	9 US-09-989-727-268	Sequence 268, App
8	24	100.0	117	10 US-09-989-731-268	Sequence 268, App
9	24	100.0	117	10 US-09-989-732-268	Sequence 268, App
10	24	100.0	117	10 US-09-991-073-268	Sequence 268, App
11	24	100.0	117	10 US-09-990-442-268	Sequence 268, App
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41	24	100.0	117	11 US-09-997-601-268	Sequence 268, App
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ALIGNMENTS

RESULT 1
US-09-853-253-4
; Sequence 4, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zslg33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-4

Query Match 100.0%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24
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Db 1 ALAGWLRPEDGGGAEGAEDELEVR 24
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RESULT 2
US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.

Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/046,479
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Query Match 100.0%; Score 24; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. NO. 3.9e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEVR 24
Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 3
US-09-853-253-2
Sequence 2, Application US/09853253
Patent No. US2002005156A1
GENERAL INFORMATION:
APPLICANT: JASPERS, STEPHEN
APPLICANT: SHEPPARD, PAUL
APPLICANT: DEISHER, THERESA
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: zsig33-like Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-853-253-2

Query Match 100.0%; Score 24; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. NO. 3.9e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 4
US-09-989-722-268
Sequence 268, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Garber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/087607
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PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04

RESULT 5

US-09-989-723-268 Application US/098987723
; Sequence 268
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grøttsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGADELEVR 24
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Db 52 ALAGWLRPEDGGGAEGADELEVR 75

RESULT 6
US-09-989-279-268
; Sequence 268, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.9e-16;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24

Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 7

US-09-989-727-268
; Sequence 268, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 24; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.9e-16;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGGAEGAEDELEVR 24
 Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 8

US-09-989-731-268
 ; Sequence 268, Application US/09989731
 ; Patent No. US20020103125A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PLC70
 ; CURRENT APPLICATION NUMBER: US/09/989,731
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.9e-16; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 52 ALAGWLRPEDGGQAEDELEVR 75

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US-09-989-732-268
 ; Sequence 268, Application US/09989732
 ; Patent No US20020123463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-991-073-268

; Sequence 268, Application US/09991073

; Patent No. US20020127576A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
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 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730PIC15
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Sco
Best Local Similarity 100.0%; Pre
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RESULT 11
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Tr
; FILE REFERENCE: P2730P1C8
; CURRENT APPLICATION NUMBER: US/09/99-11-14
; CURRENT FILING DATE: 2001-11-14
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?	PRIOR FILING DATE:	1998-06-26
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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.9e-16;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24

Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 12

US-09-991-163-268

; Sequence 268, Application US/09991163

; Patent No. US20020132253A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanebe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C17

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 24; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ALAGWLRPEDGGGAEGAEDELEVR 24
        |||
Db      52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 13
US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 24; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.9e-16;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAGWLRPEDGGGAEGAEDELEVR 24

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Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 14

US-09-990-456-268

; Sequence 268, Application US/09990456

; Patent No. US20020137890A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730PIC22

; CURRENT APPLICATION NUMBER: US/09/990,456

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

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; PRIOR APPLICATION NUMBER: 60/084600

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; PRIOR APPLICATION NUMBER: 60/087827

; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:37 ; Search time 9.1123 seconds
(without alignments)
253.289 Million cell updates/sec

Title: US-09-853-253-4

Perfect score: 24

Sequence: 1 ALAGWLRPDGGQAGAEDELEVR 24

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	24	100.0	117	1	A59316	ghrelin precursor
2	8	33.3	483	2	T04453	hypothetical prote
3	7	29.2	302	2	JH0572	hypothetical prote
4	7	29.2	344	2	A48990	transcription regu
5	7	29.2	910	2	B83451	aconitate hydratase
6	7	29.2	1239	1	Q08E10	BOLFI protein - hu
7	6	25.0	69	2	C87574	cold-shock domain
8	6	25.0	103	2	F82266	conserved hypothet
9	6	25.0	142	2	AB0401	probable membrane
10	6	25.0	175	2	E82118	conserved hypothet
11	6	25.0	178	2	A30230	quiescence-specifi
12	6	25.0	180	2	T46695	hypothetical prote
13	6	25.0	189	2	A91082	hypothetical prote
14	6	25.0	189	2	B85927	hypothetical prote
15	6	25.0	198	2	D69070	imidazoleglycerol-
16	6	25.0	223	2	A40866	HL-60-induced diff
17	6	25.0	237	2	T30002	hypothetical prote
18	6	25.0	265	2	A95298	hypothetical prote
19	6	25.0	267	1	CTGPP	corticotropin / li
20	6	25.0	284	2	B25624	tropomyosin I, tho
21	6	25.0	284	2	A25624	tropomyosin I, emb
22	6	25.0	288	2	A55737	PD-1 protein - hum
23	6	25.0	289	2	T48894	lipoprotein mtsA,
24	6	25.0	289	2	H83433	hypothetical prote
25	6	25.0	290	2	H71852	hypothetical prote
26	6	25.0	293	2	H72757	hypothetical prote
27	6	25.0	299	2	T35144	glutamate transpor
28	6	25.0	302	2	T48871	catechol 1,2-dioxy
29	6	25.0	308	2	F72508	probable hydrogena

ALIGNMENTS

RESULT 1

A59316

ghrelin precursor - human

N:Alternate names: preproghrelin

C:Species: Homo sapiens (man)

C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000

C:Accession: A59316

R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A:Reference number: A59316; MUID:20067959; PMID:10604470

A:Accession: A59316

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-117 <KOJ>

A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BAA89371.1; PID:g6691572

A:Experimental source: tissue stomach endocrine cells

A>Note: submitted to GenBank, June 1999

C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gr

C:Superfamily: motilin

C:Keywords: hormone; lipoprotein; stomach

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-51/Product: ghrelin #status predicted <MAT>

F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match	100.0%	Score 24;	DB 1;	Length 117;
Best Local Similarity	100.0%;	Pred. No. 3.3e-17;		
Matches 24;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 ALAGWLRPDGGQAGAEDELEVR 24

DB 52 ALAGWLRPDGGQAGAEDELEVR 75

RESULT 2

T04453

hypothetical protein F4D11.80 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999

C:Accession: T04453

R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Hohelsel, J.; Mewes,

submitted to the Protein Sequence Database, April 1998

A:Reference number: Z15360

A:Accession: T04453

A:Molecule type: DNA

A:Residues: 1-483 <BEV>

A:Cross-references: EMBL:AL022537

A:Experimental source: cultivar Columbia; BAC clone F4D11

C:Genetics:

A:Map position: 4

A:Introns: 17/3; 44/1; 94/1; 141/3; 206/2; 247/2; 345/3; 395/1; 434/2

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31	6	25.0	315	2	F64129	probable phosphogl
32	6	25.0	326	1	E69690	transcription repr
33	6	25.0	343	2	AH1823	30S ribosomal prot
34	6	25.0	343	2	T35063	probable prolipopr
35	6	25.0	345	2	A83526	hypothetical prote
36	6	25.0	346	2	AE3323	sam-dependent meth
37	6	25.0	350	2	S71923	cysteine proteinase
38	6	25.0	360	2	S59598	cysteine proteinase
39	6	25.0	368	2	G96668	protein FIN19.7 [l
40	6	25.0	376	2	AD2697	hypothetical prote
41	6	25.0	377	2	G97314	alcohol dehydrogen
42	6	25.0	377	2	T47471	cysteine proteinase
43	6	25.0	379	1	DCBSPK	phosphoribosylamin
44	6	25.0	379	2	D82801	molybdopterin bios
45	6	25.0	383	2	F83321	hypothetical prote

A>Note: F4D11.80

Query Match 33.3%; Score 8; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAED 20
| | | | | | | |
Db 302 QAEGAED 309

RESULT 3

JH0572

hypothetical protein - Streptomyces lividans (fragment)

C:Species: Streptomyces lividans
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-1999
R:Lichenstein, H.S.; Busse, L.A.; Smith, G.A.; Narhl, L.O.; McGinley, M.O.; Rohde, M.F.;
Gene 111, 125-130, 1992
A:Title: Cloning and characterization of a gene encoding extracellular metalloprotease
A:Reference number: JH0571; MUID:92192468; PMID:1547948
A:Accession: JH0572
A:Molecule type: DNA
A:Residues: 1-302 <LIC>
A:Cross-references: GB:M89476; NID:g153411; PIDN:AAA26804.1; PID:g153412
A:Experimental source: strain TK24
A>Note: the authors translated the codon GTA for residue 260 as Asp
A>Note: this protein has a strong similarity to LysR family of transcriptional regulator
C:Superfamily: Pseudomonas putida regulatory protein catR

Query Match 29.2%; Score 7; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7
| | | | | | | |
Db 100 ALAGWLR 106

RESULT 4

A48990

transcription regulator LysR family homolog Snpr - Streptomyces lividans

C:Species: Streptomyces lividans
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
R:Butler, M.J.; Davey, C.C.; Krygsman, P.; Walczyk, E.; Malek, L.T.
Can. J. Microbiol. 38, 912-920, 1992
A:Title: Cloning of genetic loci involved in endoprotease activity in Streptomyces lividans
A:Reference number: A48990; MUID:93099553; PMID:11464066
A:Contents: 66
A:Accession: A48990
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-344 <BUT>
A>Note: sequence extracted from NCBI backbone (NCBIN:121210, NCBIP:121213)
C:Superfamily: Pseudomonas putida regulatory protein catR

Query Match 29.2%; Score 7; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7
| | | | | | | |
Db 104 ALAGWLR 110

RESULT 5

B83451

aconitate hydratase 1 PA1562 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83451
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.;
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83451
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-910 <STO>
A:Cross-references: GB:AE004584; GB:AE004091; NID:9947516; PIDN:AA04951.1; GSPDB:GN
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: acnA; PA1562
C:Superfamily: iron-responsive element-binding protein

Query Match 29.2%; Score 7; DB 2; Length 910;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7
| | | | | | | |
Db 65 ALAGWLR 71

RESULT 6

QB0E10

BOLFI protein - human herpesvirus 4 (strain B95-8)

C:Species: human herpesvirus 4, Epstein-Barr virus
C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
C:Accession: A43041; A03752; S32995
R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi
A:Reference number: A93065; MUID:85035713; PMID:6092825
A:Accession: A43041
A:Molecule type: DNA
A:Residues: 1-1239 <BAN>
A:Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24841.1; PID:g1334855
R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.

Nature 310, 207-211, 1984
A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A:Reference number: A03794; MUID:84270667; PMID:6087149
A:Contents: annotation; protein coding region
C:Superfamily: human herpesvirus 4 BOLFI protein

Query Match 29.2%; Score 7; DB 1; Length 1239;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AEGAED 20
| | | | | | | |
Db 696 AEGAED 702

RESULT 7

C87574

cold-shock domain family protein [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C:Accession: C87574
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87574
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-69 <STO>
A:Cross-references: GB:AE005673; NID:g13424199; PIDN:AAK24591.1; GSPDB:GN00148
C:Genetics:

A:Gene: CC2623

C:Superfamily: major cold shock protein; cold shock domain homology

Query Match 25.0%; Score 6; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PEDGGQ 13
|||||
DB 20 PEDGGQ 25

RESULT 8

F82266 conserved hypothetical protein VC0887 [imported] - Vibrio cholerae (strain N16961 serogr

C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Dec-2002
C:Accession: F82266
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301

A:Accession: F82266
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <HE>
A:Cross-references: GB:AE004173; GB:AE003852; NID:g9655341; PIDN:AAF94049.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0887
A:Map position: 1
C:Superfamily: uncharacterized conserved protein

Query Match 25.0%; Score 6; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 DELEVR 24
|||||
DB 12 DELEVR 17

RESULT 9

AB0401 probable membrane protein YPO3302 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0401
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AB0401
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92534.1; PID:gl5981232; GSPDB:GN00175
C:Genetics:
A:Gene: YPO3302
C:Superfamily: hypothetical protein HI0489

Query Match 25.0%; Score 6; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAGWLR 7
|||||
DB 104 LAGWLR 109

RESULT 10

E82118 conserved hypothetical protein VC2111 [imported] - Vibrio cholerae (strain N16961 ser

C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82118
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301

A:Accession: E82118
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-175 <HE>
A:Cross-references: GB:AE004284; GB:AE003852; NID:g96556649; PIDN:AAF95256.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2111
A:Map position: 1

Query Match 25.0%; Score 6; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GOAEGA 17
|||||
DB 54 GOAEGA 59

RESULT 11

A30230 quiescence-specific protein precursor - chicken

N:Alternate names: Ch21 protein
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 15-Nov-1996
C:Accession: A30230; A42581; A36595; A35491
R:Bedard, P.A.; Yannoni, Y.; Simmons, D.L.; Erikson, R.L.
Mol. Cell. Biol. 9, 1371-1375, 1989
A:Title: Rapid repression of quiescence-specific gene expression by epidermal growth
A:Reference number: A30230; MUID:89261749; PMID:2498647

A:Accession: A30230
A:Molecule type: mRNA
A:Residues: 1-178 <BED>
R:Dozin, B.; Descalzi, F.; Briata, L.; Hayashi, M.; Gentili, C.; Hayashi, K.; Quarto,
J. Biol. Chem. 267, 2979-2985, 1992
A:Title: Expression, regulation, and tissue distribution of the Ch21 protein during c
A:Reference number: A42581; MUID:92147639; PMID:1737754

A:Accession: A42581
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-95, 'L', 97-178 <DOZ>
A:Experimental source: tibia hypertrophic cartilage
A:Note: sequence extracted from NCBI backbone (NCBIN:80796, NCBIP:80797)
R:Cancedda, F.D.; Dozin, B.; Rossi, F.; Molina, F.; Cancedda, R.; Negri, A.; Ronchi,
J. Biol. Chem. 265, 19060-19064, 1990
A:Title: The Ch21 protein, developmentally regulated in chick embryo, belongs to the
A:Reference number: A36595; MUID:91035433; PMID:2229062

A:Accession: A36595
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 21-95, 'L', 97-178 <CAN>
A:Cross-references: GB:M37611
R:Cancedda, F.D.; Asaro, D.; Molina, F.; Cancedda, R.; Caruso, C.; Camardella, L.; Ne
Biochem. Biophys. Res. Commun. 168, 933-938, 1990
A:Title: The amino terminal sequence of the developmentally regulated CH21 protein sh
A:Reference number: A35491; MUID:90267487; PMID:2346493

A:Accession: A35491
A:Status: preliminary
A:Molecule type: protein
A:Residues: 21-48 <CA2>
C:Superfamily: lipocalin; lipocalin homology

F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-178/Product: quiescence-specific protein #status predicted <MAT>
F:25-173/Domain: lipocalin homology <LIP>

Query Match 25.0%; Score 6; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EDELEV 23
|||||
Db 65 EDELEV 70

RESULT 12

T46695

hypothetical protein ORF-180 [imported] - Lactobacillus helveticus plasmid pLH1

C:Species: Lactobacillus helveticus

C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 04-Mar-2000

C:Accession: T46695

R:Thompson, K.; McConville, K.J.; McReynolds, C.; Foley, S.

submitted to the EMBL Data Library, December 1997

A:Description: Complete sequence of plasmid pLH1 from Lactobacillus helveticus ATCC15009

A:Reference number: 223135

A:Accession: T46695

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-180 <THO>

A:Cross-references: EMBL:AJ222725; PIDN:CAA10962.1

A:Experimental source: ATCC 15009

C:Genetics:

A:Genome: plasmid pLH1

C:Superfamily: Lactobacillus helveticus plasmid pLH1 hypothetical protein ORF-180

Query Match 25.0%; Score 6; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
|||||
Db 31 ALAGWL 36

RESULT 13

A91082

hypothetical protein ECS3625 [imported] - Escherichia coli (strain O157:H7, substrain R)

C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C:Accession: A91082

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: A91082

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-189 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA037048.1; PID:q13363096; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: ECS3625

Query Match 25.0%; Score 6; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
|||||
Db 14 ALAGWL 19

RESULT 14

B85927

hypothetical protein 24080 [imported] - Escherichia coli (strain O157:H7, substrain E
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: B85927

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apoda

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B85927

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-189 <STO>

A:Cross-references: GB:AE005174; NID:q12517231; PIDN:AAG57878.1; GSPDB:GN00145; UWGP:

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: 24080

Query Match 25.0%; Score 6; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWL 6
|||||
Db 14 ALAGWL 19

RESULT 15

D69070

imidazoleglycerol-phosphate synthase - Methanobacterium thermoautotrophicum (strain D

C:Species: Methanobacterium thermoautotrophicum

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C:Accession: D69070

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T

; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, I.

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: D69070

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-198 <MTH>

A:Cross-references: GB:AE000912; GB:AE000666; NID:g2622632; PIDN:AAB85999.1; PID:g262

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH1524

A:Start codon: TTG

C:Superfamily: amidotransferase hish; trpG homology

Query Match 25.0%; Score 6; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EGAEDE 20
|||||
Db 130 EGAEDE 135

Search completed: September 11, 2003, 17:57:05

Job time : 11.1123 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:30:37 ; Search time 4.62032 Seconds
(without alignments)
244.278 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 24
Sequence: 1 ALAGWLRPEDGGQAEARDELEVR 24

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	24	100.0	117	GHRL_HUMAN	Q9ubu3 homo sapien
2	10	41.7	116	GHRL_BOVIN	Q9bdj6 bos taurus
3	7	29.2	328	MPR2_STRCO	Q91127 streptomyc
4	7	29.2	344	MPR2_STRLI	P31161 streptomyc
5	7	29.2	1239	V120_EBV	P03189 epstein-bar
6	6	25.0	117	GHRL_CANFA	Q9bef8 canis famil
7	6	25.0	178	EFAB_CHICK	P21760 gallus gall
8	6	25.0	198	HIS5_METHH	O27568 methanobact
9	6	25.0	267	COLI_PIG	P01192 s corticotr
10	6	25.0	284	TPM2_DROME	P09491 drosophila
11	6	25.0	288	PCD1_HUMAN	Q15116 homo sapien
12	6	25.0	289	OPSD_LIMPA	O42431 limnocottus
13	6	25.0	290	PARB_HELPJ	Q92x75 helicobacte
14	6	25.0	310	MTSA_STRP8	Q8p280 streptococc
15	6	25.0	310	MTSA_STRPY	Q9af88 xyliella fas
16	6	25.0	313	MRW_XYLFA	P12045 bacillus su
17	6	25.0	315	YF56_HAEIN	Q09689 schizosacch
18	6	25.0	326	RSBR_BACSU	Q09t16 staphylococ
19	6	25.0	346	MRW_BRUME	Q8y174 bruceella me
20	6	25.0	360	CYS2_MAIZE	Q10717 zea mays (m
21	6	25.0	379	PURK_BACSU	P12045 bacillus su
22	6	25.0	395	IF5_SCHPO	Q09689 schizosacch
23	6	25.0	433	TIG_STAAM	Q09t16 staphylococ
24	6	25.0	436	CUS1_YEAST	Q02554 saccharomyc
25	6	25.0	497	RPSD_MYCGE	P47491 mycoplasma
26	6	25.0	499	RPSD_MYCPN	P78022 mycoplasma
27	6	25.0	511	SYS_MOUSE	P26638 mus musculu
28	6	25.0	513	SYS_BOVIN	Q9gmb8 bos taurus
29	6	25.0	513	SYS_HUMAN	P43591 homo sapien
30	6	25.0	535	AMYB_HORVU	P16098 hordeum vul
31	6	25.0	539	Z173_HUMAN	Q12899 homo sapien
32	6	25.0	547	CH60_BUCTC	Q8k1x3 buchnera ap
33	6	25.0	566	HS60_CANAL	O74261 candida alb

RESULT 1
GHRL_HUMAN
ID GHRL_HUMAN STANDARD; PRT; 117 AA.
AC Q9UBU3: Q8TAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRL OR MTLRP
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach."
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Stomach;
RA Tomasetto C., Karam S.M., Rio M.-C.;
RT "Identification of a novel gastric protein m46."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wajnarajch M.P., Ten I.S., Gertner J.M., Leibell R.L.;
RT "Genomic organization of the human Ghrelin gene."
RL J. Endocrinol. Genet. 1:231-233(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RL MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Dattaletskiy M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

34 6 25.0 572 1 HS60_YEAST P19882 saccharomyc
35 6 25.0 590 1 HS60_AJECA P50142 ajellomyces
36 6 25.0 620 1 SMP_COTJA Q92154 coturnix co
37 6 25.0 641 1 DXS_RHOCA P26242 rhodobacter
38 6 25.0 650 1 APPI_HUMAN P31693 homo sapien
39 6 25.0 657 1 HUTH_MOUSE P33492 mus musculu
40 6 25.0 683 1 HELS_HUMAN Q14978 homo sapien
41 6 25.0 702 1 HELS_AERPE O9yfq8 aeropyrum p
42 6 25.0 728 1 UVRC_STRCO Q95112 streptomyc
43 6 25.0 886 1 SM6B_MOUSE O54951 mus musculu
44 6 25.0 887 1 SM6B_RAT O70141 rattus norv
45 6 25.0 890 1 ACOL_ECOLI P22516 escherichia

ALIGNMENTS

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 24-33.
 RX TISSUE=Stomach;
 RC MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [7]
 RP REVIEW
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=O9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=dal-Gln14-ghrelin;
 CC IsoId=O9UBU3-2; Sequence=VSP_003245;
 CC -1- PTM: O-n-octanoylation is essential for activity.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobogen.fr/services/chromancer/Genes/GhrelinID327.html".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB029434; BAA89371.1; -;
 CC EMBL; AB035700; BAB19045.1; -;
 CC EMBL; AJ252278; CAB65733.1; -;
 CC EMBL; AF296558; AAG10300.1; -;
 CC EMBL; BC025791; AAH25791.1; -;
 CC PIR; A59316; A59316.
 CC MIM; 605353; -;
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0005331; P:cell growth hormone receptor ligand activity; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0007186; P:G-protein coupled receptor protein signaling. . . ; TAS.
 CC InterPro; IPR006737; motilin_assoc.
 CC InterPro; IPR006738; motilin_ghrelin.
 CC InterPro; IPR005441; Preproghrelin.
 CC Pfam; PF04643; motilin_assoc.1.
 CC Pfam; PF04644; motilin_ghrelin.1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD332162; Preproghrelin.1.
 CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing
 KW SIGNAL 1 23
 FT PEPTIDE 24 51 GHRELIN.
 FT PROPEP 52 117 REMOVED IN MATURE FORM.
 FT LIPID 26 26 N-OCTANOATE.
 FT VARSPIC 37 37 Missing (in isoform 2).
 FT CONFLICT 72 72 L -> M (IN REF. 5).
 FT

SQ SEQUENCE 117 AA; 12911 MW; 39C0572EBECAA2755 CRC64;
 Query Match 100.0%; Score 24; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 6e-18;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 DB 52 ALAGWLRPEDGGQAGAEDELEVR 75
 RESULT 2
 GHRL_BOVIN STANDARD; PRT; 116 AA.
 ID GHRL_BOVIN STANDARD; PRT; 116 AA.
 AC Q9BDJ6; O9GKY6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ghrelin precursor (growth hormone secretagogue) (growth hormone
 DE releasing peptide).
 GN GHRL.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kita K., Harada K., Yokota H.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 24-99 FROM N.A.
 RA Kojima M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF350329; AAK18612.1; -;
 CC EMBL; AB035702; BAB19047.1; -;
 CC InterPro; IPR006737; motilin_assoc.
 CC InterPro; IPR006738; motilin_ghrelin.
 CC InterPro; IPR005441; Preproghrelin.
 CC Pfam; PF04643; motilin_assoc.1.
 CC Pfam; PF04644; motilin_ghrelin.1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD332162; Preproghrelin.1.
 CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
 KW Alternative splicing
 KW SIGNAL 1 23 BY SIMILARITY.
 FT PEPTIDE 24 50 GHRELIN (BY SIMILARITY).
 FT PROPEP 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).
 FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
 FT CONFLICT 34 34 K -> E (IN REF. 2).
 SQ SEQUENCE 116 AA; 12792 MW; F55536DAC5FA59B6 CRC64;
 Query Match 41.7%; Score 10; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. NO. 0.0014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 QAQGADELE 22

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Db      63 QAEGAEDELE 72
|||||||
RESULT 3
MPR2_STRCO
ID      MPR2_STRCO      STANDARD;      PRT;      328 AA.
AC      Q9L127;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Small neutral protease regulatory protein.
GN      MPRR OR MPRR2 OR SCO7433 OR SC6011.29.
OS      Streptomyces coelicolor.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Streptomyces; Streptomycetaceae; Streptomyces.
OX      NCBI_TaxID=1902;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=A3(2) / M145;
RX      MEDLINE=21396410; PubMed=12000953;
RA      Bentley S.D., Chater K.F., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA      Thomson N.R., Bateson A., Brown S., Chandra G., Chen C.W., Collins M.,
RA      Cronin A., Fraser A., Godle A., Hidaigo J., Hornsby T., Howarth S.,
RA      Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA      Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA      Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA      Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA      Hopwood D.A.;
RT      "Complete genome sequence of the model actinomycete Streptomyces
RT      coelicolor A3(2).";
RL      Nature 417:141-147(2002).
CC      -!- FUNCTION: TRANSCRIPTIONAL TRANS-ACTIVATOR OF THE GENE (MPRA) FOR
CC      THE SMALL NEUTRAL PROTEASE.
CC      -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC      REGULATORS.
CC      -----
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CC      -----
CC      EMBL; AL939131; CAB76352.1; -
CC      InterPro; IPR000847; HTH_LysR.
CC      Pfam; PF00126; HTH_1; 1.
CC      PRINTS; PR00039; HTHLYSR.
CC      PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
CC      DNA-binding; Protease; Transcription regulation; Complete proteome.
CC      DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
CC      FT SEQUENCE 328 AA; 35885 MW; 2BA97730AB4FA16B CRC64;
CC      -----
Query Match 29.2%; Score 7; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLR 7
Db 104 ALAGWLR 110
|||||
RESULT 4
MPR2_STRLI
ID      MPR2_STRLI      STANDARD;      PRT;      344 AA.
AC      P43161;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Small neutral protease regulatory protein.
GN      MPRR OR MPRR2 OR SCO7433 OR SC6011.29.
OS      Streptomyces coelicolor.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Streptomyces; Streptomycetaceae; Streptomyces.
OX      NCBI_TaxID=1902;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=A3(2) / M145;
RX      MEDLINE=21396410; PubMed=12000953;
RA      Bentley S.D., Chater K.F., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA      Thomson N.R., Bateson A., Brown S., Chandra G., Chen C.W., Collins M.,
RA      Cronin A., Fraser A., Godle A., Hidaigo J., Hornsby T., Howarth S.,
RA      Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA      Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA      Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA      Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA      Hopwood D.A.;
RT      "Complete genome sequence of the model actinomycete Streptomyces
RT      coelicolor A3(2).";
RL      Nature 417:141-147(2002).
CC      -!- FUNCTION: TRANSCRIPTIONAL TRANS-ACTIVATOR OF THE GENE (MPRA) FOR
CC      THE SMALL NEUTRAL PROTEASE.
CC      -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC      REGULATORS.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; M81703; AAA26739.1; -
CC      InterPro; IPR000847; HTH_LysR.
CC      Pfam; PF00126; HTH_1; 1.
CC      PRINTS; PR00039; HTHLYSR.
CC      PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
CC      DNA-binding; Protease; Transcription regulation; Complete proteome.
CC      DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
CC      FT SEQUENCE 344 AA; 37415 MW; 485C82C813B52312 CRC64;
CC      -----
Query Match 29.2%; Score 7; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLR 7
Db 104 ALAGWLR 110
|||||
RESULT 5
V120_EBV
ID      V120_EBV      STANDARD;      PRT;      1239 AA.
AC      P03189;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      01-OCT-1996 (Rel. 34, Last annotation update)
DE      Capsid assembly protein BOLF1.
GN      BOLF1.
OS      Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
OC      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC      Gammaherpesvirinae; Lymphocryptovirus.
OX      NCBI_TaxID=10377;
RN      [1]
RP      SEQUENCE FROM N.A.

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RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tufnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
CC EH-V 1 23, EBV BOLE1, VZV 21, HVS-1 63, AND HCMV UL47.
CC -----
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CC -----
DR EMBL; V01555; CAA24841.1; -
DR PIR; A43041; QQBE10.
KW Capsid assembly.
SQ SEQUENCE 1239 AA; 132748 MW; 6C5DBFC55F2FF729 CRC64;

Query Match 29.28; Score 7; DB 1; Length 1239;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AEGAED 20
Db 696 AEGAED 702
|||||

RESULT 6
GHRL_CANFA STANDARD; PRT; 117 AA.
AC Q9BEF8: Q9BEF7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide).
GN GHRL OR MTLRP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Gastric fundus;
RA Tomasetto C., Wendling C., Rio M.-C., Poltras P.;
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
RT fundus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9BEF8-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9BEF8-2; Sequence=VSP_003244;
CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
DR EMBL; AJ298295; CAC29155.1; -
DR EMBL; AJ298296; CAC29156.1; -
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin-ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin-ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPLOC 37 37 Missing (in isoform 2).
FT FTID=VSP_003244.
SQ SEQUENCE 117 AA; 13007 MW; 3E57ED9D1847CF7 CRC64;

Query Match 25.08; Score 6; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 AEDELE 22
Db 68 AEDELE 73
|||||

RESULT 7
EFAB_CHICK STANDARD; PRT; 178 AA.
AC P21760: P21928; Q9PWN9;
DT 01-MAY-1991 (Rel. 18, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Extracellular fatty acid binding protein precursor (Ex-FABP)
DE (Quiescence-specific protein) (p20K) (Ch21 protein).
GN EXFABP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89261749; PubMed=2498647;
RA Bedard P.-A., Yannoni Y., Simmons D.L., Erikson R.L.;
RT "Rapid repression of quiescence-specific gene expression by epidermal
RT growth factor, insulin, and pp60v-src.";
RL Mol. Cell. Biol. 9:1371-1375(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92147639; PubMed=1737754;
RA Dozin B., Descalzi F., Briata L., Hayashi M., Gentili C.,
RA Hayashi K., Quarto R., Cancedda R.;
RT "Expression, regulation, and tissue distribution of the Ch21 protein
RT during chicken embryogenesis.";
RL J. Biol. Chem. 267:2979-2985(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Leghorn;
RA Giannoni P., Dozin B., Zambotti A., Neri M., Cancedda R.;
RT "Differentiation-dependent activation of the extracellular fatty acid
RT binding protein (EXFABP) gene in chicken embryo chondrocytes.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 25-178 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91035433; PubMed=2225062;
RA Cancedda F.D., Dozin B., Rossi F., Molina F., Cancedda R.,
RA Negri A., Ronchi S.;
RT "The Ch21 protein, developmentally regulated in chick embryo, belongs

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to the superfamily of lipophilic molecule carrier proteins.";
 J. Biol. Chem. 265:19060-19064(1990).
 [5]
 SEQUENCE OF 21-48.
 MEDLINE-90267487; PubMed-2346493;
 Cancedda F.D., Asaro D., Molina F., Cancedda R., Caruso C.,
 Camardella L., Negri A., Ronchi S.;
 "The amino terminal sequence of the developmentally regulated Ch21
 protein shows homology with amino terminal sequences of low molecular
 weight proteins binding hydrophobic molecules";
 Biochem. Biophys. Res. Commun. 168:933-938(1990).
 [6]
 SEQUENCE OF 103-178 FROM N.A.
 STRAIN-White leghorn; TISSUE-Bone marrow;
 MEDLINE-92195690; PubMed-1549365;
 Nakano T., Graf T.;
 "Identification of genes differentially expressed in two types of
 v-myd-transformed avian myelomonocytic cells";
 Oncogene 7:527-534(1992).
 [7]
 CHARACTERIZATION.
 MEDLINE-96355330; PubMed-8702740;
 Cancedda F.D., Malpeli M., Gentili C., Di Marzo V., Bet P.,
 Carlevaro M., Cermelli S., Cancedda R.;
 "The developmentally regulated avian Ch21 lipocalin is an
 extracellular fatty acid-binding protein.";
 J. Biol. Chem. 271:20163-20169(1996).
 [8]
 CHARACTERIZATION.
 MEDLINE-20513977; PubMed-11058755;
 Descalzi Cancedda F., Dozin B., Zeraga B., Cermelli S., Cancedda R.;
 "Ex-FABP: a fatty acid binding lipocalin developmentally regulated in
 chicken endochondral bone formation and myogenesis.";
 Biochim. Biophys. Acta 1482:127-135(2000).
 CC -1- FUNCTION: Preferentially binds long-chain unsaturated fatty acids
 such as linoleic acid, oleic acid, arachidonic acid. Also binds
 with a lower affinity long chain saturated fatty acids such as
 stearic acid. May act as survival protein by playing a role in
 maintaining cell viability.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY SYNTHESIZED IN NONPROLIFERATING
 CELLS.
 CC -1- PTM: Does not seem to be glycosylated.
 CC -1- MISCELLANEOUS: Developmentally regulated in chick embryo.
 CC -1- SIMILARITY: Belongs to the lipocalin family.

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 CC EMBL: M25784; AAA53371.1; -;
 CC EMBL: M55644; AAA48677.1; -;
 CC EMBL: AF121346; RAD23569.1; -;
 CC EMBL: X61199; -; NOT_ANNOTATED_CDS.
 CC PIR: A30230; A30230.
 CC InterPro: IPR002345; Lipocalin.
 CC InterPro: IPR000566; Lipocaln_cytFABP.
 CC Pfam: PF00061; Lipocalin; 1.
 CC PRINTS: PR00179; LIPOCALIN.
 CC PROSITE: PS00123; LIPOCALIN; 1.
 CC Lipocalin; Transport; Signal.
 KW SIGNAL 1 20
 FT CHAIN 21 178 EXTRACELLULAR FATTY ACID BINDING PROTEIN.
 FT MOD_RES 21 21 BLOCKED.
 FT DISULFID 80 173 BY SIMILARITY.
 FT CONFLICT 4 4 L -> S (IN REF. 2).
 FT CONFLICT 27 27 R -> S (IN REF. 2 AND 4).
 FT CONFLICT 45 45 F -> S (IN REF. 2 AND 4).

FT CONFLICT 62 62 F -> S (IN REF. 1).
 FT CONFLICT 96 96 L -> V (IN REF. 1).
 SQ SEQUENCE 178 AA; 20201 MW; 0DDBDC33C1A0C6B8 CRC64;
 Query Match 25.0%; Score 6; DB 1; Length 178;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 EDELEV 23
 Db 65 EDELEV 70
 RESULT 8
 HIS5_METTH STANDARD; PRT; 198 AA.
 ID AC 027568;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Imidazole glycerol phosphate synthase subunit hish (EC 2.4.2.-) (IGP
 synthase glutamine amidotransferase subunit) (IGP synthase subunit
 hish) (ImGP synthase subunit hish) (IGP subunit hish).
 GN HISH OR MTH1524.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OC NCBI_Taxid=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-Delta H;
 RX MEDLINE-98037514; PubMed-9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M.,
 Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 "Complete genome sequence of Methanobacterium thermoautotrophicum
 deltaH: functional analysis and comparative genomics.";
 J. Bacteriol. 179:7135-7155(1997).
 CC -1- FUNCTION: IGPs catalyzes the conversion of PRFAR and glutamine to
 IGP, AICAR and glutamate. The hish subunit provides the glutamine
 amidotransferase activity that produces the ammonia necessary to
 hifp for the synthesis of IGP and AICAR (By similarity).
 CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulo-1-
 ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
 carboxamide + L-glutamine -> imidazole-glycerol phosphate + 5-
 aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
 CC -1- PATHWAY: Histidine biosynthesis; fifth step.
 CC -1- SUBUNIT: Heterodimer of hish and hifp (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.

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 or send an email to license@isb-sib.ch).

 CC EMBL: A5000912; AAB85999.1; -;
 CC PIR: D69070; D69070.
 CC HAMAP: MF_00278; -; 1.
 CC InterPro: IPR000991; GATase_1.
 CC Pfam: PF00117; GATase; 1.
 CC PROSITE: PS00442; GATASE_TYPE_I; 1.
 CC Histidine biosynthesis; Transferase; Glutamine amidotransferase;
 KW Complete proteome.
 FT ACT_SITE 77 77
 FT ACT_SITE 177 177 BY SIMILARITY.
 FT CONFLICT 177 177 BY SIMILARITY.

FT ACT_SITE 179 179 BY SIMILARITY.
 SQ SEQUENCE 198 AA; 21348 MW; E8EFA43EC9163AEF CRC64;

Query Match 25.0%; Score 6; DB 1; Length 198;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 EGADE 20
 |||||
 Db 130 EGADE 135

RESULT 9
 COLI_PIG STANDARD; PRT; 267 AA.

AC P01192; O95246;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Corticotropin-lipotropin precursor (Pro-opiomelanocortin) (POMC)
 DE (Contains: NPP; Melanotropin gamma (Gamma-MSH); Corticotropin
 DE (Adrenocorticotrophic hormone) (ACTH); Melanotropin alpha (Alpha-MSH);
 DE Corticotropin-like intermediary peptide (CLIP); Lipotropin beta (Beta-
 DE LPH); Lipotropin gamma (Gamma-LPH); Melanotropin beta (Beta-MSH);
 DE Beta-endorphin; Met-enkephalin].
 GN POMC.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;

[1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86131687; PubMed=3753882;
 RA Gossard F.J., Chang A.C.Y., Cohen S.N.;
 RT "Sequence of the cDNA encoding porcine pro-opiomelanocortin.";
 RL Biochim. Biophys. Acta 866:68-74 (1986).
 RN [2]

[2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84069823; PubMed=6196724;
 RA Boileau G., Barbeau C., Jeannotte L., Chretien M., Drouin J.;
 RT "Complete structure of the porcine pro-opiomelanocortin mRNA derived
 from the nucleotide sequence of cloned cDNA.";
 RL Nucleic Acids Res. 11:8063-8071 (1983).
 RN [3]

[3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95046835; PubMed=7958386;
 RA Gen K., Hirai T., Kato T., Kato Y.;
 RT "Presence of the same transcript of pro-opiomelanocortin (POMC) genes
 in the porcine anterior and intermediate pituitary lobes.";
 RL Mol. Cell. Endocrinol. 103:101-108 (1994).
 RN [4]

[4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84239667; PubMed=6547437;
 RA Oakes E., Herbert E.;
 RT "5' sequence of porcine and rat pro-opiomelanocortin mRNA. One porcine
 and two rat forms.";
 RL J. Biol. Chem. 259:7421-7425 (1984).
 RN [5]

[5]
 RP SEQUENCE OF 136-174.
 RA Shepherd R.G., Willson S.D., Howard K.S., Bell P.H., Davies D.S.,
 RA Davis S.B., Eigner E.A., Shakespeare N.E.;
 RT "Studies with corticotropin. III. Determination of the structure of
 beta-corticotropin and its active degradation products.";
 RL J. Am. Chem. Soc. 78:5067-5076 (1956).
 RN [6]

[6]
 RP REVISIONS TO 160 AND 165.
 RX MEDLINE=72114902; PubMed=4334191;
 RA Riniker B., Sieber P., Rittel W., Zuber H.;
 RT "Revised amino-acid sequences for porcine and human
 adrenocorticotrophic hormone.";
 RL Nature New Biol. 235:114-115 (1972).
 RN [7]

[7]
 RP REVISIONS (CORTICOTROPIN).

RX MEDLINE=74306590; PubMed=4369114;
 RA Graf L.;
 RT "Re-examination of the sequence of the C-terminal tryptic fragment
 from porcine adrenocorticotrophic hormone.";
 RL Acta Biochim. Biophys. Acad. Sci. Hung. 7:293-297 (1972).
 RN [8]

[8]
 RP SEQUENCE OF 136-174.
 RX MEDLINE=91071194; PubMed=2174774;
 RA Voigt K., Stegmaier W., McGregor G.P., Roesch H., Selliger H.;
 RT "Isolation and full structural characterisation of six
 adrenocorticotropin-like peptides from porcine pituitary gland.
 RT Identification of three novel fragments of adrenocorticotropin and of
 two forms of a novel adrenocorticotropin-like peptide.";
 RL Eur. J. Biochem. 194:225-236 (1990).
 RN [9]

[9]
 RP SEQUENCE OF 136-148.
 RA Harris J.I., Lerner A.B.;
 RT "Amino-acid sequence of the alpha-melanocyte-stimulating hormone.";
 RL Nature 179:1346-1347 (1957).
 RN [10]

[10]
 RP SEQUENCE OF 177-267.
 RX MEDLINE=71111231; PubMed=5543613;
 RA Graf L., Barat E., Cseh G., Sejgo M.;
 RT "Amino acid sequence of porcine beta-lipotrophic hormone.";
 RL Biochim. Biophys. Acta 229:276-278 (1971).
 RN [11]

[11]
 RP REVISIONS (LIPOTROPIN).
 RA Gilardeau C., Chretien M.;
 RT "Complete amino acid sequence of porcine beta-lipotrophic hormone
 (beta-LPH)."
 RL (In) Meienhofer J. (eds.);
 RL Chemistry and biology of peptides, pp.609-611, Ann Arbor Sci. Pub.,
 RL Ann Arbor (1972).
 RN [12]

[12]
 RP REVISION TO 211.
 RX MEDLINE=73048217; PubMed=4673865;
 RA Pankov Y.A., Yudaev N.A.;
 RT "Complete amino acid sequence in the molecule of porcine beta-
 lipotropin.";
 RL Biokhimiia 37:991-1004 (1972).
 RN [13]

[13]
 RP SEQUENCE OF 217-234.
 RA Harris J.I., Roos P.;
 RT "Amino-acid sequence of a melanophore-stimulating peptide.";
 RL Nature 178:90-90 (1956).
 RN [14]

[14]
 RP SEQUENCE OF 217-234.
 RA Geschwind I.I., Li C.H., Barnafi L.;
 RT "The structure of the beta-melanocyte-stimulating hormone.";
 RL J. Am. Chem. Soc. 79:620-625 (1957).
 RN [15]

[15]
 RP SEQUENCE OF 237-241.
 RX MEDLINE=76100762; PubMed=1207728;
 RA Hughes J., Smith T.W., Kosterlitz H.W., Fothergill L.A., Morgan B.A.,
 RA Morris H.R.;
 RT "Identification of two related pentapeptides from the brain with
 potent opiate agonist activity.";
 RL Nature 258:577-579 (1975).
 RN [16]

[16]
 RP SEQUENCE OF 237-267.
 RX MEDLINE=77084500; PubMed=1007884;
 RA Graf L., Barat E., Patthy A.;
 RT "Isolation of a COOH-terminal beta-lipotropin fragment (residues
 61-91) with morphine-like analgesic activity from porcine pituitary
 glands.";
 RL Acta Biochim. Biophys. Acad. Sci. Hung. 11:121-122 (1976).
 RN [17]

[17]
 CC -1- FUNCTION: ACTH STIMULATES THE ADRENAL GLANDS TO RELEASE CORTISOL.
 CC -1- FUNCTION: MSH (MELANOCYTE-STIMULATING HORMONE) INCREASES THE
 CC PIGMENTATION OF SKIN BY INCREASING MELANIN PRODUCTION IN
 CC MELANOCYTES.
 CC -1- FUNCTION: BETA-ENDORPHIN AND MET-ENKEPHALIN ARE ENDOGENOUS
 CC OPIATES.
 CC -1- TISSUE SPECIFICITY: ACTH AND MSH ARE PRODUCED BY THE PITUITARY

CC GLAND.
CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
CC THE DIFFERENT ACTIVE PEPTIDES
CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X03561; CAA27248.1; -
CC EMBL: X00135; CAA24968.1; -
CC EMBL: S73519; AAB32312.1; -
CC EMBL: K01879; AAB31104.1; -
CC FIC: A93496; CTPGP.
CC InterPro: IPR001941; Mcoctin_ACTH.
CC Pfam: PF00976; ACTH_domain; 1.
CC PRINTS: PR00383; MELANOCORTIN.
CC Endorphin; Hormone; Cleavage on pair of basic residues; Amidation;
CC Glycoprotein; Signal.
CC SIGNAL 1 26
CC PEPTIDE 27 106
CC PEPTIDE 77 87
CC PEPTIDE 136 174
CC PEPTIDE 136 148
CC PEPTIDE 134 174
CC PEPTIDE 177 267
CC PEPTIDE 177 234
CC PEPTIDE 217 234
CC PEPTIDE 237 267
CC PEPTIDE 237 241
CC PEPTIDE 237 241
CC MOD_RES 87 87
CC MOD_RES 148 148
CC CARBOHYD 91 91
CC VARIANT 143 143
CC CONFLICT 6 6
CC CONFLICT 15 15
CC CONFLICT 23 23
CC CONFLICT 49 49
CC SEQUENCE 267 AA; 28894 MW; A6DB487A5032B648 CRC64;

CC Query Match 25.0%; Score 6; DB 1; Length 267;
CC Best Local Similarity 100.0%; Pred. No. 38;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 16 GAEDEL 21
CC Db 161 GAEDEL 166

CC RESULT 10
CC TPMD2_DROME STANDARD; PRT; 284 AA.
CC AC P09491; P09490; Q24408; Q24427; Q24428; Q8S265; Q9VF95;
CC DT 01-WAR-1989 (Rel. 10, Created)
CC DT 01-WAR-1989 (Rel. 10, Last sequence update)
CC DE 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Tropomyosin 2 (Tropomyosin I).
CC TM2 OR TMI OR CG4843.
CC OS Drosophila melanogaster (Fruit fly).
CC OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC OC Ephydroidea; Drosophilidae; Drosophila.
CC ON NCBI_TaxID=7227;
CC RN [1]
CC RP SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
CC RC TISSUE=Embryo. Larva, and Pupae;
CC RX MEDLINE=84205681; PubMed=6202423;
CC RA Karlik C.C., Mahaffey J.W., Coutu M.D., Fyrberg E.A.;
CC "Organization of contractile protein genes within the 88F subdivision
RT

RT of the D. melanogaster third chromosome.";
RL Cell 37:469-481(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
RX MEDLINE=86085920; PubMed=3079761;
RA Basi G.S., Storti R.V.;
RT "Structure and DNA sequence of the tropomyosin I gene from Drosophila
RT melanogaster";
RL J. Biol. Chem. 261:817-827(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S.Q.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [4]
RP REVISIONS.
RC STRAIN=Berkley;
RX MEDLINE=22426069; PubMed=12537572;
RA Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM EMBRYONIC).
RC STRAIN=Berkley; TISSUE=Embryo;
RX PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource";

Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
[6]
SEQUENCE OF 258-284 FROM N.A. (ISOFORM EMBRYONIC).
MEDLINE=85215579; PubMed=4000944;
Boardman M., Basi G.S., Storti R.V.;
"Multiple polyadenylation sites in a Drosophila tropomyosin gene are
used to generate functional mRNAs";
Nucleic Acids Res. 13:1763-1776(1985).
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Thoracic; Synonyms=127, t;
IsoId=P09491-1; Sequence=Displayed;
Name=Embryonic; Synonyms=129, A, B, e;
IsoId=P09491-2; Sequence=VSP_006616;
-1- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE
EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
-1- SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY.
-1- CAUTION: Ref.6 sequence differs from that shown due to erroneous
gene model prediction.

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EMBL; K02622; AAA28970.1; -;
EMBL; K02623; AAA28971.1; -;
EMBL; K02622; AAA28971.1; JOINED.
EMBL; K02627; AAA28973.1; -;
EMBL; K03277; AAA28974.1; -;
EMBL; AE003708; AAN13652.1; -;
EMBL; AY071087; AAL48709.1; -;
EMBL; X02220; CAA26142.1; ALT_SEQ.
PIR; A25624; A25624.
PIR; B25624; B25624.
FlyBase; FBgn0004117; Tm2.
InterPro; IPR000533; Tropomyosin.
Pfam; PF00261; Tropomyosin; 1.
PRINTS; PR00194; TROPOMYOSIN.
PROSITE; PS00326; TROPOMYOSIN; 1.
Muscle protein; Coiled coil; Repeat; Alternative splicing;
Multigene family.
VARSPPLIC 259 284 RLNEKEKYKAICDDLDTFAELTGY -> ELGINKORYKS
LADMDSTFAELAGY (in isoform Embryonic).
/FTid=VSP_006616.
M -> V (IN REF. 1).
Q -> L (IN REF. 1).
I -> T (IN REF. 1).
R -> D (IN REF. 1).
SEQUENCE 284 AA; 32981 MW; 07AD03FDD304EA5F CRC64;
Query Match 25.0%; Score 6; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 EDELEV 23
|||||
Db 173 EDELEV 178
RESULT 11
PCD1_HUMAN STANDARD; PRT; 288 AA.
AC Q15116; Q00517;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Programmed cell death protein 1 precursor (Protein PD-1) (hpd-1).
GN PDCD1 OR PDL.
OS Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
NCBI_TaxID=9606;
SEQUENCE FROM N.A.
MEDLINE=95154844; PubMed=7851902;
Shinohara T., Tanikawa M., Ishida Y., Kawaich M., Honjo T.;
"Structure and chromosomal localization of the human PD-1 gene
(PDCD1).";
Genomics 23:704-706(1994).
[2]
SEQUENCE FROM N.A.
MEDLINE=97473511; PubMed=9332365;
Finger L.R., Pu J., Wasserman R., Vibhakhar R., Louie E., Hardy R.R.,
Burrows P.D., Billips L.D.;
"The human PD-1 gene: complete cDNA, genomic organization, and
developmentally regulated expression in B cell progenitors.";
Gene 197:177-187(1997).
[3]
ERRATUM.
Finger L.R., Pu J., Wasserman R., Vibhakhar R., Louie E., Hardy R.R.,
Burrows P.D., Billips L.D.;
Gene 203:253-253(1997).
-1- FUNCTION: POSSIBLE CELL DEATH INDUCER, IN ASSOCIATION WITH
OTHER FACTORS.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- DEVELOPMENTAL STAGE: INDUCED AT PROGRAMMED CELL DEATH.
-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

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EMBL; L27440; AAC41700.1; -;
EMBL; U64863; AAC51773.1; -;
PIR; A55737; A55737.
HSP; P01607; IREI.
Genew; HGNC:8760; PDCD1.
MIM; 600244; -;
GO; GO:0004871; F:signal transducer activity; TAS.
GO; GO:0006915; P:apoptosis; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0006959; P:humoral immune response; TAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IgV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; Apoptosis.
SIGNAL 1 20
CHAIN 21 288
PROGRAMMED CELL DEATH PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
F -> S (IN REF. 1).
P -> S (IN REF. 1).
SEQUENCE 288 AA; 31707 MW; A5210AD50C3046C7 CRC64;
Query Match 25.0%; Score 6; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      6 LRPEDG 11
Db      277 LRPEDG 282

RESULT 12
OPSD_LIMPA
ID OPSD_LIMPA STANDARD; PRT; 289 AA.
AC 042431.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Rhodopsin (Fragment).
GN RHO.
OS Limnocottus pallidus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Scorpaeniformes;
OC Cottidae; Abyssocottidae; Limnocottus.
OX NCBI_TaxID=61634;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98086781; PubMed=9417898;
RA Hunt D.M., Fitzgibbon J., Slobodyanyuk S.J., Bowmaker J.K.,
RA Dulai K.S.;
RT "Molecular evolution of the cottoid fish endemic to Lake Baikal
RT deduced from nuclear DNA evidence.";
RL Mol. Phylogenet. Evol. 8:415-422(1997).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES
CC VISION IN DIM LIGHT.
CC -!- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
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CC -----
DR EMBL; U97271; AAB61725.1; -.
DR HSSP; P02699; 1BOJ.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001760; Opsin.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECF_1_1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN_RECF_1_2; 1.
DR PROSITE; PS00238; OPSIN; 1.
KW Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
FT NON_TER 1
FT DOMAIN <1 7 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 8 32 1 (POTENTIAL).
FT DOMAIN 33 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 69 2 (POTENTIAL).
FT DOMAIN 70 84 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 85 104 3 (POTENTIAL).
FT DOMAIN 105 123 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 124 147 4 (POTENTIAL).
FT DOMAIN 148 173 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 174 201 5 (POTENTIAL).
FT DOMAIN 202 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 247 6 (POTENTIAL).
FT DOMAIN 248 255 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 256 280 7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
RETINAL CHROMOPHORE (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
>289
281
81 158
267 267
171 171
289 289
160D08E17E5E1280 CRC64;
25.0%; Score 6; DB 1; Length 289;
100.0%; Pred. No. 41;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 LAGWLR 7
111111
143 LAGWLR 148

RESULT 13
PARB_HELPJ
ID PARB_HELPJ STANDARD; PRT; 290 AA.
AC Q92K75;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable chromosome partitioning protein parB.
GN PARB OR JHP1066.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: INVOLVED IN CHROMOSOME PARTITION. LOCALIZE TO BOTH POLES
CC OF THE PREDIVISIONAL CELL FOLLOWING COMPLETION OF DNA REPLICATION.
CC BINDS TO THE DNA ORIGIN OF REPLICATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARB FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001534; AAD06646.1; -.
DR FIC; H71852; H71852.
DR InterPro; IPR004437; ParB_part.
DR InterPro; IPR003115; ParBC.
DR Pfam; PF02195; ParBC; 1.
DR SMART; SM00470; ParB; 1.
DR TIGRFAMs; TIGR00180; parB_part; 1.
DR Chromosome partitioning; DNA-binding; Complete proteome.
KW Chromosome partitioning; DNA-binding; Complete proteome.
SQ SEQUENCE 290 AA; 33405 MW; 6709BA0547A55A4F CRC64;
25.0%; Score 6; DB 1; Length 290;
100.0%; Pred. No. 41;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
17 AEDELE 22
111111
245 AEDELE 250

RESULT 14

```

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MTSA_STRP8
ID Q8P280; STANDARD; PRT; 310 AA.
AC
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metal ABC transporter substrate-binding lipoprotein precursor.
GN MTSA OR SPY18_0494.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OC NCBI_TaxID=186103;
RN
RP
RC
RX STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RA "Genome sequence and comparative microarray analysis of serotype M18
RA group A Streptococcus strains associated with acute rheumatic fever
RA outbreaks.";
RC Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC
CC -1- FUNCTION: Part of an ATP-driven transport system for a metal; this
CC protein has affinity for Zn(II), Fe(III) and Cu(II).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC -1- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC 9. Lipoprotein receptor antigen (Lrai) subfamily.
CC
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CC -----
DR EMBL; AE009988; AAL97215.1; -
DR InterPro; IPR006128; Lipoprotein_4.
DR Pfam; PF01297; SBP_bac_9.1;
DR PRINTS; PR00690; ADHESNFAMILY.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Transport; zinc transport; Iron transport; Copper; Membrane;
KW Lipoprotein; Signal; Complete proteome.
FT SIGNAL 1 20 PROBABLE.
FT CHAIN 21 310 METAL ABC TRANSPORTER SUBSTRATE-
FT LIPID 21 21 BINDING LIPOPROTEIN.
FT N-ACYL DIGLYCERIDE (PROBABLE).
SQ SEQUENCE 310 AA; 34330 MW; 40F613659AAD1768 CRC64;
Query Match 25.0%; Score 6; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 EDGQQA 14
DQ 94 EDGQQA 99
|||||
DQ 94 EDGQQA 99

RESULT 15
MTSA_STRPY
ID Q9A157; Q9RNJ0; STANDARD; PRT; 310 AA.
AC
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Metal ABC transporter substrate-binding lipoprotein precursor.
GN MTSA OR SPY0453 OR SPY3_0318 OR SP51539.
OS Streptococcus pyogenes, and
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

```

```

Streptococcus.
NCBI_TaxID=1314, 198466;
[1]
SEQUENCE FROM N.A., SEQUENCE OF 30-39, AND CHARACTERIZATION.
STRAIN-SF370 / ATCC 700294 / Serotype M1, and API / Serotype M1;
MEDLINE=20032372; PubMed=10564500;
RA Janulczyk R., Pallon J., Bjoerck L.;
RA "Identification and characterization of a Streptococcus pyogenes ABC
RA transporter with multiple specificity for metal cations.";
RL Mol. Microbiol. 34:596-606(1999).
[2]
SEQUENCE FROM N.A.
STRAIN-SF370 / ATCC 700294 / Serotype M1;
MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
[3]
SEQUENCE FROM N.A.
STRAIN-MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RA "Genome sequence of a serotype M3 strain of group A Streptococcus:
RA phage-encoded toxins, the high-virulence phenotype, and clone
RA emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
[4]
SEQUENCE FROM N.A.
STRAIN-SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RA "The genome of invasive Streptococcus pyogenes; a comparative analysis
RA of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: Part of an ATP-driven transport system for a metal; this
CC protein has affinity for Zn(II), Fe(III) and Cu(II).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC -1- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC 9. Lipoprotein receptor antigen (Lrai) subfamily.
CC
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CC -----
DR EMBL; AF180520; AAD56936.1; -
DR EMBL; AF180521; AAD56939.1; -
DR EMBL; AE006505; AAK33468.1; -
DR EMBL; AE014143; AAM78925.1; ALT_INIT.
DR EMBL; AP005145; BAC64634.1; ALT_INIT.
DR HSPSP; P96116; ITOA.
DR InterPro; IPR006128; Lipoprotein_4.
DR InterPro; IPR006127; SBP_bac_9.
DR Pfam; PF01297; SBP_bac_9.1;
DR PRINTS; PR00690; ADHESNFAMILY.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Transport; zinc transport; Iron transport; Copper; Membrane;
KW Lipoprotein; Signal; Complete proteome.
FT SIGNAL 1 20 PROBABLE.
FT CHAIN 21 310 METAL ABC TRANSPORTER SUBSTRATE-
FT LIPID 21 21 BINDING LIPOPROTEIN.
FT N-ACYL DIGLYCERIDE (PROBABLE).
FT VARIANT 21 77 V -> A (IN STRAIN AFL).

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FT CONFLICT 26 26 T -> A (IN REF. 1).
FT CONFLICT 30 30 K -> E (IN REF. 1).
FT CONFLICT 44 44 A -> G (IN REF. 1).
FT CONFLICT 49 50 AI -> VM (IN REF. 1).
SQ SEQUENCE 310 AA; 34358 MW; B0F829EF1C72CADC CRC64;

Query Match 25.0%; Score 6; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 EDGGA 14
Db 94 EDGGA 99

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Search completed: September 11, 2003, 17:52:40
 Job time : 6.62032 secs

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:46:02 ; Search time 22.9733 Seconds
(without alignments)
269.586 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 24
Sequence: 1 ALAGWLRPDGGQAEAGAELEVR 24

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	83.3	117	4	Q8TAT9
2	11	45.8	117	11	Q8CH53
3	8	33.3	433	10	Q93ZV7
4	8	33.3	433	10	Q8L7B4
5	8	33.3	483	10	Q65529
6	7	29.2	103	16	Q9L063
7	7	29.2	313	2	Q8VP52
8	7	29.2	433	16	Q8CNY4
9	7	29.2	887	16	Q8XY49
10	7	29.2	910	16	Q9I3F5
11	7	29.2	2376	5	Q9V5J0
12	7	29.2	2376	5	Q966V1
13	6	25.0	69	16	Q9A542
14	6	25.0	88	17	Q8ZXR1
15	6	25.0	98	5	P91785
16	6	25.0	100	16	Q8PBN4

17	6	25.0	103	16	Q9KTL5
18	6	25.0	106	10	P93359
19	6	25.0	110	2	O87801
20	6	25.0	112	5	Q26847
21	6	25.0	113	16	Q8G7N5
22	6	25.0	117	12	Q65548
23	6	25.0	129	4	O43180
24	6	25.0	133	13	Q8JFY6
25	6	25.0	137	4	Q8N8H9
26	6	25.0	138	16	Q9RD30
27	6	25.0	142	16	Q8ZBU1
28	6	25.0	147	5	Q25622
29	6	25.0	148	5	Q8WT59
30	6	25.0	154	5	Q8WT58
31	6	25.0	154	5	O8WT56
32	6	25.0	154	5	Q8WT57
33	6	25.0	159	3	Q05697
34	6	25.0	159	4	Q8N9A4
35	6	25.0	161	10	Q9LWY4
36	6	25.0	163	17	Q8TMV7
37	6	25.0	165	2	Q9BNJ3
38	6	25.0	165	16	Q8XXY6
39	6	25.0	171	5	Q25624
40	6	25.0	175	13	Q8JFY7
41	6	25.0	175	16	Q9KQ90
42	6	25.0	177	11	O8CI08
43	6	25.0	178	5	Q25619
44	6	25.0	178	5	Q8NZJ8
45	6	25.0	178	16	Q98IM5

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY; PRT; 117 AA.
AC Q8TAT9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025791; AAH25791.1; -
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
SQ SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;

Query Match 83.3%; Score 20; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.1e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRPDGGQAEAGAE 20
DB 52 ALAGWLRPDGGQAEAGAE 71

RESULT 2
Q8CH53 PRELIMINARY; PRT; 117 AA.
AC Q8CH53;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF42491; AAC06965.1; -
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 45.8%; Score 11; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QAEGAEDELE 22
Db 63 QAEGAEDELE 73

RESULT 3
Q932V7 PRELIMINARY; PRT; 433 AA.
ID Q932V7
AC Q932V7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DR 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative RNA-binding protein LAH1.
GN A74G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koesena E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene AT4g32720 (GI:7270219).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY056237; AAL07086.1; -
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 433 AA; 48126 MW; E58EBAF51C35A8F7 CRC64;

Query Match 33.3%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAEDE 20
Db 287 QAEGAEDE 294

RESULT 4
Q8L7E4 PRELIMINARY; PRT; 433 AA.
ID Q8L7E4
AC Q8L7E4
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DR 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN A74G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Shinn P., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
RA Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY136302; AAM96968.1; -
DR EMBL; BT000396; AAN15715.1; -
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 433 AA; 48126 MW; CFF6F611A29AA0318 CRC64;

Query Match 33.3%; Score 8; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAEDE 20
Db 287 QAEGAEDE 294

RESULT 5
O65529 PRELIMINARY; PRT; 483 AA.
ID O65529
AC O65529
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DR 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 54.1 kDa protein.
GN F4D11.80 OR AT4G32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoorge W., Hohelsel J.,
RA Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]

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RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W., Lemcke K.,
RL Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022537; CAA18589.1; -.
DR EMBL; AL161582; CAB79989.1; -.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rtm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RM; 1.
DR PROSITE; PS0102; RRM; 1.
KW Hypothetical protein.
SQ SEQUENCE 483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;

Query Match 33.3%; Score 8; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAED 20
DB 302 QAEGAED 309

RESULT 6
Q9L063
ID Q9L063 PRELIMINARY; PRT; 103 AA.
AC Q9L063;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SC02791.
GN SCO2791 OR SCG105.22C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders A., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939114; CAB87228.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;

Query Match 29.2%; Score 7; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAEG 16
DB 48 DGGQAEG 54

RESULT 7

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Q8VP52
ID Q8VP52 PRELIMINARY; PRT; 313 AA.
AC Q8VP52;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE LysR-like transcriptional activator SnpR.
OS Streptomyces sp. C5.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=45212;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C5;
RA DeSanti C.L., Strohl W.R.;
RT "Characterization of the Streptomyces sp. strain C5 snp locus and
development of an snp-derived expression vector family.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AY072041; AAL61992.1; -.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW DNA-binding; Transcription; Transcription regulation.
SQ SEQUENCE 313 AA; 34258 MW; C907C8AF51C3FA13 CRC64;

Query Match 29.2%; Score 7; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLR 7
DB 103 ALAGWLR 109

RESULT 8
Q8CNY4
ID Q8CNY4 PRELIMINARY; PRT; 433 AA.
AC Q8CNY4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Trigger factor.
GN SE1350.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RA Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016748; AAO04949.1; -.
KW Complete proteome.
SQ SEQUENCE 433 AA; 48732 MW; FF2490AD097F437D CRC64;

Query Match 29.2%; Score 7; DB 16; Length 433;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAEG 16
DB 180 DGGQAEG 186

RESULT 9
Q8XY49
ID Q8XY49 PRELIMINARY; PRT; 887 AA.

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Q8XY49;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Probable phage-related tail transmembrane protein.
GN RSC1914 OR RS03483.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schliex T.,
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002)
DR EMBL; AL646067; CAD15616.1; -
KW Complete proteome.
SQ SEQUENCE 887 AA; 94105 MW; 9A8840E5362E740E CRC64;

Query Match          29.2%; Score 7; DB 16; Length 887;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QGAEAG 18
Db 290 QGAEAG 296
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      |||||

RESULT 10
Q913F5
ID Q913F5 PRELIMINARY; PRT; 910 AA.
AC Q913F5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aconitase hydratase 1.
GN ACNA OR PA1562.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria.
OC Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004584; AAG04951.1; -
DR HSP; P20004; IACO.
DR InterPro; IPR006249; Aconitase_1.
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR001030; Aconitase_N.
DR Pfam; PF00330; aconitase; 1.
DR Pfam; PF00694; Aconitase_C; 1.
DR PRINTS; PR00415; ACONITASE.
DR PRODOM; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR01341; aconitase_1; 1.
DR PROSITE; PS00405; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.

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KW Complete proteome.
SQ SEQUENCE 910 AA; 99147 MW; C65F23CDB6FA0E1C CRC64;

Query Match          29.2%; Score 7; DB 16; Length 910;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLR 7
Db 65 ALAGWLR 71
      |||||
      |||||

RESULT 11
Q9V5J0
ID Q9V5J0 PRELIMINARY; PRT; 2376 AA.
AC Q9V5J0;
DT 01-MAR-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG18408 protein.
GN REXIN OR CG3451 OR CG18408 OR CG18409.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkelley;
RX MEDLINE=20196008; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rehnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC Celisner S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

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RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Matteli B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.B., Bergman C., Bernan B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003830; AAF58816.2; -;
DR FlyBase; FBgn0033504; rexin.
DR InterPro; IPR001452; SH3.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 3.
DR SMART; SM00326; SH3; 3.
DR PROSITE; PS50002; SH3; 3.
SQ SEQUENCE 2376 AA; 267666 MW; A5F2D0589B8B695C CRC64;

Query Match 29.2%; Score 7; DB 5; Length 2376;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAEED 19
Db 37 QAEGAEED 43

RESULT 12
Q966V1 PRELIMINARY; PRT; 2376 AA.
AC Q966V1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
REXIN LI.
GN REXIN OR RXN OR CG3451 OR CG18408 OR CG18409.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki H.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamazaki H., Willert K., Fish M., Nusse R.;
RT "Drosophila Rexin, a Novel SH3 Adaptor Protein of Axin and Arrow that
RT Is Essential for Living in Late Stage Embryo.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: CONTAINS 3 SH3 DOMAINS.
DR EMBL; AB053478; BAB62017.1; -;
DR FlyBase; FBgn0033504; rexin.
DR InterPro; IPR002965; P_FICH_extensan.
DR Pfam; IPR001452; SH3.
DR Pfam; PF00018; SH3; 3.
DR PRINTS; PR01217; PRICHEXTENS.
DR PRODOM; PD000066; SH3; 3.
DR SMART; SM00326; SH3; 3.
DR PROSITE; PS50002; SH3; 3.
KW SH3 domain.
SQ SEQUENCE 2376 AA; 267657 MW; 9C7BD6C7A705C888 CRC64;

Query Match 29.2%; Score 7; DB 5; Length 2376;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QAEGAEED 19
Db 37 QAEGAEED 43

RESULT 13
Q9A542 PRELIMINARY; PRT; 69 AA.
AC Q9A542;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cold-shock domain family protein.
GN CC2623.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=153892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR EMBL; AE005930; AAK24591.1; -;
DR HSP; F15277; IMJC.
DR TIGR; CC2623; -;
DR InterPro; IPR002059; Cold_shock.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000821; Cold_shock; 1.
DR SMART; SM00357; Csp; 1.
KW Activator; DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 69 AA; 7450 MW; 8EA80BE9EE56853C CRC64;

Query Match 25.0%; Score 6; DB 16; Length 69;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PEDGGQ 13
Db 20 PEDGGQ 25

RESULT 14
Q8Z2R1 PRELIMINARY; PRT; 88 AA.
ID Q8Z2R1

AC Q82ZRI;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PAE0124.
GN PAE0124.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Muller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009752; AAL62578.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 88 AA; 9492 MW; 22091651B45CADD1 CRC64;

Query Match 25.0%; Score 6; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWL 6
Db 45 ALAGWL 50

RESULT 15
P91785
ID P91785 PRELIMINARY; PRT; 98 AA.
AC P91785;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Antigen maltose binding protein (Fragment).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94336252; PubMed=8058358;
RA Trenholme K.R., Tree T.I., Gillespie A.J., Guderian R., Maizels R.M.,
RA Bradley J.E.;
RT "Heterogeneity of IgG antibody responses to cloned Onchocerca volvulus
RT antigens in microfiladermia positive individuals from Esmeraldas
RT Province, Ecuador.";
RL Parasite Immunol. 16:201-209(1994).
DR EMBL; S71371; AAC60510.2; -;
FT NON_TER 1 1
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11165 MW; 221BEPFEBE14DC76 CRC64;

Query Match 25.0%; Score 6; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LRPEDG 11
Db 51 LRPEDG 56

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 16.893 Seconds
(without alignments)
325.703 Million cell updates/sec

Title: US-09-853-253-2
Perfect score: 611
Sequence: 1 MPSPTGVCSSLLGLMLDL.....LGKFLQDILWEEAKEAPADK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Watch 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	611	100.0	117	1	GHRL_HUMAN
2	524	85.8	117	1	GHRL_MOUSE
3	518	84.8	117	1	GHRL_RAT
4	476	77.9	117	1	GHRL_CANFA
5	472.5	77.3	118	1	GHRL_PIG
6	417.5	68.3	116	1	GHRL_BOVIN
7	92	15.1	115	1	MOTI_MACMU
8	88.5	14.5	115	1	MOTI_HUMAN
9	86.5	14.2	127	1	MOTI_CAVPO
10	86	14.1	92	1	MOTI_HORSE
11	82	13.4	119	1	MOTI_PIG
12	72.5	11.9	115	1	MOTI_SHEEP
13	72.5	11.9	482	1	TYPH_HUMAN
14	72	11.8	147	1	H2B_GOSHI
15	71	11.6	1236	1	MOTI_LEICH
16	70	11.5	116	1	MOTI_FELCA
17	70	11.5	220	1	WFDL_HUMAN
18	69	11.3	792	1	NEKA_MOUSE
19	69	11.3	2424	1	CCAA_RABIT
20	68.5	11.2	115	1	MOTI_BOVIN
21	68.5	11.2	133	1	MOTI_RABIT
22	68.5	11.2	340	1	GBX2_XENLA
23	68.5	11.2	533	1	CUEQ_YERPE
24	68	11.1	330	1	NAG2_VIBCH
25	67.5	11.0	416	1	TC10_HUMAN
26	67.5	11.0	1878	1	BA2A_HUMAN
27	67	11.0	2164	1	CCAA_MOUSE
28	67	11.0	2212	1	CCAA_RAT
29	66.5	10.9	575	1	PTL_LACLA
30	66.5	10.9	575	1	PTL_LACIC
31	66.5	10.9	577	1	PTI_STRBO
32	66	10.8	247	1	MOG_HUMAN
33	66	10.8	589	1	IF2P_THEVO

34	66	10.8	770	1	STA3_HUMAN	P40763 homo sapien
35	66	10.8	770	1	STA3_MOUSE	P42227 mus musculus
36	66	10.8	770	1	STA3_RAT	P52631 rattus norv
37	66	10.8	3462	1	RELN_RAT	P58751 rattus norv
38	65.5	10.7	262	1	TRUA_PYRHO	O58941 pyrococcus
39	65.5	10.7	333	1	TALI_KLULA	P34214 kluyveromyc
40	65.5	10.7	692	1	FLHA_SALTY	P40729 salmonella
41	65	10.6	155	1	RS15_HALMA	P05762 haloarcula
42	65	10.6	458	1	HN3B_RAT	P32182 rattus norv
43	65	10.6	554	1	SAP_RAT	P10960 rattus norv
44	65	10.6	795	1	SYFB_HAEIN	P43820 haemophilus
45	64.5	10.6	447	1	CPXU_RHISN	P55340 rhizobium s

ALIGNMENTS

RESULT 1
GHRL_HUMAN STANDARD; PRT; 117 AA.
AC Q9UBU3; O8TAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
DE releasing peptide) (Motilin-related peptide) (M46 protein).
GN GHRL OR MTLRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
RX Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach.";
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Stomach;
RC Tomasetto C., Karam S.M., Rio M.-C.;
RT "Identification of a novel gastric protein m46.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wajnsrajch M.P., Ten I.S., Gertner J.M., Leibell R.L.;
RL "Genomic organization of the human Ghrelin gene.";
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RC MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [6]
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [7]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -!- PTM: O-n-octanoylation is essential for activity.
 CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infoblog.fr/services/chromocancer/Genes/GhrelinID327.html".
 CC -----
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 CC -----
 DR EMBL; AB029434; BA89371.1; -;
 DR EMBL; AB035700; BAB19045.1; -;
 DR EMBL; AJ252278; CAB65733.1; -;
 DR EMBL; AF296558; AAG10300.1; -;
 DR EMBL; BC025791; AAH25791.1; -;
 DR PIR; A59316; A59316.
 DR MIM; 605353; -;
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
 DR GO; GO:0007287; P:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc.1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD32162; Preproghrelin; 1.
 KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23 GHRELIN.
 FT PEPTIDE 24 51
 FT PROPEP 52 117 REMOVED IN MATURE FORM.
 FT LIPID 26 26 N-OCTANOATE.
 FT VARSPLIC 37 37 Missing (in Isoform 2).
 FT FT /FTid=VSP_003245.
 FT CONFLICT 72 72 L -> M (IN REF. 5).

SQ SEQUENCE 117 AA; 12911 MW; 39C0572BECA2755 CRC64;
 Query Match 100.0%; Score 611; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.1e-54;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPGTVCSSLLLLGLMLDLAMAGSSFLSPHORVQQRKESKPPAKLQPRALAGWLRLPE 60
 DB 1 MPSPGTVCSSLLLLGLMLDLAMAGSSFLSPHORVQQRKESKPPAKLQPRALAGWLRLPE 60
 QY 61 DGGQAEAGAEDELEVRFNAPFDVGKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAEAGAEDELEVRFNAPFDVGKLSGVYQQHSQALGKFLQDILWEEAKEAPADK 117
 RESULT 2
 GHRL_MOUSE
 ID GHRL_MOUSE STANDARD; PRT; 117 AA.
 AC Q9BQX0; Q9MUZ1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide) (Motilin-related peptide) (M46 protein).
 GN GHRL OR MTLRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Kojima M.;
 RT "Mouse mRNA for preproghrelin.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Stomach;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavita H.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann C., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyono-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RN Nature 409:685-690(2001).
 RP [5]
 RP REVIEW.


```

RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulation of gastric acid secretion. Involved in
CC growth regulation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9EQX0-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9EQX0-2; Sequence=VSP_003246;
CC -!- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
CC with higher levels in the stomach, medium levels in the duodenum,
CC jejunum, ileum and colon. Low expression in the testis and brain.
CC Not detected in the salivary gland, pancreas, liver and lung.
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC
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CC -----
DR EMBL; AJ243503; CAB46500.1; -
DR EMBL; AB035701; BAB19046.1; -
DR EMBL; AB060078; BAB69857.1; -
DR EMBL; AK008658; BAB25814.1; -
DR EMBL; AK008860; BAB25934.1; -
DR MGI; MGI:1930008; Ghrl.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005576; C:extracellular; IDA.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_assoc.1.
DR Pfam; PF04644; motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
KW Hormone: Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23
FT PEPTIDE 24 51
FT PROPEP 52 117
FT LIPID 26 26
FT VARSPLIC 37 37
FT FTID=VSP_003246;
SQ SEQUENCE 117 AA; 13207 MW; EACB49D2E3CA7203 CRC64;

Query Match 85.8%; Score 524; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 1.le-45;
Matches 98; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MPSPGTGCSLLLLGLMLDLAMAGSFLSPHQVRQKESKPPAKLPQPRALAGWLKPE 60
Db 1 MLSSGTCISLLLSMLMDMAMAGSFLSPHQKQAKQKESKPPAKLPQPRALAGWLKPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOQSALGKFLQDILWEEAKEAPADK 117
Db 61 DRGQAEETEELIRNAPFDVGIKLSGAQYQOQGRALGKFLQDILWEEAKEAPADK 117

RESULT 3
GHRL_RAT
ID GHRL_RAT STANDARD; PRT: 117 AA.

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AG Q9QYH7: Q9ET69;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide).
GN GHRL.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,
RP AND ACYLATION OF SER-26.
RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX MEDLINE=20067959; PubMed=10604470;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from
RT stomach.";
RL Nature 402:656-660(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS
RP SPECTROMETRY, AND ACYLATION OF SER-26.
RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX MEDLINE=20357315; PubMed=10801861;
RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT "Purification and characterization of rat des-Gln14-ghrelin, a second
RT endogenous ligand for the growth hormone secretagogue receptor.";
RL J. Biol. Chem. 275:21995-22000(2000).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=21092536; PubMed=11162448;
RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
RT in gastrointestinal tissue.";
RL Biochem. Biophys. Res. Commun. 279:909-913(2000).
RN [4]
RP STRUCTURE-ACTIVITY RELATIONSHIP.
RX MEDLINE=21433488; PubMed=11549267;
RA Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
RT "Structure-activity relationship of ghrelin: pharmacological study of
RT ghrelin peptides.";
RL Biochem. Biophys. Res. Commun. 287:142-146(2001).
RN [5]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9QYH7-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9QYH7-2; Sequence=VSP_003248;
CC -!- TISSUE SPECIFICITY: Broadly expressed with higher expression in
CC the stomach. Very low levels are detected in the hypothalamus,
CC heart, lung, pancreas, intestine and adipose tissue.
CC -!- PTM: O-n-octanoylation is essential for activity. The replacement
CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.
CC -!- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;
CC RANGE=24-51.
CC -!- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;
CC RANGE=24-36, 38-51.
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.

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-----
EMBL; AB029433; BAA89370.1; -
EMBL; AB035699; BAB11956.1; -
PIR; B59316; B59316.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
PRINTS; PR01624; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23 GHRELIN.
FT PEPTIDE 24 51 REMOVED IN MATURE FORM.
FT PROPEP 52 117 N-OCTANOATE.
FT LIPID 26 26 Missing (in isoform 2).
FT VARSPPLIC 37 37 /FTid=VSP_003248.
SQ SEQUENCE 117 AA; 13176 MW; 8857546FE51A7691 CRC64;

Query Match 84.8%; Score 518; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 4.2e-45;
Matches 97; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 1 MPSPTGVCSSLLGLMGLDLAMAGSSFLSPHEQVQORQKSKPPAKLQPRALAGWLRLPE 60
DB 1 MVSATTCSSLLLSMLMDMAMAGSSFLSPHEQAKQORQKSKPPAKLQPRALGWLRLPE 60

OY 61 DGGQAEAGDELEVRFPDVGILSGVQYQOHSQALGKFLQDLILWEEAKEAPADK 117
DB 61 DRGQAEAEDELEIRFNPFDVGILSGVQYQOHSQALGKFLQDLILWEEVKEAPANK 117

RESULT 4
GHRLL_CANFA STANDARD; PRT; 117 AA.
ID GHRLL_CANFA Q9BEF8; Q9BEF7;
AC Q9BEF8; Q9BEF7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (growth hormone secretagogue) (growth hormone
releasing peptide) (Motilin-related peptide).
GN GHRLL OR MTLRP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
[1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RN Tissue=Stomach;
RA Tomasetto C., Wendling C., Rio M.-C., Poltras P.;
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
fundus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Specific ligand for the growth hormone secretagogue
receptor type 1 (GHSR) inducing the release of growth hormone from
the pituitary. Has an appetite-stimulating effect, induces
adiposity and stimulates gastric acid secretion. Involved in
growth regulation (By similarity).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9BEF8-1; Sequence=Displayed;

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Name=2; Synonyms=del-Gln14-ghrelin;
IsoId=Q9BEF8-2; Sequence=VSP_003244;
-|- PTM: O-n-octanoylation is essential for activity (By similarity).
-|- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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-----
EMBL; AJ298295; CAC29155.1; -
EMBL; AJ298296; CAC29156.1; -
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
PRINTS; PR01624; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPPLIC 37 37 Missing (in isoform 2).
FT /FTid=VSP_003244.
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Query Match 77.9%; Score 476; DB 1; Length 117;
Best Local Similarity 77.8%; Pred. No. 6.7e-41;
Matches 91; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

OY 1 MPSPTGVCSSLLGLMGLDLAMAGSSFLSPHEQVQORQKSKPPAKLQPRALAGWLRLPE 60
DB 1 MPSLGTCSLLLSVLMVLDLAMAGSSFLSPHEQKQKSKPPAKLQPRALGSLGPE 60

OY 61 DGGQAEAGDELEVRFPDVGILSGVQYQOHSQALGKFLQDLILWEEAKEAPADK 117
DB 61 DTSQVEAEDELEIRFNPFDVGILSGVQYQOHSQALGKFLQDLILWEDTNEALADE 117

RESULT 5
GHRLL_PIG STANDARD; PRT; 118 AA.
ID GHRLL_PIG Q9GKY5; Q9BGD8; Q9GKY4;
AC Q9GKY5; Q9BGD8; Q9GKY4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (growth hormone secretagogue) (growth hormone
releasing peptide).
GN GHRLL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RN Kojima M.;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC Tissue=Stomach;
RA Rousselle J., Lacroix D., Dubreuil P.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Specific ligand for the growth hormone secretagogue
receptor type 1 (GHSR) inducing the release of growth hormone from
the pituitary. Has an appetite-stimulating effect, induces
adiposity and stimulates gastric acid secretion. Involved in
growth regulation (By similarity).
CC

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CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Name=1; Synonyms=Ghrelin; Named isoforms=2;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC Name=3; Synonyms=del-Gln14-ghrelin;
CC Name=4; Synonyms=del-Gln14-ghrelin;
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB035703; BAB19048.1; -
CC EMBL; AB035704; BAB19049.1; -
CC EMBL; AF308930; AAK19243.1; -
CC EMBL; AY028942; AAK30002.1; -
CC InterPro: IPR006737; motilin_assoc.
CC InterPro: IPR006738; motilin_ghrelin.
CC InterPro: IPR005441; Preproghrelin.
CC Pfam: PF04643; motilin_assoc; 1.
CC Pfam: PF04644; motilin_ghrelin; 1.
CC PRINTS: PR01624; GHRELIN.
CC ProDom: PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 24 BY SIMILARITY.
FT PEPTIDE 25 52 GHRELIN.
FT PROPEP 53 118 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 27 27 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC 38 38 Missing (in isoform 2).
FT CONFLICT 17 17 L -> P (IN REF. 2; AAK30002).
FT CONFLICT 72 72 K -> E (IN REF. 2; AAK30002).
FT SEQUENCE. 118 AA; 12785 MW; 856D3E1D6DABA76 CRC64;
SQ
Query Match 77.3%; Score 472.5; DB 1; Length 118;
Best Local Similarity 78.0%; Pred. No. 1.5e-40;
Matches 92; Conservative 8; Mismatches 17; Indels 1; Gaps 1;
QY 1 MSPSGTVCSSLLGLMLWLDLAWAGSSFLSPHQVQQRKSKPKPAKLQPRALAGWLRP 59
Db 1 MSPSTGTCSSLLGLMLWLDLAWAGSSFLSPHQVQQRKSKPKPAKLQPRALAGWLRP 60
QY 60 EDGQAGAEDELEVRNAPFDVGIKLSGVQYQHQSQLGKFLQDILWEAKEAPADK 117
Db 61 EDGSEVEGTEDKLEIRFNAPCDVGIKLSGAQSDQHQPLGKFLQDILWEAVEAPADK 118
RESULT 6
GHRL_BOVIN
ID GHRL_BOVIN STANDARD; PRT; 116 AA.
AC Q9BD76; Q9CKY6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide).
GN GHRL
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Kita K., Harada K., Yokota H.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

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RN SEQUENCE OF 24-99 FROM N.A.
RP Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF350329; AAK18612.1; -
CC EMBL; AB035702; BAB19047.1; -
CC InterPro: IPR006737; motilin_assoc.
CC InterPro: IPR006738; motilin_ghrelin.
CC InterPro: IPR005441; Preproghrelin.
CC Pfam: PF04643; motilin_assoc; 1.
CC Pfam: PF04644; motilin_ghrelin; 1.
CC PRINTS: PR01624; GHRELIN.
CC ProDom: PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 50 GHRELIN (BY SIMILARITY).
FT PROPEP 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT CONFLICT 34 34 K -> E (IN REF. 2).
FT SEQUENCE. 116 AA; 12792 MW; F55536DAC5FA59B6 CRC64;
SQ
Query Match 68.3%; Score 417.5; DB 1; Length 116;
Best Local Similarity 69.2%; Pred. No. 4.8e-35;
Matches 81; Conservative 16; Mismatches 19; Indels 1; Gaps 1;
QY 1 MSPSGTVCSSLLGLMLWLDLAWAGSSFLSPHQVQQRKSKPKPAKLQPRALAGWLRP 60
Db 1 MPAPWTICSSLLGLMLWLDLAWAGSSFLSPHQVQQRKSKPKPAKLQPRALAGWLRP 59
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQHQSQLGKFLQDILWEAKEAPADK 117
Db 60 VGSQAGAEDELEIRFNAPFNIGIKLAGAQLHGQTLGKFLQDILWEAEETLANE 116
RESULT 7
MOTIL_MACMU
ID MOTIL_MACMU STANDARD; PRT; 115 AA.
AC O18811;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Motilin precursor [Contains: Motilin; Motilin associated peptide
DE (MAP)].
GN MLN
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Z., De Clercq P., Depoortere I., Peeters T.L.;
RL MEDLINE=98433861; PubMed=9762897;
RT "Isolation and sequence of cDNA encoding the motilin precursor from
RT monkey intestine. Demonstration of the motilin precursor in the

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RT monkey brain."
RL FEBS Lett. 435:149-152(1998).
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
CC INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
CC RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
DR EMBL; AF016372; AAC82510.1; -
DR InterPro; IPR006737; motilin_assoc.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
DR Hormone; Cleavage on pair of basic residues; Signal.
ET SIGNAL 1 25 BY SIMILARITY.
FT PEPTIDE 26 47 MOTILIN.
FT PEPTIDE 50 115 MOTILIN ASSOCIATED PEPTIDE.
SQ SEQUENCE 115 AA; 12821 MW; FB67E1080E989159 CRC64;

Query Match 15,18; Score 92; DB 1; Length 115;
Best Local Similarity 27,08; Pred. No. 0.018;
Matches 24; Conservative 23; Mismatches 32; Indels 10; Gaps 2;

Qy 27 FLSPHQVQVQKESKPPAKLPALAGWLRPDGGQAGAEDELE-----VRFNAPFD 81
Db 30 FTYGELQMQEKESKG-----QKKSLSVMQSGEGCPDPAEPLEEGNEMIKLTAPLE 84

Qy 82 VGKLSGVQVQVQHSQALGKFLQDILWEEA 110
Db 85 IGRMNSRQLEKYRAALEGLLSEMLPQHA 113

RESULT 8
MOTIL_HUMAN STANDARD; PRT; 115 AA.
AC P12872;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Motilin precursor (Contains: Motilin; Motilin associated peptide
DE (MAP)).
GN MLN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=9289989; PubMed=2737284;
RA Yano H., Sano Y., Fujita J., Yamada Y., Inagaki N., Takeda J.,
RA Bell G.I., Eddy R.L., Fan Y.-S., Byers M.G., Shows T.B., Imura H.;
RT "Exon-intron organization, expression, and chromosomal localization
RT of the human motilin gene.";
RL FEBS Lett. 249:248-252(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88030048; PubMed=3666144;
RA Sano Y., Tanaka K., Takeda J., Takahashi H., Mitani T., Kurono M.,
RA Kayano T., Koh G., Fukumoto H., Yano H., Fujita J., Inagaki N.,
RA Yamada Y., Imura H.;
RT "Sequence of an intestinal cDNA encoding human motilin precursor.";
RL FEBS Lett. 223:74-76(1987).
RN [3]
RP SEQUENCE FROM N.A.

RX MEDLINE=90091748; PubMed=2574660;
RA Daikh D.I., Douglass J.O., Adelman J.P.;
RT "Structure and expression of the human motilin gene.";
RL DNA 8:615-621(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89121385; PubMed=2914635;
RA Dea D., Boileau G., Poltras P., Lahaie R.G.;
RT "Molecular heterogeneity of human motilinlike immunoreactivity
RT explained by the processing of prepromotilin.";
RL Gastroenterology 96:695-703(1989).
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
CC INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
CC RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
DR EMBL; X15393; CAA33448.1; -
DR EMBL; X15396; CAA33448.1; JOINED.
DR EMBL; X15395; CAA33448.1; JOINED.
DR EMBL; X15394; CAA33448.1; JOINED.
DR EMBL; Y06695; CAA68690.1; -
DR EMBL; M30281; AAA59860.1; -
DR EMBL; M30278; AAA59860.1; JOINED.
DR EMBL; M30279; AAA59860.1; JOINED.
DR EMBL; M30280; AAA59860.1; JOINED.
DR PIR; A33233; A33233.
DR PDB; 1LBJ; 20-NOV-02.
DR Genev; HGNC:7141; MLN.
DR MIN; 158270; -
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
DR Hormone; Cleavage on pair of basic residues; Signal; 3D-structure.
ET SIGNAL 1 25
FT PEPTIDE 26 47 MOTILIN.
FT PEPTIDE 50 115 MOTILIN ASSOCIATED PEPTIDE.
SQ SEQUENCE 115 AA; 12920 MW; 30D4BB59B2F42783 CRC64;

Query Match 14,58; Score 88,5; DB 1; Length 115;
Best Local Similarity 25,48; Pred. No. 0.041;
Matches 31; Conservative 29; Mismatches 41; Indels 21; Gaps 5;

Qy 1 MPSPGTVCSLLLGLMLDLAMAGSS-----FLSPHQVQVQKESKPPAKLPAL 53
Db 1 MYSRKAVALLVHVH----AAMLASQTEAFVPIFYGELQMQEKERNG-----QKKS 51

Qy 54 AGWLRPDGGQAGAE-----EDELV-VRFNAPFDVGKLSGVQVQHSQALGKFLQDILWE 108
Db 52 SVMQSGEGVPDPAEPREENEMIKLTAPLEIGMRMNSRQLEKYPATLEGLLSEMLPQ 111

Qy 109 EA 110
Db 112 HA 113

RESULT 9
MOTI_CAVPO
ID MOTI_CAVPO STANDARD; PRT; 127 AA.
AC Q99MPS;
DT 28-FEB-2003 (Rel. 41, Created)
```

DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Motilin precursor [Contains: Motilin; Motilin associated peptide
(MAP)].
GN MLN.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
ON NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=2109894; PubMed=11172801;
RA Xu L., Depoortere I., Tang M., Peeters T.L.;
RT "Identification and expression of the motilin precursor in the guinea
pig";
RL FEBS Lett. 490:7-10(2001).
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Present in the gut mucosa with the exception
of the gastric corpus. Also present in medulla oblongata, nucleus
of the solitary tract, hypophysis, spinal cord, hypothalamus, and
cerebellum but not in the cerebral cortex.
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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CC -----
CC EMBL: AF323752; AAK07442.1; -
DR InterPro: IPR006737; motilin_assoc.
DR InterPro: IPR006738; motilin_ghrelin.
DR Pfam: PF04643; motilin_assoc; 1.
DR Pfam: PF04644; motilin_ghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT PEPTIDE 26 47 MOTILIN.
FT PEPTIDE 50 127 MOTILIN ASSOCIATED PEPTIDE.
SQ SEQUENCE 127 AA; 14156 MW; A45E90C0E7EFC220 CRC64;
Query Match 14.2%; Score 86.5; DB 1; Length 127;
Best Local Similarity 27.6%; Pred. No. 0.072;
Matches 32; Conservative 23; Mismatches 44; Indels 17; Gaps 5;
QY 1 MFPGTVCSLLGLGLWLDLMAAGSS-----FLSPHQVQQRKSK--KPPAKLQPR 51
DB 1 MLRSKRAVALLVHV-----TAMLASQTEGFVIFTYSELRRTQREQNRRLRSURVQOR 56
QY 52 A-LAGWLRPEDGQAGAELEVRFNAPFDVGIKLSGVQYQOHSQALCKFLQDIL 106
DB 57 SKAAGRLRPQ---EVMNEENGVIKLTAPVEIGVGLSSRQLEKRAVLEALLSEAL 109
RESULT 10
MOTI_HORSE
ID MOTI_HORSE STANDARD; PRT; 92 AA.
AC O46617;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Motilin precursor [Contains: Motilin; Motilin associated peptide
(MAP)] (Fragment).
GN MLN.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=DuoDenal mucosa;
RX MEDLINE=20033565; PubMed=10564829;
RA Huang Z., Depoortere I., De Clercq P., Peeters T.;
RT "Sequence and characterization of cDNA encoding the motilin precursor
from chicken, dog, cow and horse. Evidence of mosaic evolution in
premotilin";
RL Gene 240:217-226(1999).
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF047520; AAC03790.1; -
DR InterPro: IPR006737; motilin_assoc.
DR InterPro: IPR006738; motilin_ghrelin.
DR Pfam: PF04643; motilin_assoc; 1.
DR Pfam: PF04644; motilin_ghrelin; 1.
KW Hormone; Cleavage on pair of basic residues.
FT NON_TER 1 1
FT PEPTIDE 1 22 MOTILIN.
FT PEPTIDE 25 92 MOTILIN ASSOCIATED PEPTIDE.
SQ SEQUENCE 92 AA; 10410 MW; 99DCA503EAFE4C8 CRC64;
Query Match 14.1%; Score 86; DB 1; Length 92;
Best Local Similarity 28.9%; Pred. No. 0.057;
Matches 24; Conservative 19; Mismatches 34; Indels 6; Gaps 3;
QY 27 FLSPHQVQ--QRKSKPPAKLQPR--LAGWLRPEDGQAGAELEVRFNAPFDV 83
DB 5 FTYSELQRMQEKERNRQKSLGLQORSEVGLDPTAEAEKGEK---VIKLTAPVEIG 61
QY 84 IKLSGVQYQOHSQALCKFLQDIL 106
DB 62 MRNRSQLEKYRAALEGLLEVL 84
RESULT 11
MOTI_PIG
ID MOTI_PIG STANDARD; PRT; 119 AA.
AC P01307;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Motilin precursor [Contains: Motilin; Motilin associated peptide
(MAP)].
GN MLN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88288231; PubMed=2456453;
RA Bond C.T., Nilaver G., Godfrey B., Zimmerman E.A., Adelman J.P.;
RT "Characterization of complementary deoxyribonucleic acid for
precursor of porcine motilin";
RL Mol. Endocrinol. 2:175-180(1988).
RN [2]
RP SEQUENCE OF 26-47.
RX MEDLINE=73184120; PubMed=4706833;

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Db          90 DSRQLEKYRATLERLL 105

RESULT 12
MOTIL_SHEEP
ID MOTI_SHEEP STANDARD; PRT; 115 AA.
AC Q18845;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Motilin precursor [Contains: Motilin; Motilin associated peptide
DE (MAP)].
GN MLN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=98087436; PubMed=9427564;
RA De Clercq P., Depoortere I., Peeters T.L.;
RT "Isolation and sequencing of the cDNA encoding the motilin precursor
RT from sheep intestine.";
RL Gene 202187-191(1997).
CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
CC INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
CC RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF022771; AAB80930.1; -
CC PIR; JC6511; JC6511.
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC Pfam; PF04643; motilin_assoc.1.
CC Pfam; PF04644; motilin_ghrelin.1.
CC Hormone; Cleavage on pair of basic residues; Signal.
KW SIGNAL
FT SIGNAL 1 25 BY SIMILARITY.
FT PEPTIDE 26 47 MOTILIN.
FT PEPTIDE 50 115 MOTILIN ASSOCIATED PEPTIDE.
SQ SEQUENCE 115 AA; 12956 MW; 383892C2AD7EC5D CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 115;
Best Local Similarity 25.0%; Pred. No.1.6;
Matches 21; Conservative 21; Mismatches 33; Indels 9; Gaps 2;

QY 27 FLSPHQVRQVRKSKPPAKLQPRLAGWLRPEDGGQAGAEDELE----VRFNAPFOV 82
Db 30 FTYGEVQRMQEKERYKG----QKSLSVQQRSEEVGPDPAEPREKQEVKLTAPVEI 84
QY 83 GIKLSGVQVQOHSQALGKFKLODIL 106
Db 85 GMRMNSRQLEKYQATLEGLLRKAL 108

RESULT 13
TYPH_HUMAN
ID TYPH_HUMAN STANDARD; PRT; 482 AA.
AC P19971; Q13390;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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```
Db 60 AVVNGSQAQIGAML-----MAIRLRGMDLETSVLTQALASGQGLEWPEAWRQOL 112
Qy 115 ADK 117
Db 113 VDK 115

RESULT 14
H2B_GOSHI
ID H2B_GOSHI STANDARD; PRT; 147 AA.
AC O22582;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histone H2B.
GN HIS2B.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Deltapine 62; TISSUE=Etiolated cotyledon;
RA Turley R.B.;
RT "cDNA clones encoding histone H3 and histone H2B from upland cotton
(Gossypium hirsutum L.).";
RL (In) Plant Gene Register PGR97-182.
CC -1- SUBUNIT: The nucleosome is an octamer containing two molecules
each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
BP of DNA.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the histone H2B family.
CC
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CC
CC EMBL; AF025667; AAB97163.1; -.
DR PIR; T09722; T09722.
DR InterPro; IPR004822; Histone_Core.
DR InterPro; IPR000558; Histone_H2B.
DR Pfam; PF00125; histone.1
DR PRINTS; PR00621; HISTONEH2B.
DR PRODOM; PD000497; Histone_H2B; 1.
DR SMART; SM00427; H2B; 1.
DR PROSITE; PS00357; HISTONE_H2B; 1.
DR KW Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
SQ SEQUENCE 147 AA; 16087 MW; CEFDS774E6E11F6 CRC64;

Query Match 11.8%; Score 72; DB 1; Length 147;
Best Local Similarity 25.2%; Pred. No. 2.4;
Matches 28; Conservative 22; Mismatches 31; Indels 30; Gaps 5;

Qy 22 MAGSSFLSPHORVQORKE--SKKPPAKLOPRALAGWLRPEDGGQAGAEDELEVRFNAP 79
Db 1 MAPKAEEKPAEKKPAEKKVAEKAPEAKPK--AGKKLPKEGGAAGDKKKRVKKSVE 58
Qy 80 F-----DVGIKSLGVQYQOHSQALG---KFLQDILWEBAKEA 113
Db 59 TYKIYIFKLVKQVHPDIGIS-----SKAMGIMNSFINDIFEKLAQEA 100

RESULT 15
TOP2_LEICH
ID TOP2_LEICH STANDARD; PRT; 1236 AA.
AC O61078;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
```

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA topoisomerase II (EC 5.99.1.3).
GN TOP2.
OS Leishmania chagasi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=44271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MHOM/BR/86/L669;
RA Tepe-Lansdell T., Mann B.J., Labombard M., Macdonald T., Slunt K.M.,
RA Pearson R.D.;
RT "Isolation of a gene encoding a DNA topoisomerase II of Leishmania
(Leishmania chagasi).";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
MAKES DOUBLE-STRAND BREAKS.
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
RELAX ONLY NEGATIVE SUPERCOILS.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC
CC EMBL; AF051307; AAC05295.2; -.
DR HSSP; P06786; 1BGW.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR001241; DNA_topoisoiI.
DR InterPro; IPR002205; DNA_topoisoiV.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF00521; DNA_topoisoiV; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR PRODOM; PD000742; DNA_topoisoiV; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00433; TOP2C; 1.
DR SMART; SM00434; TOP4C; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR KW Isomerase; Topoisomerase; ATP-binding.
DR NP_BIND 137 142 ATP (POTENTIAL).
FT ACT_SITE 775 775 DNA CLEAVAGE (BY SIMILARITY).
SQ SEQUENCE 1236 AA; 138968 MW; A3209B95A078045C CRC64;

Query Match 11.6%; Score 71; DB 1; Length 1236;
Best Local Similarity 27.4%; Pred. No. 30;
Matches 26; Conservative 13; Mismatches 48; Indels 8; Gaps 2;

Qy 20 LAMAGSSFLSPHORVQORKE--SKKPPAKLOPRALAGWLRPED-----GGQAGAEDELE 73
Db 1141 LLMLGASAKGATATRVHACQYKPPPPSKRRPGESVGGARPSDSAAARTVGRKRLVGRSEFK 1200
Qy 74 VR--FNAPFDVQKLSGVQYQOHSQALGKFLQDIL 106
Db 1201 NKKPMRSKKNVKSLSLSTRTVAQPGCAQLGRLLPHVL 1235

Search completed: September 11, 2003, 17:21:41
Job time : 18.893 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 25.0267 Seconds
(without alignments)
152.215 Million cell updates/sec

Title: US-09-853-253-4

Perfect score: 126

Sequence: 1 ALAGWLRPEDGGQAEAGAELEVR 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126	100.0	24	AAE23839	Human zsig33-linker
2	126	100.0	24	AAE15884	Human zsig33-linker
3	126	100.0	91	AAE33410	Human exon 3-delet
4	126	100.0	116	AAE60517	Human des-Gln14-gh
5	126	100.0	117	AAW87991	Protein designated
6	126	100.0	117	AAW87236	Human signal pepti
7	126	100.0	117	AAW38890	Human polypeptide
8	126	100.0	117	AAE62649	Human zsig33 polyp
9	126	100.0	117	AAE20101	Zsig33 protein. H

10	126	100.0	117	22	AAE60511	Human ghrelin prep
11	126	100.0	117	23	ABW78319	Amino acid sequenc
12	126	100.0	117	23	AAE23838	Human zsig33 prote
13	126	100.0	117	23	AAE15883	Human zsig33 prote
14	126	100.0	117	24	ABU66790	Human PRO polypept
15	126	100.0	117	24	ABU67066	Human secreted/tra
16	126	100.0	117	24	ABU59871	Novel secreted and
17	126	100.0	117	24	ABU59124	Novel human secret
18	126	100.0	117	24	ABU59271	Human secreted/tra
19	126	100.0	117	24	ABU59420	Novel human secret
20	126	100.0	117	24	ABU60555	Human secreted/tra
21	126	100.0	117	24	ABU58046	Human PRO polypept
22	126	100.0	117	24	ABU58977	Human secreted/tr
23	126	100.0	117	24	AAE33409	Human preproghreli
24	126	100.0	117	24	ABU13937	Human PRO1066 poly
25	126	100.0	117	24	ABU10892	Human PRO polypept
26	126	100.0	118	21	AAE66708	Membrane-bound pro
27	126	100.0	118	22	AAU12392	Human PRO1066 poly
28	126	100.0	118	22	AAE65231	Human PRO1066 (UNQ
29	126	100.0	126	22	AAE40676	Human polypeptide
30	121	96.0	23	23	AAE23840	Human zsig33-linker
31	121	96.0	23	23	AAE23841	Human zsig33-linker
32	121	96.0	23	23	AAE15885	Human zsig33-linker
33	121	96.0	23	23	AAE15886	Human zsig33-linker
34	95	75.4	90	23	ABP08975	Human ORFX protein
35	95	75.4	116	22	AAE60516	Rat des-Gln14-ghre
36	95	75.4	117	22	AAE60510	Rat ghrelin prepro
37	92	73.0	117	22	AAE60521	Porcine des-Gln14-
38	92	73.0	118	22	AAE60520	Porcine ghrelin pr
39	67.5	53.6	89	22	AAE60523	Bovine ghrelin pre
40	54	42.9	200	24	ABP58240	Xenopus laevis nuc
41	50	39.7	653	17	AAE8903	Murine APLP1. Mus
42	48	38.1	82	22	AAE73526	Human colon cancer
43	48	38.1	287	22	ABG15575	Novel human diagno
44	48	38.1	570	22	ABG20671	Novel human diagno
45	48	38.1	2836	22	ABE62719	Drosophila melanog

ALIGNMENTS

RESULT 1	AAE23839	AAE23839 standard; peptide; 24 AA.
ID	AAE23839	standard; peptide; 24 AA.
XX	AAE23839	
AC	AAE23839	
XX	AAE23839	
DT	10-SEP-2002	(first entry)
XX	10-SEP-2002	(first entry)
DE	Human zsig33-linker peptide #1.	
XX	Human zsig33-linker peptide #1.	
KW	Human; zsig33-like peptide; gastric contractility; nutrient uptake;	
KW	growth hormone; digestive enzyme; restorative therapy; gene therapy;	
KW	protein therapy; gastrointestinal; endocrine; anabolic.	
XX	Human; zsig33-like peptide; gastric contractility; nutrient uptake;	
OS	Homo sapiens.	
XX	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Region	7..18
FT	FT	/note= "Hydrophilic region"
XX	US2002055156-A1.	
XX	US2002055156-A1.	
PD	09-MAY-2002.	
XX	09-MAY-2002.	
PF	10-MAY-2001; 2001US-0853253.	
XX	10-MAY-2001; 2001US-0853253.	
PR	11-MAY-2000; 2000US-203300P.	
XX	11-MAY-2000; 2000US-203300P.	
PA	(JASP/) JASPERS S R.	
PA	(SHEP/) SHEPPARD P O.	
PA	(DEIS/) DEISHER T A.	
PA	(BISH/) BISHOP P D.	

```

XX PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX PR WPI: 2002-443750/47.
XX PA N-PSDB; AAD38239.
XX DR
XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
XX FT contractility, nutrient uptake, growth hormones and/or secretion of
XX PT digestive/pancreatic enzymes and hormones -
XX DR
XX Claim 1: Page 28; 34pp; English.
XX PS
XX The invention relates to zsig33-like peptides and their corresponding
XX CC nucleic acids and methods for modulating gastric contractility, nutrient
XX CC uptake, growth hormones, secretion of digestive enzymes and hormones.
XX CC The sequences of the invention are used in the prevention, diagnosis and
XX CC treatment of diseases associated with inappropriate ZSIG33 expression.
XX CC The nucleic acids of the invention and their complements are used as
XX CC DNA probes in diagnostic assays to detect and quantitate the presence
XX CC of similar nucleic acids in samples, and therefore which patients may be
XX CC in need of restorative therapy. The ZSIG33 peptides are used as antigens
XX CC in the production of antibodies against ZSIG33 and in assays to identify
XX CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
XX CC and antagonists are used to down regulate expression and activity. The
XX CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
XX CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
XX CC assay (ELISA)). The peptides and nucleic acids of the invention are used
XX CC to modulate gastric contractility, nutrient uptake, growth hormones, the
XX CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
XX CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
XX CC and zsig33-like peptide is used in protein therapy. The present sequence
XX CC is human zsig33-like peptide, zsig33-linker peptide.
XX SQ Sequence 24 AA;
    Query Match 100.0%; Score 126; DB 23; Length 24;
    Best Local Similarity 100.0%; Pred. No. 5.7e-12;
    Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ALAGWLRPEDGGQAGAEDELEVR 24
    |||||
Db 1 ALAGWLRPEDGGQAGAEDELEVR 24
    |||||
RESULT 2
AAE15884
ID AAE15884 standard; peptide; 24 AA.
XX AC AAE15884;
XX DT 26-MAR-2002 (first entry)
XX DE Human zsig33-linker peptide #1.
XX KW Human: zsig33-like peptide; ZS33LP; immunity; developmental process;
XX KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
XX KW adsorption enhancer; gastrointestinal disease; growth related disease;
XX KW inflammation; gene therapy; growth regulation; blood vessel formation;
XX KW HIV; zsig33-linker peptide.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Region 6..22
XX FT /note= "Hydrophilic antigenic site"
XX FT Region 7..18
XX FT /note= "Hydrophilic region"
XX FT
XX KW WO200187933-A2.
XX PN 22-NOV-2001.
XX PD
XX FF 10-MAY-2001; 2001WO-US15091.

```

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XX 11-MAY-2000; 2000US-0569271.
XX PR (ZYMO ) ZYMOGENETICS INC.
XX PA
XX PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX DR WPI: 2002-082982/11.
XX DR N-PSDB; AAD25760.
XX PS
XX New polypeptides, useful for modulating gastric contractility, nutrient
XX FT uptake, pancreatic secretion of hormones, digestive enzymes and
XX PT treating gastrointestinal and growth related diseases, comprises
XX CC zsig33-like peptides -
XX PS
XX Claim 1a; Page 81; 89pp; English.
XX CC The invention relates to zsig33-like peptides (ZS33LP) including
XX CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and
XX CC zsig33-epsilon peptides and nucleic acid molecules encoding such
XX CC zsig33-like peptides. ZS33LP peptides activate the immune system
XX CC in boosting immunity to infectious diseases, treating immunocompromised
XX CC patients such as human immunodeficiency virus (HIV) patients, in
XX CC improving vaccines and in treatment of bacterial, viral, protozoal and
XX CC fungal infections. Peptides of the invention are used to identify and
XX CC isolate receptors involved in growth regulation in the liver, blood
XX CC vessel formation and other developmental processes. They are useful for
XX CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
XX CC growth and/or differentiation of tumour cells, as additives to anti-
XX CC hypoglycaemic preparations containing glucose and as adsorption
XX CC enhancers for oral drugs which require fast nutrient action and to
XX CC stimulate glucose-induced insulin release. They are also useful as
XX CC research reagents for the expansion, differentiation, growth factor and
XX CC hormone secretion and/or cell-cell interactions of tissues associated
XX CC with gastrointestinal system, brain and central nervous system. These
XX CC molecules are useful for treating dysfunction associated with contractile
XX CC tissues or to suppress or enhance contractility in vivo and to treat
XX CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
XX CC acids and/or antibodies are useful for treating disorders associated
XX CC with gastrointestinal contractility, secretion of digestive enzymes,
XX CC hormone and acids, secretion of hormones in the pancreas and/or brain,
XX CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
XX CC and regulation of nutrient absorption. Sequences of the invention are
XX CC useful in gene therapy. The present sequence is human zsig33-linker
XX CC peptide.
XX SQ Sequence 24 AA;
    Query Match 100.0%; Score 126; DB 23; Length 24;
    Best Local Similarity 100.0%; Pred. No. 5.7e-12;
    Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ALAGWLRPEDGGQAGAEDELEVR 24
    |||||
Db 1 ALAGWLRPEDGGQAGAEDELEVR 24
    |||||
RESULT 3
AAE33410
ID AAE33410 standard; Protein; 91 AA.
XX AC AAE33410;
XX DT 02-APR-2003 (first entry)
XX DE Human exon 3-deleted ghrelin protein..
XX KW Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
XX KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
XX KW cancer; human.
XX OS Homo sapiens.

```

PN WO20020387-A1.
 XX 14-NOV-2002.
 XX 10-MAY-2002; 2002WO-AU00582.
 XX 10-MAY-2001; 2001AU-0004919.
 PR 17-DEC-2001; 2001AU-0009567.
 XX (UYOU-) UNIV QUEENSLAND TECHNOLOGY.
 XX Chopin LK, Jeffery PL, Herington AC;
 XX WPI; 2003-1111957/10.
 DR N-PSDB; AAD50726.
 XX Identifying a cancer cell or tissue for treating prostate, ovarian,
 PT breast cancer, or benign prostatic hyperplasia, by detecting the
 PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
 PT 1b proteins or nucleic acids -
 XX Claim 14; Page 34; 50pp; English.
 XX The invention relates to a method for identifying a cancer cell or
 CC tissue of the reproductive system by detecting expression of a ghrelin,
 CC an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic
 CC acids. The antibodies, exon 3-deleted form of preproghrelin and
 CC antagonists are useful for treating cancer of the reproductive system
 CC such as prostate, ovarian, breast, cervical or uterine cancer,
 CC choriocarcinoma or benign prostatic hyperplasia. The present sequence
 CC is human exon 3-deleted ghrelin protein.
 XX Sequence 91 AA;
 SQ Query Match 100.0%; Score 126; DB 24; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRLPEDGGQAGAEDELEVR 24
 DB 52 ALAGWLRLPEDGGQAGAEDELEVR 75
 RESULT 4
 AAB60517
 ID AAB60517 standard; Protein; 116 AA.
 XX AAB60517;
 XX 24-APR-2001 (first entry)
 XX Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
 XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX Homo sapiens.
 OS WO200107475-A1.
 XX 01-FEB-2001.
 XX 24-JUL-2000; 2000WO-JP04907.
 XX 23-JUL-1999; 95JP-0210002.
 PR 29-NOV-1999; 95JP-0338841.
 PR 26-APR-2000; 2000JP-0126623.
 XX (KANG/) KANGAWA K.
 PA Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 XX WPI; 1999-070071/06.

DR WPI; 2001-159704/16.
 DR N-PSDB; AAF59647.
 XX New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 XX Claim 3; Page 186-187; 210pp; Japanese.
 XX The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX Sequence 116 AA;
 SQ Query Match 100.0%; Score 126; DB 22; Length 116;
 Best Local Similarity 100.0%; Pred. No. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRLPEDGGQAGAEDELEVR 24
 DB 51 ALAGWLRLPEDGGQAGAEDELEVR 74
 RESULT 5
 AAW87991
 ID AAW87991 standard; Protein; 117 AA.
 XX AAW87991;
 AC 07-APR-1999 (first entry)
 DT Protein designated zsig33.
 XX Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
 KW nutrient absorption regulation; obesity; metabolic disorder.
 KW Homo sapiens.
 OS Key Location/Qualifiers
 FH Key 1..23
 FT Peptide /note= "signal peptide"
 FT Protein 24..117
 FT /note= "mature protein"
 XX WO9842840-A1.
 XX 01-OCT-1998.
 XX 23-MAR-1998; 98WO-US05620.
 XX 24-MAR-1997; 97US-0822897.
 PR 24-MAR-1997; 97US-0041102.
 XX (ZYMO) ZYMOGENETICS INC.
 PA Delisher TA, Sheppard PO;
 XX WPI; 1999-070071/06.

DR N-PSDB; AAX04550.

XX Human polypeptide having homology to motilin, zsig33 - useful e.g.

PT to treat gastrointestinal motility disorders, obesity etc. and to

PT identify antagonists to treat gastrointestinal hypermotility

PS Claim 13; Page 55-56; 69pp; English.

XX

CC The present sequence represents a protein designated zsig33. The nucleic

CC acids are strongly expressed in stomach tissue. The polypeptide (or

CC allelic variants/orthologs) can be used to stimulate gastric motility,

CC measured as increased transit time or gastric emptying of an ingested

CC substance in mammals. The products are used to treat disorders associated

CC with gastrointestinal cell contractility, secretion of digestive

CC enzymes/acids, gastrointestinal inflammation, reflux disease and nutrient

CC absorption regulation. Zsig33 polypeptides may also be important

CC neurologically, since the family of gut-brain peptides to which the

CC homologous protein motilin belongs has been associated with neurological

CC and CNS functions. They may therefore be used e.g. to regulate satiety

CC or treat obesity and other metabolic disorders where neurological

CC feedback modulates nutritional absorption. They are useful to identify

CC zsig33 agonists, antagonists and ligands and to produce antibodies.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 126; DB 20; Length 117;

Best Local Similarity 100.0%; Pred. NO. 3.4e-11;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24

DB 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 6

AAY87236

ID AAY87236 standard; Protein; 117 AA.

XX

AC AAY87236;

XX

DT 11-MAY-2000 (first entry)

XX

DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.

XX

KW Human; signal peptide-containing protein; HSPP; diagnosis: cancer;

KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;

KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;

KW antiasthmatic; gene therapy; cell proliferation; neurodegenerative disorder;

KW reproductive disorder; developmental disorder; arteriosclerosis;

KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;

KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;

KW Parkinson's disease; Huntington's disease; muscular dystrophy;

XX

OS Homo sapiens.

XX

PN WO200000610-A2.

XX

PD 06-JAN-2000.

XX

PF 25-JUN-1999; 99WO-US14484.

XX

XX 26-JUN-1998; 98US-0090762.

PR 31-JUL-1998; 98US-0094983.

PR 01-OCT-1998; 98US-0102686.

PR 11-DEC-1998; 98US-0112129.

XX

PA (INCYTE) INCYTE PHARM INC.

XX

XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;

PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;

PI Bandman O;

XX WPI; 2000-160673/14.

DR N-PSDB; AAZ98121.

XX

PT New human signal peptide-containing proteins useful in treatment,

PT prevention and diagnosis of e.g. cancer, inflammation and

PT cardiovascular disease

XX

PS Claim 1; Page 168-169; 327pp; English.

XX

CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the

CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have

CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,

CC neuroprotective, cardiovascular and antiasthmatic activities, and can

CC be used in gene therapy. HSPPs can be used to treat or prevent disorders

CC associated with decreased activity or function of HSPP. Antagonists of

CC HSPP are used to treat or prevent disorders associated with increased

CC activity or function of HSPP. Such diseases include cell proliferation

CC (including cancer), inflammation, cardiovascular, neurological,

CC reproductive or developmental disorders, (e.g. arteriosclerosis,

CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,

CC asthma, Crohn's disease, microbial or other infections, congestive or

CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's

CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP

CC nucleic acids can be used for the recombinant production of HSPP, for

CC detecting HSPP in standard hybridisation and amplification assays (for

CC diagnosis and monitoring), in gene therapy, as antisense,

CC triplex-forming or ribozyme therapeutics, for detecting related sequences

CC or genetic variations, and for chromosomal mapping. HSPP are also used

CC to raise specific antibodies (Ab) and to screen for agonists and

CC antagonists (potential therapeutic agents). Ab are used to diagnose, or

CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic

CC antagonists, in competitive drug screens, and for purification of HSPP

CC from natural sources.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 126; DB 21; Length 117;

Best Local Similarity 100.0%; Pred. NO. 3.4e-11;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24

DB 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 7

AAM38890

ID AAM38890 standard; Protein; 117 AA.

XX

AC AAM38890;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 2035.

XX

DE Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

XX 26-JUL-2001.

XX

XX 26-DEC-2000; 2000WO-US34263.

PF

XX 21-JAN-2000; 2000US-0488725.

PR 23-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB; AAI58046.
 XX
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 PT
 PS Example 3; SEQ ID NO 2035; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAW42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activity, chemotactic/chemokinetic activity, haemostatic
 CC Activin/inhibin activity, cancer diagnosis and therapy, drug screening,
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: the sequence data for this patent did not form part of the printed
 CC specification.
 XX
 XX Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 126; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 Db 52 ALAGWLRPEDGGQAGAEDELEVR 75
 RESULT 8
 AAB62649
 ID AAB62649 standard; Protein; 117 AA.
 XX
 AC AAB62649;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Human zsig33 polypeptide.
 XX
 KW zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
 KW G-protein coupled receptor.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 24..37
 FT Peptide /note= "specifically claimed fragment that binds to
 FT the GHS-R"
 XX
 PN W0200138355-A2.

XX 31-MAY-2001.
 PD
 XX 22-NOV-2000; 2000WO-US32074.
 PF
 XX 22-NOV-1999; 99US-0166765.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 PI WPI: 2001-355879/37.
 DR N-PSDB; AAF83678.
 DR
 XX
 PT Forming reversible peptide receptor complex for purifying cell and
 PT peptides, stimulating signal transduction and modulating hormone
 PT secretion, involves contacting a receptor with zsig33 polypeptide -
 XX
 PS Claim 1; Page 93-94; 111pp; English.
 XX
 CC The invention relates to a method of forming a reversible peptide-
 CC receptor complex that involves providing an immobilized receptor, and
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
 CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
 CC is useful for purifying cells, purifying a peptide, stimulating signal
 CC transduction in a cell expressing a receptor. It is also useful for
 CC modulating secretion of hormones, neural development and/or utilization,
 CC gastric contractility, nutrient uptake, secretion of digestive and
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
 CC hormone secretion in a mammal having a disease associated with abnormal
 CC levels of growth hormone, such as osteoporosis, bone repair, bone
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,
 CC protein catabolic responses after surgery, cachexia, protein loss,
 CC dwarfism, wound healing and ovulation induction, treating a mammal having
 CC a metabolic disorder requiring neurological feedback, such as satiety
 CC regulation, glucose absorption and metabolism and neuropathy-associated
 CC gastrointestinal disorders, and stimulating glucose-induced insulin
 CC release in a mammal. The present sequence represents the human zsig33
 CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 126; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 Db 52 ALAGWLRPEDGGQAGAEDELEVR 75
 RESULT 9
 AAB20101
 ID AAB20101 standard; Protein; 117 AA.
 XX
 AC AAB20101;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Zsig33 protein.
 XX
 KW SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
 KW nutritional absorption modulator; growth hormone secretagogue;
 KW therapy; human.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1..23
 FT Peptide /label= Signal_peptide
 FT Protein 24..117

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FT Peptide /label= Mature_protein
FT 24..34
FT /label= SGIP_peptide
FT /note= "this peptide is claimed in Claim 1"
PN WO200100830-A1.
XX
XX
XX 04-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-US18306.
XX
XX 30-JUN-1999; 99US-0345157.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
XX WPI; 2001-123010/13.
XX N-PSDB; AAF30033.
XX
XX Novel variants of SGIP peptides for modulating contractility in
XX duodenum or jejunum tissue, pancreatic secretion of hormones and
XX digestive enzymes, inducing growth hormone secretion or modulating
XX gastric emptying -
XX
XX Disclosure: 54; 61pp; English.
XX
XX The present sequence is that of zsig33, a secreted protein with
XX homology to motilin (see AAB20102). Zsig33 is expressed at high
XX levels in the stomach, and at lower levels in the small intestine
XX and pancreas. A novel peptide fragment of zsig33, termed SGIP (see
XX AAB20100), is claimed. SGIP is a ligand for growth hormone
XX secretagogue receptor, and is therefore useful for modulating
XX secretion of growth hormone and insulin like growth factor 1.
XX SGIP, and variant SGIP peptides, are used in claimed methods for
XX stimulating contractility in duodenum or jejunum tissue,
XX modulating pancreatic secretion of hormones and digestive enzymes,
XX inducing growth hormone secretion, and modulating gastric emptying.
XX
XX Sequence 117 AA;

Query Match 100.0%; Score 126; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. NO. 3.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
DB 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 10
AAB60511
ID AAB60511 standard; Protein; 117 AA.
XX
XX AAB60511;
XX
XX 24-APR-2001 (first entry)
XX
XX Human ghrelin preproprotein, SEQ ID NO:5.
XX
XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
XX calcium concentration elevation; infant growth disorder;
XX growth hormone deficiency.
XX
XX Homo sapiens.
XX
XX WO200107475-A1.
XX
XX 01-FEB-2001.
XX
XX 24-JUL-2000; 2000WO-JP04907.
XX
XX 23-JUL-1999; 99JP-0210002.
XX

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PR 29-NOV-1999; 99JP-0338841.
PR 26-APR-2000; 2000JP-0126623.
PA (KANG/) KANGAWA K.
XX
XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
XX
XX WPI; 2001-159704/16.
XX N-PSDB; AAF59645.
XX
XX New peptide compounds which induce growth hormone secretion and
XX elevate cell calcium concentrations, useful in treatment and diagnosis
XX of infant growth disorders -
XX
XX Claim 3; Page 182; 210pp; Japanese.
XX
XX The invention relates to a novel peptide compound or its salt which
XX induces the secretion of growth hormone and/or elevates calcium ion
XX concentration in cells. The peptides are ghrelin homologues and are
XX characterised in that at least one amino acid has been substituted by
XX a modified amino acid and/or a non-amino acid compound. The invention
XX also encompasses the unmodified peptides; the DNA encoding the peptides;
XX vectors and host cells comprising such DNA; a method of producing the
XX peptides comprising recombinant production, optionally followed by
XX chemical modification; an antibody specific for a peptide of the
XX invention; and an assay and kit for detecting the peptides. The peptides
XX of the invention are useful for treating and/or diagnosing diseases
XX caused by a deficiency in growth hormone expression or activity. In
XX particular, they are useful for promoting infant growth due to growth
XX hormone deficiency. The compounds of the invention are safe with
XX no accompanying side effects. The present sequence represents a
XX ghrelin-type growth hormone secretagogue (GHS) precursor protein
XX of the invention.
XX
XX Sequence 117 AA;

Query Match 100.0%; Score 126; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. NO. 3.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
DB 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 11
AAB78319
ID AAB78319 standard; Protein; 117 AA.
XX
XX ABB78319;
XX
XX 05-DEC-2002 (first entry)
XX
XX Amino acid sequence of a human zsig33.
XX
XX Short gastrointestinal peptide; SGIP; zsig33; motilin.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX /note= "signal peptide"
XX Protein 24..119
XX /note= "mature protein"
XX
XX US6420521-B1.
XX
XX 16-JUL-2002.
XX
XX 30-JUN-2000; 2000US-0608810.
XX
XX 30-JUN-1999; 99US-141592P.
XX

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PA (ZYMO) ZYMOGENETICS INC.
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 PI WPI: 2002-634794/68.
 XX N-PSDB; ABV72214.
 DR New Short Gastrointestinal Peptide, which has homology to motilin,
 XX useful for preventing, diagnosing and treating gastrointestinal
 PT disorders -
 XX Disclosure: Columns 39-40; 23pp; English.
 PS The present sequence represents human zsig33. The specification describes
 CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.
 CC SGIP has homology to motilin. The SGIP peptide may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate SGIP expression. For example, SGIP may be used to treat
 CC disorders associated with decreased expression by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of SGIP by
 CC expressing inactive proteins or to supplement the patients own production
 CC of SGIP. SGIP may also be used as an antigen in the production of
 CC antibodies against SGIP and in assays to identify modulators of SGIP
 CC expression and activity. The anti-SGIP antibodies, agonists and
 CC antagonists may also be used to regulate expression and activity. The
 CC anti-SGIP antibodies may also be used as diagnostic agents for detecting
 CC the presence of SGIP in samples.
 XX SQ Sequence 117 AA;
 SQ Query Match 100.0%; Score 126; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 DB 52 ALAGWLRPEDGGQAGAEDELEVR 75
 RESULT 12
 AAE23838
 ID AAE23838 standard; Protein; 117 AA.
 XX AC AAE23838;
 XX 10-SEP-2002 (first entry)
 XX Human zsig33 protein.
 DE Human;
 XX Human; zsig33-like peptide; gastric contractility; nutrient uptake;
 KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
 KW protein therapy; gastrointestinal; endocrine; anabolic.
 XX Homo sapiens.
 OS US2002055156-A1.
 XX US2002055156-A1.
 XX 09-MAY-2002.
 XX 10-MAY-2001; 2001US-0853253.
 XX 11-MAY-2000; 2000US-203300P.
 XX (JASP/) JASPERS S R.
 PA (SHEP/) SHEPPARD P O.
 PA (DEIS/) DEISHER T A.
 PA (BISH/) BISHOP P D.
 XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 PI WPI: 2002-443750/47.
 XX N-PSDB; AAD38238.
 XX

PT ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
 PT contractility, nutrient uptake, growth hormones and/or secretion of
 XX digestive/pancreatic enzymes and hormones -
 PS Disclosure: Page 27; 34pp; English.
 XX The invention relates to zsig33-like peptides and their corresponding
 CC nucleic acids and methods for modulating gastric contractility, nutrient
 CC uptake, growth hormones, secretion of digestive enzymes and hormones.
 CC The sequences of the invention are used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate zsig33 expression.
 CC The nucleic acids of the invention and their components are used as
 CC DNA probes in diagnostic assays to detect and quantitate the presence
 CC of similar nucleic acids in samples, and therefore which patients may be
 CC in need of restorative therapy. The zsig33 peptides are used as antigens
 CC in the production of antibodies against zsig33 and in assays to identify
 CC modulators of zsig33 expression and activity. The anti-zsig33 antibodies
 CC and antagonists are used to down regulate expression and activity. The
 CC anti-zsig33 antibodies are also used as diagnostic agents for detecting
 CC the presence of zsig33 in samples (e.g. by enzyme linked immunosorbent
 CC assay (ELISA)). The peptides and nucleic acids of the invention are used
 CC to modulate gastric contractility, nutrient uptake, growth hormones, the
 CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
 CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
 CC and zsig33-like peptide is used in protein therapy. The present sequence
 XX is human zsig33 protein.
 XX SQ Sequence 117 AA;
 SQ Query Match 100.0%; Score 126; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 DB 52 ALAGWLRPEDGGQAGAEDELEVR 75
 RESULT 13
 AAE15883
 ID AAE15883 standard; Protein; 117 AA.
 XX AC AAE15883;
 XX 26-MAR-2002 (first entry)
 XX Human zsig33 protein.
 DE Human;
 XX Human; zsig33-like peptide; zsig33LP; immunity; developmental process;
 KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
 KW adsorption enhancer; gastrointestinal disease; growth related disease;
 KW inflammation; gene therapy; growth regulation; blood vessel formation;
 KW HIV; zsig33 protein.
 XX Homo sapiens.
 OS WO200187933-A2.
 XX WO200187933-A2.
 XX 22-NOV-2001.
 XX 10-MAY-2001; 2001WO-US15091.
 XX 11-MAY-2000; 2000US-0569271.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
 PI

XX WPI; 2002-082982/11.
DR N-PSDB; RAD25759.
XX
XX New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and
PT treating gastrointestinal and growth related diseases, comprises
PT zsig33-like peptides -
XX
XX Disclosure; Page 80-81; 89pp; English.
XX
XX The invention relates to zsig33-like peptides (ZS33LP) including
CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and
CC zsig33-epsilon peptides and nucleic acid molecules encoding such
CC zsig33-like peptides. ZS33LP peptides activate the immune system
CC in boosting immunity to infectious diseases, treating immunocompromised
CC patients such as human immunodeficiency virus (HIV) patients, in
CC improving vaccines and in treatment of bacterial, viral, protozoal and
CC fungal infections. Peptides of the invention are used to identify and
CC isolate receptors involved in growth regulation in the liver, blood
CC vessel formation and other developmental processes. They are useful for
CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
CC growth and/or differentiation of tumour cells, as additives to anti-
CC hypoglycaemic preparations containing glucose and as adsorption
CC enhancers for oral drugs which require fast nutrient action and to
CC stimulate glucose-induced insulin release. They are also useful as
CC research reagents for the expansion, differentiation, growth factor and
CC hormone secretion and/or cell-cell interactions of tissues associated
CC with gastrointestinal system, brain and central nervous system. These
CC molecules are useful for treating dysfunction associated with contractile
CC tissues or to suppress or enhance contractility in vivo and to treat
CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
CC acids and/or antibodies are useful for treating disorders associated
CC with gastrointestinal contractility, secretion of digestive enzymes,
CC hormone and acids, secretion of hormones in the pancreas and/or brain,
CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
CC and regulation of nutrient absorption. Sequences of the invention are
CC useful in gene therapy. The present sequence is human zsig33 protein.
XX
XX Sequence 117 AA;
SQ

Query Match 100.0%; Score 126; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ALAGWLRPEDGGQAGAEDELEVR 24
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75
|||||

RESULT 14
ABU66790
ID ABU66790 standard; Protein; 117 AA.
XX
XX AC ABU66790;
XX
XX DT 23-MAY-2003 (first entry)
XX
XX DE Human PRO polypeptide #221.
XX
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytostatic.
XX
XX KW Homo sapiens.
OS
XX FN US2003036180-A1.
XX
XX XX 20-FEB-2003.
XX
XX PF 09-MAY-2002; 2002US-0143114.
XX

31-MAR-1997; 97WO-US05230.
12-JUN-1998; 98WO-US12456.
14-JUL-1998; 98WO-US14552.
28-AUG-1998; 98WO-US17888.
10-SEP-1998; 98WO-US18824.
14-SEP-1998; 98WO-US19093.
14-SEP-1998; 98WO-US19094.
14-SEP-1998; 98WO-US19177.
16-SEP-1998; 98WO-US19330.
17-SEP-1998; 98WO-US19437.
07-OCT-1998; 98WO-US21141.
29-OCT-1998; 98WO-US22991.
29-OCT-1998; 98WO-US22992.
20-NOV-1998; 98WO-US24855.
01-DEC-1998; 98WO-US25108.
05-JAN-1999; 98WO-US00106.
08-MAR-1999; 98WO-US05028.
10-MAR-1999; 98WO-US05190.
20-APR-1999; 98WO-US08615.
14-MAY-1999; 98WO-US10733.
02-JUN-1999; 98WO-US12252.
01-SEP-1999; 98WO-US20111.
08-SEP-1999; 98WO-US20594.
13-SEP-1999; 98WO-US20944.
15-SEP-1999; 98WO-US21090.
15-SEP-1999; 98WO-US21547.
05-OCT-1999; 98WO-US23089.
29-NOV-1999; 98WO-US28214.
30-NOV-1999; 98WO-US28313.
30-NOV-1999; 98WO-US28409.
01-DEC-1999; 98WO-US28301.
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02-DEC-1999; 98WO-US28651.
02-DEC-1999; 98WO-US28564.
02-DEC-1999; 98WO-US28565.
16-DEC-1999; 98WO-US30095.
20-DEC-1999; 98WO-US30911.
20-DEC-1999; 98WO-US30999.
22-DEC-1999; 98WO-US30720.
30-DEC-1999; 98WO-US31243.
30-DEC-1999; 98WO-US31274.
05-JAN-2000; 2000WO-US00219.
06-JAN-2000; 2000WO-US00277.
06-JAN-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US03565.
18-FEB-2000; 2000WO-US04341.
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
24-FEB-2000; 2000WO-US04914.
24-FEB-2000; 2000WO-US05004.
01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05746.
02-MAR-2000; 2000WO-US05841.
10-MAR-2000; 2000WO-US06319.
15-MAR-2000; 2000WO-US06884.
20-MAR-2000; 2000WO-US07377.
21-MAR-2000; 2000WO-US07532.
30-MAR-2000; 2000WO-US08439.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-JUN-2000; 2000WO-US15264.
28-JUL-2000; 2000WO-US20710.
11-AUG-2000; 2000WO-US22031.
23-AUG-2000; 2000WO-US23522.
24-AUG-2000; 2000WO-US23328.
08-NOV-2000; 2000WO-US30952.
10-NOV-2000; 2000WO-US30873.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US06520.
01-MAR-2001; 2001WO-US06666.
25-MAY-2001; 2001WO-US17092.

01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0865034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI: 2003-332040/31.
 DR N-PSDB; ACA03823.
 XX
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification -
 XX
 PS Claim 12; Fig 442; 660pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. ABU66570-ABU66844 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsdIDEntry.html.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 126; DB 24; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGGQAGAELEVR 24
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 DB 52 ALAGWLRPDGGGQAGAELEVR 75

RESULT 15
 ABU67066
 ID ABU67066 standard; Protein; 117 AA.
 XX
 AC ABU67066;
 XX
 DT 27-MAY-2003 (first entry)
 XX
 DE Human secreted/transmembrane, PRO, protein SEQ ID 442.
 KW Human; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioindicator; tumour.
 XX
 OS Homo sapiens.
 XX
 PN US2003032155-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 03-MAY-2002; 2002US-0137865.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
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 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
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 PR 02-DEC-1999; 99WO-US28564.
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 PR 16-DEC-1999; 99WO-US30095.
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 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05061.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAR-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 01-JUN-2001; 2001US-0866034.
PR 05-JUN-2001; 2001US-0872035.
PR 14-JUN-2001; 2001US-0874503.
PR 19-JUN-2001; 2001US-0882636.
PR 21-JUN-2001; 2001US-0886342.
PR 18-JUL-2001; 2001US-0887879.
PR 06-AUG-2001; 2001US-0908827.
PR 09-AUG-2001; 2001US-0924419.
PR 16-AUG-2001; 2001US-0927796.
PR 19-DEC-2001; 2001US-0931836.
PR 2001US-0028072.
XX PA (GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2003-331925/31.
DR N-PSDB: ACA04244.

XX New secreted and transmembrane nucleic acids and polypeptides,
PT designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer
XX

PS Claim 12: Fig 442: 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid
CC further comprises the full-length coding sequence of the DNA deposited

CC under American Type Culture Collection (ATCC) accession number in a list
CC given in the specification. Also included are vectors and host
CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
CC antibodies, PRO extracellular domains and mature sequences, methods
CC of detecting PRO proteins, methods for stimulating the release of
CC TNF-alpha (tumour necrosis factor alpha) from human blood,
CC and the proliferation of differentiation of chondrocyte cells, the
CC proliferation of, or gene expression in pericyte cells, the release or
CC proteoglycans from cartilage, proliferation of inner ear utricular
CC supporting cells, the proliferation of T-lymphocyte cells, the release
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
CC proliferation of endothelial cells), a method for modulating the uptake
CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
CC a method for inhibiting the binding of A-peptide to factor VIIA,
CC or the differentiation of adipocyte cells, a method for detecting the
CC presence of a tumour in a mammal and an oligonucleotide probe derived
CC from any of the nucleotide sequences cited above. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
CC diabetic complications. The nucleic acids are useful as hybridisation
CC probes, in chromosome and gene mapping, and in generating antisense RNA
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors. Both are useful in tissue typing.
CC The present sequence represents a PRO protein of the invention.
XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 126; DB 24; Length 117;
Best Local Similarity 100.0%; Pred. NO. 3.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
|||||
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

Search completed: September 11, 2003, 17:25:02
Job time : 25.0267 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 6.41711 Seconds
(without alignments)
158.243 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 126
Sequence: 1 ALAGWLRPEDGGQAEGBEDEVLR 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents_AA:*
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 - 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
 - 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
 - 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
 - 5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
 - 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126	100.0	117	3	US-09-046-479-2
2	126	100.0	117	4	US-08-822-897C-2
3	126	100.0	117	4	US-09-608-810A-4
4	126	100.0	117	4	US-09-996-243-268
5	52	41.3	233	4	US-09-252-991A-27758
6	50	39.7	518	4	US-09-252-991A-23604
7	50	39.7	634	1	US-08-339-152A-17
8	50	39.7	653	2	US-08-339-152A-16
9	50	39.7	653	2	US-08-007-999B-3
10	50	39.7	653	2	US-08-689-276A-3
11	49	38.9	139	2	US-08-039-1988-10
12	48	38.1	428	4	US-09-252-991A-19723
13	47	37.3	283	4	US-09-252-991A-29700
14	47	37.3	405	4	US-09-252-991A-20326
15	47	37.3	468	4	US-09-252-991A-24394
16	46	36.5	341	4	US-09-252-991A-27327
17	46	36.5	517	4	US-09-252-991A-25921
18	46	36.5	1044	4	US-09-252-991A-18853
19	45.5	36.1	551	4	US-09-252-991A-20358
20	45.5	36.1	579	3	US-08-704-711A-1
21	45.5	36.1	579	4	US-09-521-220-1
22	45.5	36.1	582	3	US-08-704-711A-2
23	45.5	36.1	582	3	US-08-448-489-1
24	45.5	36.1	582	3	US-09-211-704A-9
25	45.5	36.1	582	4	US-09-521-220-2
26	45.5	36.1	582	4	US-09-391-104-28
27	45.5	36.1	591	2	US-08-889-402-1

28	45	35.7	174	4	US-09-252-991A-18600	Sequence 18600, A
29	45	35.7	494	1	US-08-464-340A-4	Sequence 4, Appl1
30	45	35.7	494	5	PCT-US94-08449A-4	Sequence 4, Appl1
31	45	35.7	1059	4	US-09-394-272-5	Sequence 5, Appl1
32	45	35.7	1185	3	US-08-664-962B-2	Sequence 2, Appl1
33	45	35.7	1185	3	US-09-311-743-2	Sequence 2, Appl1
34	44	34.9	298	4	US-09-252-991A-32302	Sequence 32302, A
35	43	34.1	118	3	US-08-482-304-12	Sequence 12, Appl
36	43	34.1	118	3	US-08-483-474-12	Sequence 12, Appl
37	43	34.1	140	3	US-08-482-304-9	Sequence 9, Appl1
38	43	34.1	140	3	US-08-483-474-9	Sequence 9, Appl1
39	43	34.1	162	4	US-09-252-991A-24838	Sequence 24838, A
40	43	34.1	191	4	US-09-252-991A-21437	Sequence 21437, A
41	43	34.1	212	3	US-09-154-083-4	Sequence 4, Appl1
42	43	34.1	247	4	US-09-252-991A-27419	Sequence 27419, A
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44	43	34.1	281	2	US-08-900-565-1	Sequence 1, Appl1
45	43	34.1	281	4	US-09-149-534-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 126; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
 |||||
 Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 2

US-08-822-897C-2
 ; Sequence 2, Application US/08822897C
 ; Patent No. 6380158
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Delsher, Theresa A.
 ; TITLE OF INVENTION: MOTILIN HOMOLOGS
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZymoGenetics, Inc.
 ; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/822,897C
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sawistak, Deborah A.
 ; REGISTRATION NUMBER: 37,438
 ; REFERENCE/DOCKET NUMBER: 97-04
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-442-6672
 ; TELEFAX: 206-442-6678
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 117 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-822-897C-2

Query Match 100.0%; Score 126; DB 4; Length 117;
 Best Local Similarity 100.0%; Pred. No. 9.9e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
 |||||
 Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 3

US-09-608-810A-4
 ; Sequence 4, Application US/09608810A
 ; Patent No. 6420521
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Jaspers, Stephen R.
 ; APPLICANT: Delsher, Theresa A.
 ; APPLICANT: Bishop, Paul D.
 ; TITLE OF INVENTION: SGIP PEPTIDES
 ; FILE REFERENCE: 99-51
 ; CURRENT APPLICATION NUMBER: US/09/608,810A
 ; CURRENT FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 60/141,592
 ; PRIOR FILING DATE: 1999-06-30
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 117
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(23)
 ; US-09-608-810A-4

Query Match 100.0%; Score 126; DB 4; Length 117;
 Best Local Similarity 100.0%; Pred. No. 9.9e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
 |||||
 Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 4

US-09-996-243-268
 ; Sequence 268, Application US/09996243
 ; Patent No. 6478825
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Grittisen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C13
 ; CURRENT APPLICATION NUMBER: US/09/996,243
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/084600

1	PRIOR FILING DATE: 1998-05-07	2	PRIOR APPLICATION NUMBER: 60/089655
2	PRIOR APPLICATION NUMBER: 60/087106	3	PRIOR FILING DATE: 1998-06-17
3	PRIOR FILING DATE: 1998-05-28	4	PRIOR APPLICATION NUMBER: 60/089801
4	PRIOR APPLICATION NUMBER: 60/087607	5	PRIOR FILING DATE: 1998-06-18
5	PRIOR FILING DATE: 1998-06-02	6	PRIOR APPLICATION NUMBER: 60/089907
6	PRIOR APPLICATION NUMBER: 60/087609	7	PRIOR FILING DATE: 1998-06-18
7	PRIOR FILING DATE: 1998-06-02	8	PRIOR APPLICATION NUMBER: 60/089908
8	PRIOR APPLICATION NUMBER: 60/087759	9	PRIOR FILING DATE: 1998-06-18
9	PRIOR FILING DATE: 1998-06-02	10	PRIOR APPLICATION NUMBER: 60/089947
10	PRIOR APPLICATION NUMBER: 60/087827	11	PRIOR FILING DATE: 1998-06-19
11	PRIOR FILING DATE: 1998-06-03	12	PRIOR APPLICATION NUMBER: 60/089948
12	PRIOR APPLICATION NUMBER: 60/088021	13	PRIOR FILING DATE: 1998-06-19
13	PRIOR FILING DATE: 1998-06-04	14	PRIOR APPLICATION NUMBER: 60/089952
14	PRIOR APPLICATION NUMBER: 60/088025	15	PRIOR FILING DATE: 1998-06-19
15	PRIOR FILING DATE: 1998-06-04	16	PRIOR APPLICATION NUMBER: 60/090246
16	PRIOR APPLICATION NUMBER: 60/088026	17	PRIOR FILING DATE: 1998-06-22
17	PRIOR FILING DATE: 1998-06-04	18	PRIOR APPLICATION NUMBER: 60/090252
18	PRIOR APPLICATION NUMBER: 60/088028	19	PRIOR FILING DATE: 1998-06-22
19	PRIOR FILING DATE: 1998-06-04	20	PRIOR APPLICATION NUMBER: 60/090254
20	PRIOR APPLICATION NUMBER: 60/088029	21	PRIOR FILING DATE: 1998-06-22
21	PRIOR FILING DATE: 1998-06-04	22	PRIOR APPLICATION NUMBER: 60/090349
22	PRIOR APPLICATION NUMBER: 60/088030	23	PRIOR FILING DATE: 1998-06-23
23	PRIOR FILING DATE: 1998-06-04	24	PRIOR APPLICATION NUMBER: 60/090355
24	PRIOR APPLICATION NUMBER: 60/088033	25	PRIOR FILING DATE: 1998-06-23
25	PRIOR FILING DATE: 1998-06-04	26	PRIOR APPLICATION NUMBER: 60/090429
26	PRIOR APPLICATION NUMBER: 60/088326	27	PRIOR FILING DATE: 1998-06-24
27	PRIOR FILING DATE: 1998-06-04	28	PRIOR APPLICATION NUMBER: 60/090431
28	PRIOR APPLICATION NUMBER: 60/088167	29	PRIOR FILING DATE: 1998-06-24
29	PRIOR FILING DATE: 1998-06-05	30	PRIOR APPLICATION NUMBER: 60/090435
30	PRIOR APPLICATION NUMBER: 60/088202	31	PRIOR FILING DATE: 1998-06-24
31	PRIOR FILING DATE: 1998-06-05	32	PRIOR APPLICATION NUMBER: 60/090444
32	PRIOR APPLICATION NUMBER: 60/088212	33	PRIOR FILING DATE: 1998-06-24
33	PRIOR FILING DATE: 1998-06-05	34	PRIOR APPLICATION NUMBER: 60/090445
34	PRIOR APPLICATION NUMBER: 60/088217	35	PRIOR FILING DATE: 1998-06-24
35	PRIOR FILING DATE: 1998-06-05	36	PRIOR APPLICATION NUMBER: 60/090472
36	PRIOR APPLICATION NUMBER: 60/088655	37	PRIOR FILING DATE: 1998-06-24
37	PRIOR FILING DATE: 1998-06-09	38	PRIOR APPLICATION NUMBER: 60/090535
38	PRIOR APPLICATION NUMBER: 60/088734	39	PRIOR FILING DATE: 1998-06-24
39	PRIOR FILING DATE: 1998-06-10	40	PRIOR APPLICATION NUMBER: 60/090540
40	PRIOR APPLICATION NUMBER: 60/088738	41	PRIOR FILING DATE: 1998-06-24
41	PRIOR FILING DATE: 1998-06-10	42	PRIOR APPLICATION NUMBER: 60/090542
42	PRIOR APPLICATION NUMBER: 60/088742	43	PRIOR FILING DATE: 1998-06-24
43	PRIOR FILING DATE: 1998-06-10	44	PRIOR APPLICATION NUMBER: 60/090557
44	PRIOR APPLICATION NUMBER: 60/088810	45	PRIOR FILING DATE: 1998-06-24
45	PRIOR FILING DATE: 1998-06-10	46	PRIOR APPLICATION NUMBER: 60/090576
46	PRIOR APPLICATION NUMBER: 60/088824	47	PRIOR FILING DATE: 1998-06-25
47	PRIOR FILING DATE: 1998-06-10	48	PRIOR APPLICATION NUMBER: 60/090678
48	PRIOR APPLICATION NUMBER: 60/088826	49	PRIOR FILING DATE: 1998-06-25
49	PRIOR FILING DATE: 1998-06-10	50	PRIOR APPLICATION NUMBER: 60/090690
50	PRIOR APPLICATION NUMBER: 60/088858	51	PRIOR FILING DATE: 1998-06-25
51	PRIOR FILING DATE: 1998-06-11	52	PRIOR APPLICATION NUMBER: 60/090694
52	PRIOR APPLICATION NUMBER: 60/088861	53	PRIOR FILING DATE: 1998-06-25
53	PRIOR FILING DATE: 1998-06-11	54	PRIOR APPLICATION NUMBER: 60/090695
54	PRIOR APPLICATION NUMBER: 60/088876	55	PRIOR FILING DATE: 1998-06-25
55	PRIOR FILING DATE: 1998-06-11	56	PRIOR APPLICATION NUMBER: 60/090696
56	PRIOR APPLICATION NUMBER: 60/089105	57	PRIOR FILING DATE: 1998-06-25
57	PRIOR FILING DATE: 1998-06-12	58	PRIOR APPLICATION NUMBER: 60/090862
58	PRIOR APPLICATION NUMBER: 60/089440	59	PRIOR FILING DATE: 1998-06-26
59	PRIOR FILING DATE: 1998-06-16	60	PRIOR APPLICATION NUMBER: 60/090863
60	PRIOR APPLICATION NUMBER: 60/089512	61	PRIOR FILING DATE: 1998-06-26
61	PRIOR FILING DATE: 1998-06-16	62	PRIOR APPLICATION NUMBER: 60/091360
62	PRIOR APPLICATION NUMBER: 60/089514	63	PRIOR FILING DATE: 1998-07-01
63	PRIOR FILING DATE: 1998-06-16	64	PRIOR APPLICATION NUMBER: 60/091478
64	PRIOR APPLICATION NUMBER: 60/089532	65	PRIOR FILING DATE: 1998-07-02
65	PRIOR FILING DATE: 1998-06-17	66	PRIOR APPLICATION NUMBER: 60/091544
66	PRIOR APPLICATION NUMBER: 60/089538	67	PRIOR FILING DATE: 1998-07-01
67	PRIOR FILING DATE: 1998-06-17	68	PRIOR APPLICATION NUMBER: 60/091519
68	PRIOR APPLICATION NUMBER: 60/089598	69	PRIOR FILING DATE: 1998-07-02
69	PRIOR FILING DATE: 1998-06-17		

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 126; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAGWLRPDGGGGAEGAELEVR 24
|||||
Db 52 ALAGWLRPDGGGGAEGAELEVR 75

RESULT 5

US-09-252-991A-27758
; Sequence 27758, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27758
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27758

Query Match 41.3%; Score 52; DB 4; Length 233;
Best Local Similarity 72.7%; Pred. No. 2.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWLRPDGGQA 14
|||||
Db 203 GWLRPDGSR 213

RESULT 6

US-09-252-991A-23604
; Sequence 23604, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23604
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23604

Query Match 39.7%; Score 50; DB 4; Length 518;
Best Local Similarity 45.5%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 3 AGWLRPDGGGGAEGAELEVR 24

Db 412 AGWAQPEPGCGGGAERLHRR 433
||| :||| | | : | |

RESULT 7

US-08-339-152A-17
; Sequence 17, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/339.152A
; APPLICATION NUMBER: US/08/339.152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-152A-17

Query Match 39.7%; Score 50; DB 1; Length 634;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGGAEGAEDELEV 23
||:|||||
Db 213 GGRAEGEDEEV 225

RESULT 8

US-08-339-152A-16
; Sequence 16, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,152A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 0609.4120000
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-152A-16

Query Match 39.7%; Score 50; DB 1; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGQAGAEDELEV 23
||:|||||
Db 233 GGAEGGEDEEV 245

RESULT 9
US-08-007-999B-3
Sequence 3, Application US/08007999B
Patent No. 5851787
GENERAL INFORMATION:
APPLICANT: Masco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Tanzil, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,999B
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,642
FILING DATE: 20-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 0609.3520002/JAG/GKT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2571
TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-007-999B-3

Query Match 39.7%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGQAGAEDELEV 23
||:|||||
Db 233 GGAEGGEDEEV 245

RESULT 10
US-08-689-276A-3
Sequence 3, Application US/08689276A
Patent No. 5891991
GENERAL INFORMATION:
APPLICANT: Masco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Tanzil, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,276A
FILING DATE: 06-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,999
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,642
FILING DATE: 20-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3520003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2571
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-689-276A-3

Query Match 39.7%; Score 50; DB 2; Length 653;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGGAEGAEDELEV 23
11:1111111111
Db 233 GGGAEGGEDEEV 245

RESULT 11

US-08-039-1988-10
; Sequence 10, Application US/080391988
; Patent No. 5858725
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODIES
; TITLE OF INVENTION: RECOMBINANT PCR STRATEGY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/039,1988
; FILING DATE: 29-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01744
; FILING DATE: 08-OCT-91
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-039-1988-10

Query Match 38.9%; Score 49; DB 2; Length 139;
Best Local Similarity 61.5%; Pred. No. 4.4;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGGAEG 16
11:1111111111
Db 68 GWIDPEDGGTKYG 80

RESULT 12

US-09-252-991A-19723
; Sequence 19723, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19723
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19723

Query Match 38.1%; Score 48; DB 4; Length 428;
Best Local Similarity 52.2%; Pred. No. 22;
Matches 12; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LAGWLRPEDGGGAEGAEDELEVR 24
11:1111111111111111
Db 293 LALWSLPEDPRPADMAADELSDR 315

RESULT 13

US-09-252-991A-29700
; Sequence 29700, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29700
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29700

Query Match 37.3%; Score 47; DB 4; Length 283;
Best Local Similarity 58.8%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 AGWLRPEDGGGAEGAD 19
11:1111111111111111
Db 86 AAGLRQEDGADGTGAED 102

RESULT 14

US-09-252-991A-20326
; Sequence 20326, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20326
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20326

Query Match 37.3%; Score 47; DB 4; Length 405;
Best Local Similarity 45.5%; Pred. No. 29;
Matches 10; Conservative 2; Mismatches 8; Indels 2; Gaps 1;

QY 5 WLRPEDGG--QAEGAEDELEVR 24
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Db 154 WLRPEGGADQQGVHQAQR 175

RESULT 15
US-09-252-991A-24394
; Sequence 24394, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24394
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24394

Query Match 37.3%; Score 47; DB 4; Length 468;
Best Local Similarity 57.9%; Pred. No. 34;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 6 LRPEDGGQAEGAEDELEVR 24
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Db 122 LRRSEGLAGAGDELVR 140

Search completed: September 11, 2003, 17:27:17
Job time : 7.41711 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:26:32 ; Search time 14.631 Seconds
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Title: US-09-853-253-4

Sequence: 1 ALAGWLRPEDGGQAEDELEVR 24

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	126	100.0	117	9 US-09-794-987-2	Sequence 2, Appli
3	126	100.0	117	9 US-09-853-253-2	Sequence 2, Appli
4	126	100.0	117	9 US-09-989-722-268	Sequence 268, App
5	126	100.0	117	9 US-09-989-723-268	Sequence 268, App
6	126	100.0	117	9 US-09-989-279-268	Sequence 268, App
7	126	100.0	117	9 US-09-989-727-268	Sequence 268, App
8	126	100.0	117	10 US-09-989-731-268	Sequence 268, App
9	126	100.0	117	10 US-09-989-732-268	Sequence 268, App
10	126	100.0	117	10 US-09-991-073-268	Sequence 268, App
11	126	100.0	117	10 US-09-990-442-268	Sequence 268, App
12	126	100.0	117	10 US-09-991-163-268	Sequence 268, App
13	126	100.0	117	10 US-09-993-604-268	Sequence 268, App
14	126	100.0	117	10 US-09-990-456-268	Sequence 268, App
15	126	100.0	117	10 US-09-989-721-268	Sequence 268, App

16	126	100.0	117	10	US-09-992-598-268	Sequence 268, App
17	126	100.0	117	10	US-09-989-293A-268	Sequence 268, App
18	126	100.0	117	10	US-09-989-735-268	Sequence 268, App
19	126	100.0	117	10	US-09-990-444-268	Sequence 268, App
20	126	100.0	117	10	US-09-991-181-268	Sequence 268, App
21	126	100.0	117	10	US-09-989-730-268	Sequence 268, App
22	126	100.0	117	10	US-09-990-436-268	Sequence 268, App
23	126	100.0	117	10	US-09-993-687-268	Sequence 268, App
24	126	100.0	117	11	US-09-989-734-268	Sequence 268, App
25	126	100.0	117	11	US-09-997-653-268	Sequence 268, App
26	126	100.0	117	11	US-09-993-667-268	Sequence 268, App
27	126	100.0	117	11	US-09-997-428-268	Sequence 268, App
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30	126	100.0	117	11	US-09-990-562-268	Sequence 268, App
31	126	100.0	117	11	US-09-990-711-268	Sequence 268, App
32	126	100.0	117	11	US-09-989-726-268	Sequence 268, App
33	126	100.0	117	11	US-09-998-156-268	Sequence 268, App
34	126	100.0	117	11	US-09-990-437-268	Sequence 268, App
35	126	100.0	117	11	US-09-991-157-268	Sequence 268, App
36	126	100.0	117	11	US-09-997-514-268	Sequence 268, App
37	126	100.0	117	11	US-09-997-573-268	Sequence 268, App
38	126	100.0	117	11	US-09-991-172-268	Sequence 268, App
39	126	100.0	117	11	US-09-990-726-268	Sequence 268, App
40	126	100.0	117	11	US-09-997-559-268	Sequence 268, App
41	126	100.0	117	11	US-09-997-601-268	Sequence 268, App
42	126	100.0	117	11	US-09-990-443-268	Sequence 268, App
43	126	100.0	117	11	US-09-991-854-268	Sequence 268, App
44	126	100.0	117	11	US-09-997-628-268	Sequence 268, App
45	126	100.0	117	11	US-09-997-683-268	Sequence 268, App

ALIGNMENTS

RESULT 1
US-09-853-253-4
; Sequence 4, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHOR, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig333-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-4

Query Match 100.0%; Score 126; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ALAGWLRPEDGGQAEDELEVR 24
Db 1 ALAGWLRPEDGGQAEDELEVR 24

RESULT 2
US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.

; Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Query Match 100.0%; Score 126; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 3
US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US2002005156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
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; ORGANISM: Homo sapiens
US-09-853-253-2

Query Match 100.0%; Score 126; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Caps 0;
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Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 4
US-09-989-722-268
; Sequence 268, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04

1 PRIOR APPLICATION NUMBER: 60/088025
2 PRIOR FILING DATE: 1998-06-04
3 PRIOR APPLICATION NUMBER: 60/088026
4 PRIOR FILING DATE: 1998-06-04
5 PRIOR APPLICATION NUMBER: 60/088028
6 PRIOR FILING DATE: 1998-06-04
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9 PRIOR APPLICATION NUMBER: 60/088030
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58 PRIOR APPLICATION NUMBER: 60/091633
59 PRIOR FILING DATE: 1998-07-02
60 PRIOR APPLICATION NUMBER: 60/091978
61 PRIOR FILING DATE: 1998-07-07
62 PRIOR APPLICATION NUMBER: 60/091982
63 PRIOR FILING DATE: 1998-07-07
64 PRIOR APPLICATION NUMBER: 60/092182
65 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 126; DB 9; Length 117;
Best Local Similarity 100.0%; Pred No. 1,1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 52 ALAGWLRPEDGGGAEGAELEVR 75

RESULT 5

US-09-989-723-268
; Sequence 268, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989, 723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
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Query Match 100.0%; Score 126; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPDGGQAEGAELEVR 24
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RESULT 6
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; Sequence 268, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Goddard, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
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APPLICANT: Gerber, Hanspeter
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 APPLICANT: Grimaldi, J. Christopher
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 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730PIC65
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Query Match 100.0%; Score 126; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.le-09;

Matches: 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8

US-09-989-731-268
 ; Sequence 268, Application US/09989731
 ; Patent No. US20020103125A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
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 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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 ; CURRENT FILING DATE: 2001-11-20
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
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Query Match 100.0%; Score 126; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGGAEGAEDELEVR 24
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Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75

RESULT 9
US-09-989-732-268
; Sequence 268, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC57
CURRENT FILING DATE: 2001-11-19
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PRIOR APPLICATION NUMBER: US/09/989,732
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-06-25

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 136; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 1,1e-09;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 52 ALAGWLRPEDGGQAGAEDELEVR 75
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RESULT 10

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US-09-991-073-268
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; Patent No. US2002012756A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073

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 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0% Score 126; DB 10; Length 117;
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RESULT 11
 US-09-990-442-268
 ; Sequence 268, Application US/09990442
 ; Patent No. US20020132252A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC8
 ; CURRENT APPLICATION NUMBER: US/09/990.442
 ; CURRENT FILING DATE: 2001-11-14
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 ; PRIOR FILING DATE: 1997-06-16
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; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Tumas, Daniel
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; APPLICANT: Williams, P. Mickey
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; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 126; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 52 ALAGWLRPEDGGAGAEDELEVR 75

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US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1997-06-16
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Query Match      100.0%; Score 126; DB 10; Length 117;
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC22
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Query Match 100.0%; Score 126; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Caps 0;

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 Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75
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 ; Patent No. US20020142961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
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 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-18
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; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 126; DB 10; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1,1e-09;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

Search completed: September 11, 2003, 17:48:31
 Job time : 14.631 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:48:42 ; Search time 7.87166 Seconds
(without alignments)
123.627 Million cell updates/sec

Title: US-09-853-253-5
Sequence: 23
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Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	117	3	US-09-046-479-2
2	23	100.0	117	4	US-08-822-897C-2
3	23	100.0	117	4	US-09-608-810A-4
4	23	100.0	117	4	US-09-996-243-268
5	7	30.4	442	4	US-09-134-001C-3033
6	7	30.4	552	4	US-09-252-991A-27032
7	7	30.4	599	4	US-09-252-991A-20368
8	7	30.4	981	4	US-09-252-991A-16798
9	6	26.1	39	1	US-08-428-488-13
10	6	26.1	97	2	US-08-403-852D-31
11	6	26.1	97	3	US-08-510-646B-32
12	6	26.1	97	3	US-09-231-818-31
13	6	26.1	129	3	US-09-135-994-12
14	6	26.1	129	4	US-09-684-843A-12
15	6	26.1	183	4	US-09-198-452A-612
16	6	26.1	199	4	US-09-252-991A-32089
17	6	26.1	202	4	US-09-252-991A-26333
18	6	26.1	259	4	US-09-252-991A-17300
19	6	26.1	288	1	US-08-396-650-1
20	6	26.1	288	1	US-08-768-626-1
21	6	26.1	292	4	US-09-252-991A-18951
22	6	26.1	292	4	US-09-252-991A-30162
23	6	26.1	305	4	US-09-328-352-6794
24	6	26.1	326	4	US-09-252-991A-33000
25	6	26.1	329	4	US-09-843-297-2
26	6	26.1	359	4	US-09-266-965-120
27	6	26.1	366	4	US-09-252-991A-29569

28	6	26.1	378	4	US-09-325-932A-158	Sequence 158, Appl
29	6	26.1	399	4	US-09-252-991A-25687	Sequence 25687, A
30	6	26.1	402	3	US-09-464-483-4	Sequence 4, Appl
31	6	26.1	402	3	US-09-414-684-4	Sequence 4, Appl
32	6	26.1	489	4	US-09-252-991A-22896	Sequence 22896, A
33	6	26.1	502	4	US-09-207-388-19	Sequence 19, Appl
34	6	26.1	510	4	US-09-252-991A-17695	Sequence 17695, A
35	6	26.1	529	3	US-09-464-483-2	Sequence 2, Appl
36	6	26.1	529	3	US-09-414-684-2	Sequence 2, Appl
37	6	26.1	531	1	US-08-531-601-1	Sequence 1, Appl
38	6	26.1	531	2	US-08-859-032-1	Sequence 1, Appl
39	6	26.1	535	1	US-08-737-597-10	Sequence 10, Appl
40	6	26.1	548	4	US-09-207-388-23	Sequence 23, Appl
41	6	26.1	550	4	US-09-207-388-20	Sequence 20, Appl
42	6	26.1	568	4	US-09-207-388-22	Sequence 22, Appl
43	6	26.1	568	4	US-09-207-388-24	Sequence 24, Appl
44	6	26.1	570	4	US-09-207-388-21	Sequence 21, Appl
45	6	26.1	588	4	US-09-252-991A-31356	Sequence 31356, A

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 23; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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8	PRIOR FILING DATE: 1998-06-18
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10	PRIOR FILING DATE: 1998-06-19
11	PRIOR APPLICATION NUMBER: 60/089948
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13	PRIOR APPLICATION NUMBER: 60/089952
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66	PRIOR FILING DATE: 1998-07-01
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71	PRIOR APPLICATION NUMBER: 60/091633
72	PRIOR FILING DATE: 1998-07-02
73	PRIOR APPLICATION NUMBER: 60/091978

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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52 ALAGWLRPDGGQAGAEDELEV 74

RESULT 5

US-09-134-001C-3033
; Sequence 3033, Application US/09134001C
; Patent No. 6380370

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GFC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3033

LENGTH: 442

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3033

Query Match 30.4%; Score 7; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DGGQAG 16
Db |||||||

189 DGGQAG 195

RESULT 6

US-09-252-991A-27032
; Sequence 27032, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27032

LENGTH: 552

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27032

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Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||||

22 DGGQAG 28

RESULT 7

US-09-252-991A-20368
; Sequence 20368, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20368

LENGTH: 599

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20368

Query Match 30.4%; Score 7; DB 4; Length 599;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGQAGA 17

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383 GGQAGA 389

RESULT 8

US-09-252-991A-16798
; Sequence 16798, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 16798

LENGTH: 981

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-16798

Query Match 30.4%; Score 7; DB 4; Length 981;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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136 ALAGWL 142

RESULT 9

US-08-428-488-13
; Sequence 13, Application US/08428488
; Patent No. 5624894

GENERAL INFORMATION:

; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE

TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Position 1 - H-Ser."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 39
OTHER INFORMATION: /note= "Position 39 - Phe-OH."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 30
OTHER INFORMATION: /note= "Position 30 - Glu-NH2."
US-08-428-488-13

Query Match 26.1%; Score 6; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 GADEL 21
DB 26 GADEL 31

RESULT 10
US-08-403-852D-31
Sequence 31, Application US/08403852D
Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
AND THEIR USE
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-403-852D-31

Query Match 26.1%; Score 6; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 QAEGAE 18
DB 2 QAEGAE 7

RESULT 11
US-08-510-646B-32
Sequence 32, Application US/08510646B
Patent No. 6077699
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
AND THEIR USE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510.646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-510-646B-32

Query Match 25.1%; Score 6; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAE 18
Db 2 QAEGAE 7

RESULT 12

US-09-231-818-31
Sequence 31, Application US/09231818
Patent No. 6171846

GENERAL INFORMATION:

APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Parabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
FILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-231-818-31

Query Match 26.1%; Score 6; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QAEGAE 18
Db 2 QAEGAE 7

RESULT 13

US-09-135-994-12
Sequence 12, Application US/09135994A
Patent No. 6280938

GENERAL INFORMATION:

APPLICANT: Ranum et al.
TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
US-09-135-994-12

Query Match 26.1%; Score 6; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RPEDGG 12
Db 57 RPEDGG 62

RESULT 14

US-09-684-843A-12
Sequence 12, Application US/09684843A
Patent No. 6514755

GENERAL INFORMATION:

APPLICANT: Ranum et al.
TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: Regents of the University of Minnesota
CURRENT APPLICATION NUMBER: US/09/684,843A
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/056,170
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 09/135,994

; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-843A-12

Query Match 26.1%; Score 6; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RPEDGG 12
| | | | |
Db 57 RPEDGG 62

RESULT 15

US-09-198-452A-612
; Sequence 612, Application US/09198452A
; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffals, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 612
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-612

Query Match 26.1%; Score 6; DB 4; Length 183;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | |
Db 155 AEGAED 160

Search completed: September 11, 2003, 17:58:14
Job time : 8.87166 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:27:22 ; Search time 24.2299 Seconds
(without alignments)
150.669 Million cell updates/sec

Title: US-09-853-253-5

Perfect score: 23

Sequence: 1 ALAGWLRPEDGGQAEAEDEV 23

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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 - 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
 - 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	23	AAE23840	Human zsig33-linker
2	23	100.0	23	AAE23841	Human zsig33-linker
3	23	100.0	23	AAE15885	Human zsig33-linker
4	23	100.0	23	AAE15886	Human zsig33-linker
5	23	100.0	24	AAE23839	Human zsig33-linker
6	23	100.0	24	AAE15884	Human zsig33-linker
7	23	100.0	91	AAE33410	Human exon 3-delet
8	23	100.0	116	AAE60517	Human des-Gln14-gh
9	23	100.0	117	AAW87991	Protein designated

10	23	100.0	117	21	AAE87236	Human signal pepti
11	23	100.0	117	22	AAE38890	Human polypeptide
12	23	100.0	117	22	AAE62649	Human zsig33 poly
13	23	100.0	117	22	AAE20101	Zsig33 protein. H
14	23	100.0	117	22	AAE60511	Human ghrelin prep
15	23	100.0	117	23	ABE78319	Amino acid sequenc
16	23	100.0	117	23	ABE23838	Human zsig33 prote
17	23	100.0	117	23	AAE15883	Human zsig33 prote
18	23	100.0	117	24	ABU66790	Human PRO polypept
19	23	100.0	117	24	ABU67066	Human secreted/tra
20	23	100.0	117	24	ABU59871	Novel secreted and
21	23	100.0	117	24	ABU59124	Novel human secret
22	23	100.0	117	24	ABU59271	Human secreted/tra
23	23	100.0	117	24	ABU59420	Novel human secret
24	23	100.0	117	24	ABU60555	Human secreted/tra
25	23	100.0	117	24	ABU58046	Human PRO polypept
26	23	100.0	117	24	ABU58977	Human secreted/tir
27	23	100.0	117	24	AAE33409	Human preproghreli
28	23	100.0	117	24	ABU13937	Human PRO1066 poly
29	23	100.0	117	24	ABU10892	Human PRO polypept
30	23	100.0	118	21	AAE66708	Membrane-bound pro
31	23	100.0	118	22	AAU12392	Human PRO1066 poly
32	23	100.0	118	22	AAE65231	Human PRO1066 (UNQ
33	23	100.0	126	22	AAE40676	Human polypeptide
34	10	43.5	89	22	AAE60523	Bovine ghrelin pre
35	8	34.8	334	21	AAE29677	Arabidopsis thalia
36	8	34.8	428	21	AAE29676	Arabidopsis thalia
37	8	34.8	483	21	AAE29675	Arabidopsis thalia
38	7	30.4	311	19	AAW36129	Snpr activator pro
39	7	30.4	311	21	AAE30494	Amino acid sequenc
40	7	30.4	442	23	ABP38188	Staphylococcus epi
41	7	30.4	1931	22	ABE66948	Drosophila melanog
42	6	26.1	14	22	AAE66893	Human peptide #168
43	6	26.1	26	24	AAE33406	PD-1-ctail2 peptid
44	6	26.1	26	24	ABJ18534	PD-1-related pepti
45	6	26.1	39	20	AAE50239	Neutrophil-activat

ALIGNMENTS

RESULT 1
AAE23840
ID AAE23840 standard; peptide; 23 AA.

XX AC AAE23840;

XX DT 10-SEP-2002 (first entry)

XX DE Human zsig33-linker peptide #2.

XX KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;

XX KW growth hormone; digestive enzyme; restorative therapy; gene therapy;

XX KW protein therapy; gastrointestinal; endocrine; anabolic.

XX OS Homo sapiens.

XX PN US2002055156-A1.

XX PD 09-MAY-2002.

XX PF 10-MAY-2001; 2001US-0853253.

XX PR 11-MAY-2000; 2000US-203300P.

XX PA (JASP/) JASPERS S R.

XX PA (SHEP/) SHEPPARD P O.

XX PA (DEIS/) DEISHER T A.

XX PA (BISH/) BISHOP P D.

XX PI Jaspers SR, Sheppard PO, Delsher TA, Bishop PD;

XX DR WPI; 2002-443750/47.

contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -

Claim 1; Page 28; 34pp; English.

The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate zsig33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The zsig33 peptides are used as antigens in the production of antibodies against zsig33 and in assays to identify modulators of zsig33 expression and activity. The anti-zsig33 antibodies and antagonists are used to down regulate expression and activity. The anti-zsig33 antibodies are also used as diagnostic agents for detecting the presence of zsig33 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy and zsig33-like peptide is used in protein therapy. The present sequence is human zsig33-like peptide, zsig33-linker peptide.

Sequence 23 AA:

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Query Match      100.0%; Score 23; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3	
AAE15885	
ID	AAE15885 standard; peptide; 23 AA.
XX	
AC	AAE15885;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Human zsig33-linker peptide #2.
XX	
KW	Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW	infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW	adsorption enhancer; gastrointestinal disease; growth related disease;
KW	inflammation; gene therapy; growth regulation; blood vessel formation;
KW	HIV; zsig33-linker peptide.
XX	
OS	Homo sapiens.
XX	
PN	WO200187933-A2.
XX	
PD	22-NOV-2001.
XX	
PF	10-MAY-2001; 2001WO-US15091.
XX	
PR	11-MAY-2000; 2000US-0569271.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
XX	
PI	Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX	
DR	WPI: 2002-082982/11.
DR	N-PSDB; AAD25760.
XX	
PT	New polypeptides, useful for modulating gastric contractility, nutrient
PT	uptake, pancreatic secretion of hormones, digestive enzymes and
PT	treating gastrointestinal and growth related diseases. comprises


```

PT zsig33-like peptides -
XX Claim 1b; Page 81; 89pp; English.
XX
XX The invention relates to zsig33-like peptides (ZS33LP) including
CC zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and
CC zsig33-epsilon peptides and nucleic acid molecules encoding such
CC zsig33-like peptides. ZS33LP peptides activate the immune system
CC in boosting immunity to infectious diseases, treating immunocompromised
CC patients such as human immunodeficiency virus (HIV) patients, in
CC improving vaccines and in treatment of bacterial, viral, protozoal and
CC fungal infections. Peptides of the invention are used to identify and
CC isolate receptors involved in growth regulation in the liver, blood
CC vessel formation and other developmental processes. They are useful for
CC evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate
CC growth and/or differentiation of tumour cells, as additives to anti-
CC hypoglycaemic preparations containing glucose and as adsorption
CC enhancers for oral drugs which require fast nutrient action and to
CC stimulate glucose-induced insulin release. They are also useful as
CC research reagents for the expansion, differentiation, growth factor and
CC hormone secretion and/or cell-cell interactions of tissues associated
CC with gastrointestinal system, brain and central nervous system. These
CC molecules are useful for treating dysfunction associated with contractile
CC tissues or to suppress or enhance contractility in vivo and to treat
CC gastrointestinal and growth related diseases. ZS33LP peptides, nucleic
CC acids and/or antibodies are useful for treating disorders associated
CC with gastrointestinal contractility, secretion of digestive enzymes,
CC hormone and acids, secretion of hormones in the pancreas and/or brain,
CC gastrointestinal motility, recruitment of digestive enzymes, inflammation
CC and regulation of nutrient absorption. Sequences of the invention are
CC useful in gene therapy. The present sequence is human zsig33-linker
CC peptide.
XX Sequence 23 AA;
SQ
Query Match 100.0%; Score 23; DB 23; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRPEDGGQAGAEDELEV 23
Db 1 ALAGWLRPEDGGQAGAEDELEV 23
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RESULT 4
AAE15886
ID AAE15886 standard; peptide; 23 AA.
AC AAE15886;
XX
XX 26-MAR-2002 (first entry)
DT
DE Human zsig33-linker peptide #3.
XX
Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW adsorption enhancer; gastrointestinal disease; growth related disease;
KW inflammation; gene therapy; growth regulation; blood vessel formation;
KW HIV; zsig33-linker peptide.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 23 /note= "C-terminal amide"
FT
FT
XX W0200187933-A2.
PN
XX 22-NOV-2001.
PD
XX
XX 10-MAY-2001; 2001WO-US15091.
PF
XX 11-MAY-2000; 2000US-0569271.
PR

```

(ZYMO) ZYMOGENETICS INC.

Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

WPI; 2002-082982/11.

N-PSDB; AAD25760.

New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises zsig33-like peptides -

Claim 1c; Page 82; 89pp; English.

The invention relates to zsig33-like peptides (ZS33LP) including zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and zsig33-epsilon peptides and nucleic acid molecules encoding such zsig33-like peptides. ZS33LP peptides activate the immune system in boosting immunity to infectious diseases, treating immunocompromised patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and fungal infections. Peptides of the invention are used to identify and isolate receptors involved in growth regulation in the liver, blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic preparations containing glucose and as adsorption enhancers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation, growth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These molecules are useful for treating dysfunction associated with contractile tissues or to suppress or enhance contractility in vivo and to treat gastrointestinal and growth related diseases. ZS33LP peptides, nucleic acids and/or antibodies are useful for treating disorders associated with gastrointestinal contractility, secretion of digestive enzymes, hormone and acids, secretion of hormones in the pancreas and/or brain, gastrointestinal motility, recruitment of digestive enzymes, inflammation and regulation of nutrient absorption. Sequences of the invention are useful in gene therapy. The present sequence is human zsig33-linker peptide.

Sequence 23 AA;

Query Match 100.0%; Score 23; DB 23; Length 23;

Best Local Similarity 100.0%; Pred. No. 5.9e-15;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEV 23

Db 1 ALAGWLRPEDGGQAGAEDELEV 23

|||||

RESULT 5

AAE23839

ID AAE23839 standard; peptide; 24 AA.

XX AAE23839;

AC AAE23839;

XX

XX 10-SEP-2002 (first entry)

DT

DE Human zsig33-linker peptide #1.

XX

Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.

XX Homo sapiens.

OS

XX

XX Key Location/Qualifiers

FH Region 7..18

FT

ID AAE33410 standard; Protein; 91 AA.
 XX AC AAE33410;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human exon 3-deleted ghrelin protein.
 XX
 KW Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
 KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
 KW cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200290387-A1.
 XX
 PD 14-NOV-2002.
 XX
 PF 10-MAY-2002; 2002WO-AU00582.
 XX
 PR 10-MAY-2001; 2001AU-0004919.
 XX
 PR 17-DEC-2001; 2001AU-0009567.
 XX
 PA (UYOU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 PI Chopin LK, Jeffery PL, Herington AC;
 XX
 DR WPI: 2003-111957/10.
 DR N-PSDB; AAD50726.
 XX
 XX Identifying a cancer cell or tissue for treating prostate, ovarian,
 PT breast cancer, or benign prostatic hyperplasia, by detecting the
 PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
 PT 1b proteins or nucleic acids -
 XX
 PS Claim 14; Page 34; 50pp; English.
 XX
 CC The invention relates to a method for identifying a cancer cell or
 CC tissue of the reproductive system by detecting expression of a ghrelin,
 CC an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic
 CC acids. The antibodies, exon 3-deleted form of preproghrelin and
 CC antagonists are useful for treating cancer of the reproductive system
 CC such as prostate, ovarian, breast, cervical or uterine cancer,
 CC choriocarcinoma or benign prostatic hyperplasia. The present sequence
 CC is human exon 3-deleted ghrelin protein.
 XX
 SQ Sequence 91 AA;
 Query Match 100.0%; Score 23; DB 24; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 52 ALAGWLRPEDGGQAGAEDELEV 74
 RESULT 8
 AAB60517
 ID AAB60517 standard; Protein; 116 AA.
 XX
 AC AAB60517;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
 XX
 KW Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency.
 XX
 OS Homo sapiens.
 XX

PN WO200107475-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-JP04907.
 XX
 PR 23-JUL-1999; 99JP-0210002.
 PR 29-NOV-1999; 99JP-0338841.
 PR 26-APR-2000; 2000JP-0126623.
 XX
 PA (KANG/) KANGAWA K.
 XX
 PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 XX
 DR WPI: 2001-159704/16.
 DR N-PSDB; AAF59647.
 XX
 PT New peptide compounds which induce growth hormone secretion and
 PT elevate cell calcium concentrations, useful in treatment and diagnosis
 PT of infant growth disorders -
 XX
 PS Claim 3; Page 186-187; 210pp; Japanese.
 XX
 CC The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by
 CC a modified amino acid and/or a non-amino acid compound. The invention
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with
 CC no accompanying side effects. The present sequence represents a
 CC ghrelin-type growth hormone secretagogue (GHS) precursor protein
 CC of the invention.
 XX
 SQ Sequence 116 AA;
 Query Match 100.0%; Score 23; DB 22; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEV 23
 DB 51 ALAGWLRPEDGGQAGAEDELEV 73
 RESULT 9
 AAW87991
 ID AAW87991 standard; Protein; 117 AA.
 XX
 AC AAW87991;
 XX
 DT 07-APR-1999 (first entry)
 XX
 DE Protein designated zsig33.
 XX
 KW Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
 KW nutrient absorption regulation; obesity; metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23 "signal peptide"
 FT Protein 24..117
 FT "note="mature protein"
 XX

PN W09842840-A1.
 XX 01-OCT-1998.
 XX 23-MAR-1998; 98WO-US05620.
 XX 24-MAR-1997; 97US-0822897.
 PR 24-MAR-1997; 97US-0041102.
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 PI Delsler TA, Sheppard PO;
 DR WPI; 1999-070071/06.
 DR N-PSDB; AAX04550.
 XX
 PT Human polypeptide having homology to motilin, zsig33 - useful e.g.
 PT to treat gastrointestinal motility disorders, obesity etc. and to
 PT identify antagonists to treat gastrointestinal hypermotility
 XX
 PS Claim 13; Page 55-56; 69pp; English.
 XX
 CC The present sequence represents a protein designated zsig33. The nucleic
 CC acids are strongly expressed in stomach tissue. The polypeptide (or
 CC allelic variants/orthologs) can be used to stimulate gastric motility,
 CC measured as increased transit time or gastric emptying of an ingested
 CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. Zsig33 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC and CNS functions. They may therefore be used e.g. to regulate satiety
 CC or treat obesity and other metabolic disorders where neurological
 CC feedback modulates nutritional absorption. They are useful to identify
 CC zsig33 agonists, antagonists and ligands. They are useful to identify
 XX zsig33 agonists, antagonists and ligands. They are useful to identify
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 23; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRLPEDGGQAGAEDELEV 23
 |||||
 DB 52 ALAGWLRLPEDGGQAGAEDELEV 74
 RESULT 10
 AAY87236
 ID AAY87236 standard; Protein; 117 AA.
 XX
 AC AAY87236;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
 XX
 KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX Homo sapiens.
 OS
 XX W0200000610-A2.
 PN
 XX

PD 06-JAN-2000.
 XX 25-JUN-1999; 99WO-US14484.
 XX 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX
 DR WPI; 2000-160673/14.
 DR N-PSDB; AAZ98121.
 XX
 XX New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease -
 PT
 XX
 PS Claim 1; Page 168-169; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPP
 CC from natural sources.
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 23; DB 21; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAGWLRLPEDGGQAGAEDELEV 23
 |||||
 DB 52 ALAGWLRLPEDGGQAGAEDELEV 74
 RESULT 11
 AAM38890
 ID AAM38890 standard; Protein; 117 AA.
 XX
 AC AAM38890;
 XX
 XX 22-OCT-2001 (first entry)
 DT
 XX Human polypeptide SEQ ID NO 2035.
 DE
 XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX Homo sapiens.
 OS WO200153312-A1.
 PN 26-JUL-2001.
 PD 26-DEC-2000; 2000WO-US34263.
 PF 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX WPI: 2001-442253/47.
 DR N-PSDB; AAI58046.
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX Example 3; SEQ ID NO 2035; 10078pp; English.
 PS The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 23; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ALAGWLRLPDDGGQAGGADELEV 23
 DB 52 ALAGWLRLPDDGGQAGGADELEV 74
 RESULT 12
 AAB62649
 ID AAB62649 standard; Protein; 117 AA.
 XX AAB62649;
 AC
 XX 23-JUL-2001 (first entry)
 DT
 XX Human zsig33 polypeptide.
 DE
 XX

KW zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulneryary; immunomodulator; GHS-R;
 KW G-protein coupled receptor.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 24..37
 FT /note= "specifically claimed fragment that binds to
 FT the GHS-R"
 XX WO200138355-A2.
 PN 31-MAY-2001.
 PD 22-NOV-2000; 2000WO-US32074.
 PF 22-NOV-1999; 99US-0166765.
 PR 22-NOV-1999; 99US-0166765.
 XX (ZYMO) ZYMOGENETICS INC.
 PA Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 PI WPI: 2001-355879/37.
 DR N-PSDB; AAF83678.
 DR Forming reversible peptide receptor complex for purifying cell and
 PT peptides, stimulating signal transduction and modulating hormone
 PT secretion, involves contacting a receptor with zsig33 polypeptide -
 XX Claim 1; Page 93-94; 111pp; English.
 PS The invention relates to a method of forming a reversible peptide-
 CC receptor complex that involves providing an immobilized receptor, and
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
 CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
 CC is useful for purifying cells, purifying a peptide, stimulating signal
 CC transduction in a cell expressing a receptor. It is also useful for
 CC modulating secretion of hormones, neural development and/or utilization,
 CC gastric contractility, nutrient uptake, secretion of digestive and
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
 CC hormone secretion in a mammal having a disease associated with abnormal
 CC levels of growth hormone, such as osteoporosis, bone repair, bone
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,
 CC protein catabolic responses after surgery, cachexia, protein loss,
 CC dwarfism, wound healing and ovulation induction, treating a mammal having
 CC a metabolic disorder requiring neurological feedback, such as satiety
 CC regulation, glucose absorption and metabolism and neuropathy-associated
 CC gastrointestinal disorders, and stimulating glucose-induced insulin
 CC release in a mammal. The present sequence represents the human zsig33
 CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
 XX Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 23; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ALAGWLRLPDDGGQAGGADELEV 23
 DB 52 ALAGWLRLPDDGGQAGGADELEV 74
 RESULT 13
 AAB20101
 ID AAB20101 standard; Protein; 117 AA.
 XX
 AC AAB20101;
 XX


```
FH Key Location/Qualifiers
FT Peptide 1..23
FT /note= "signal peptide"
FT Protein 24..119
FT /note= "mature protein"
XX
PN US6420521-B1.
XX
PD 16-JUL-2002.
XX
PF 30-JUN-2000; 2000US-0608810.
XX
PR 30-JUN-1999; 99US-141592P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
DR WPI; 2002-634794/68.
DR N-PSDB; ABV72214.
XX
PT New Short Gastrointestinal Peptide, which has homology to motilin,
PT useful for preventing, diagnosing and treating gastrointestinal
PT disorders
XX
PS Disclosure; Columns 39-40; 23pp; English.
XX
CC The present sequence represents human zsig33. The specification describes
CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.
CC SGIP has homology to motilin. The SGIP peptide may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate SGIP expression. For example, SGIP may be used to treat
CC disorders associated with decreased expression by rectifying mutations
CC or deletions in a patient's genome that affect the activity of SGIP by
CC expressing inactive proteins or to supplement the patients own production
CC of SGIP. SGIP may also be used as an antigen in the production of
CC antibodies against SGIP and in assays to identify modulators of SGIP
CC expression and activity. The anti-SGIP antibodies, agonists and
CC antagonists may also be used to regulate expression and activity. The
CC anti-SGIP antibodies may also be used as diagnostic agents for detecting
CC the presence of SGIP in samples.
XX
.SQ Sequence 117 AA;
Query Match 100.0%; Score 23; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-14; Mismatches 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAGWLRLPEDGGQGAEGAEDEV 23
Db 52 ALAGWLRLPEDGGQGAEGAEDEV 74
|||||
|||||
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Search completed: September 11, 2003, 17:51:54
Job time : 24.2299 secs

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 22.8449 Seconds
(without alignments)
271.100 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 126
Sequence: 1 ALAGWLRPEDGGQAGAEDELEVR 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	124	98.4	117 4 Q8TAT9	Q8tat9 homo sapien
2	97	77.0	117 11 Q8CH53	Q8ch53 meriones un
3	59	46.8	1208 5 Q8I5T3	Q8i5t3 plasmodium
4	59	46.8	1264 5 Q9U445	Q9u445 plasmodium
5	55	43.7	183 10 Q8NL6	Q8nl6 oryza sativ
6	53	42.1	202 15 Q9P58	Q9p58 human immun
7	53	42.1	1228 5 Q27724	Q27724 plasmodium
8	52	41.3	201 15 Q9P50	Q9p50 human immun
9	52	41.3	232 16 Q9I6L1	Q9i6l1 pseudomonas
10	52	41.3	249 12 Q82036	Q82036 hiram rhab
11	52	41.3	392 12 Q9L89	Q9l89 hiram rhab
12	52	41.3	977 6 Q9S169	Q9s169 capra hircu
13	51.5	40.9	436 5 Q9N638	Q9n638 caenorhabdi
14	51	40.5	158 16 Q8XW90	Q8xw90 ralstonia s
15	51	40.5	201 15 Q90NL5	Q90nl5 human immun
16	51	40.5	604 16 Q8UFA5	Q8ufa5 agrobacteri

17	51	40.5	609	2	Q9RH77	Q9rh77 bradyrhizob
18	50	39.7	131	16	Q9RV90	Q9rv90 deinococcus
19	50	39.7	202	15	Q9OP76	Q9op76 human immun
20	50	39.7	202	15	Q9OP77	Q9op77 human immun
21	50	39.7	472	10	Q8LRD5	Q8lrd5 oryza sativ
22	50	39.7	582	6	Q9XSP0	Q9xsp0 capra hircu
23	50	39.7	582	6	Q9GLE4	Q9gle4 bos taurus
24	49.5	39.3	484	16	Q9RZ17	Q9rz17 deinococcus
25	49	38.9	201	15	Q9OP55	Q9op55 human immun
26	49	38.9	201	15	Q9ONK8	Q9onk8 human immun
27	49	38.9	286	12	Q8QRU5	Q8qrus chimpanzee
28	48.5	38.5	110	10	Q93VB3	Q93vb3 oryza sativ
29	48.5	38.5	172	2	Q9RBY2	Q9rby2 pseudomonas
30	48.5	38.5	172	2	Q9R2S2	Q9r2s2 pseudomonas
31	48.5	38.5	269	2	Q9ETM8	Q9etm8 pseudomonas
32	48	38.1	106	16	Q8ELH4	Q8elh4 oceanobacil
33	48	38.1	115	10	Q8LI79	Q8li79 oryza sativ
34	48	38.1	120	15	Q78494	Q78494 human immun
35	48	38.1	201	15	Q9OP53	Q9op53 human immun
36	48	38.1	201	15	Q9ONL3	Q9onl3 human immun
37	48	38.1	201	15	Q9ONL6	Q9onl6 human immun
38	48	38.1	201	15	Q9ONL0	Q9onl0 human immun
39	48	38.1	201	15	Q9ONL1	Q9onl1 human immun
40	48	38.1	201	15	Q9ONM1	Q9onm1 human immun
41	48	38.1	201	15	Q9ONM2	Q9onm2 human immun
42	48	38.1	201	15	Q9ONL9	Q9onl9 human immun
43	48	38.1	202	15	Q9OP31	Q9op31 human immun
44	48	38.1	202	15	Q9OP37	Q9op37 human immun
45	48	38.1	211	10	Q943L4	Q943l4 oryza sativ

ALIGNMENTS

RESULT 1

Q8TAT9 PRELIMINARY; PRT; 117 AA.
AC Q8TAT9
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Ghrelin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025791; AAH25791.1; -
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_assoc.1.
DR Pfam; PF04644; motilin_ghrelin.1.
SQ SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;

Query Match 98.4%; Score 124; DB 4; Length 117;
Best Local Similarity 95.8%; Pred. No. 3.5e-10;
Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
|||||
DB 52 ALAGWLRPEDGGQAGAEDEMEVR 75

RESULT 2

Q8CH53 PRELIMINARY; PRT; 117 AA.
AC Q8CH53;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RT "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AA006965.1; -.
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Query Match 77.08; Score 97; DB 11; Length 117;
Best Local Similarity 75.08; Pred. No. 2.6e-06;
Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
II III I: |||||IIIIII:
Db 52 ALEGWLRHPDGGQAGAEDELEIR 75

RESULT 3
Q815T3 ID Q815T3 PRELIMINARY; PRT; 1208 AA.
AC Q815T3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase, putative.
GN PFL0590C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Perteira M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.W., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014846; AAN36207.1; -.
SQ SEQUENCE 1208 AA; 133873 MW; 25AA7752E707B621 CRC64;

Query Match 46.88; Score 59; DB 5; Length 1208;
Best Local Similarity 52.68; Pred. No. 9;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGQAGAEDELE 22
II III: :I ||||
Db 1072 GWCRPKDNKTSQGYNDELE 1090

RESULT 4
Q9U445 ID Q9U445 PRELIMINARY; PRT; 1264 AA.
AC Q9U445;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase4.

```

```

GN ATPASE4.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Krishna S., Woodrow C., Webb R., Penny J., Takeyasu K., Kimura M.,
RA East J.M.;
RT "Expression and Functional Characterization of a Plasmodium falciparum
RT Ca2+-ATPase (PfATP4) Belonging to a Subclass Unique to Apicomplexan
RT Organisms.";
RL J. Biol. Chem. 276:10782-10787(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
CC ATPASES).
DR EMBL; AF203980; AAF17245.1; -.
DR HSP; P04191; LEUL.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 5.
DR PROSITE; PS00154; ATPASE_E1-E2; 1.
KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SQ SEQUENCE 1264 AA; 140261 MW; 638142BB1B433640 CRC64;

Query Match 46.88; Score 59; DB 5; Length 1264;
Best Local Similarity 52.68; Pred. No. 9.4;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRPEDGGQAGAEDELE 22
II III: :I ||||
Db 1128 GWCRPKDNKTSQGYNDELE 1146

RESULT 5
Q8LNL6 ID Q8LNL6 PRELIMINARY; PRT; 183 AA.
AC Q8LNL6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0071120.2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA McCombie W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,
RA Kuit K., Nascimento L., Zutavern T., Ballia V., Bell M., Baker J.,
RA Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,
RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone
RT OSJNba0071120, from chromosome 10, complete sequence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC074355; AAM74240.1; -.
DR Gramene; Q8LNL6; -.
KW Hypothetical protein.
SQ SEQUENCE 183 AA; 20492 MW; DE73BD8607292D7B CRC64;

Query Match 43.78; Score 55; DB 10; Length 183;
Best Local Similarity 47.68; Pred. No. 4.6;
Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

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```
QY 3 AGWLRPEDGGQGAEGAEDELEV 23
   |||: ||| | | | |
Db 53 AGWIETEDGSDESDSEV 73

RESULT 6
Q90P58
ID Q90P58 PRELIMINARY; PRT; 202 AA.
AC Q90P58;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Nickle D.C.;
RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF370911; AAK66310.1; -
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 22572 MW; 4CB8ACAFBFB14314 CRC64;

Query Match 42.1%; Score 53; DB 15; Length 202;
Best Local Similarity 45.5%; Pred. No. 9.9;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQGAEGAEDELEV 23
   : | | | | | | | | |
Db 180 ITGLLLTRDGGGQGDGTDETEV 201

RESULT 7
Q27724
ID Q27724 PRELIMINARY; PRT; 1228 AA.
AC Q27724;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P-type ATPase.
GN PFATPASE4.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=96408665; PubMed=8813672;
RA Dyer M., Jackson M., McWhinney C., Zhao G., Mikkelsen R.;
RT "Analysis of a cation-transporting ATPase of Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 78:1-12(1996).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
ATPASES).
CC EMBL; U39298; AAC47167.1; -
DR HSSP; P04191; IEUL.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Hydrolase.
DR InterPro; IPR000695; H_ATPase.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
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DR PRINTS; PRO0119; CATATPASE.
DR PRINTS; PRO0120; HATPASE.
DR TIGRFS; TIGR01494; ATPase_P-type; 5.
DR PROSITE; PS00154; ATPASE_E1-E2; 1.
KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SQ SEQUENCE 1228 AA; 135989 MW; 32C3CFD324964CBE CRC64;

Query Match 42.1%; Score 53; DB 5; Length 1228;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 WLRPEDGGQGAEGAEDELE 22
   | | | | | | | | |
Db 1131 WCRPKDNKTSQGYNDELE 1148

RESULT 8
Q90P50
ID Q90P50 PRELIMINARY; PRT; 201 AA.
AC Q90P50;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Nickle D.C.;
RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF370919; AAK66318.1; -
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 201
SQ SEQUENCE 201 AA; 22550 MW; 6CAF6C460A9BA517 CRC64;

Query Match 41.3%; Score 52; DB 15; Length 201;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQGAEGAEDELEV 23
   : | | | | | | | | |
Db 179 ITGLLLTRDGGGQGDGTDETEV 200

RESULT 9
Q916L1
ID Q916L1 PRELIMINARY; PRT; 232 AA.
AC Q916L1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Probable transcriptional regulator.
GN PA0279.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.
```

RT *Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL: AE004466; AAC03668.1; -.
DR InterPro: IPR001845; HTH_ArsR.
DR Pfam: PF01022; HTH_5; 1.
DR PRINTS: PR00778; HTHARSR.
DR SMART: SM00418; HTH_ArsR; 1.
KW DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 232 AA; 24440 MW; E3C29187694CF936 CRC64;

Query Match 41.3%; Score 52; DB 16; Length 232;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWLRPDGGQA 14
Db 202 GWLRPDGSGRA 212
|||||:|:|

RESULT 10

ID Q82036 PRELIMINARY; PRT; 249 AA.
AC Q82036;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Hirame rhabdovirus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=38142;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8401-H;
RA Nishizawa T.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: D45422; BAA08261.1; -.
DR InterPro: IPR004902; Rhabdo_ncap_2.
DR Pfam: PF03216; Rhabdo_ncap_2; 1.
SQ SEQUENCE 249 AA; 26936 MW; 62FF2BFA5D47DB89 CRC64;

Query Match 41.3%; Score 52; DB 12; Length 249;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 EDGGQAEAGDE 20
Db 235 EDGGEDEGEDE 246
|||||:|:|

RESULT 11

ID Q90L89 PRELIMINARY; PRT; 392 AA.
AC Q90L89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Hirame rhabdovirus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=38142;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA 9703;
RA Oh H.K., Choi T.J.;
RL Submitted (NOV-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF104985; AAF14116.1; -.

DR InterPro: IPR004902; Rhabdo_ncap_2.
DR Pfam: PF03216; Rhabdo_ncap_2; 1.
SQ SEQUENCE 392 AA; 42465 MW; C5A282238FC7A638 CRC64;

Query Match 41.3%; Score 52; DB 12; Length 392;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 EDGGQAEAGDE 20
Db 378 EDGGEDEGEDE 389
|||||:|:|

RESULT 12

ID Q95169 PRELIMINARY; PRT; 977 AA.
AC Q95169;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Skeletal muscle voltage-gated chloride channel gC1c-1 (Fragment).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97008165; PubMed=8855341;
RA Beck C.L., Fahlke C., George A.L.;
RT "Molecular basis for decreased muscle chloride conductance in the
RT myotonic goat.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:11248-11252(1996).
DR EMBL: U60275; AAC48666.1; -.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl-channel_volt.
DR InterPro: IPR005829; Sug_transporter.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; voltage_CLC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
FT NON_TER 1
SQ SEQUENCE 977 AA; 107894 MW; 1E462B3CB307A148 CRC64;

Query Match 41.3%; Score 52; DB 6; Length 977;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRPDGGQAEAGD 19
Db 895 GWSLPEDGAGATGAGD 910
|||:|||||:|

RESULT 13

ID Q9N638 PRELIMINARY; PRT; 436 AA.
AC Q9N638;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F37D6.6 protein.
GN F37D6.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;

RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT Investigating biology."
 RL Science 282:2012-2018(1998).
 RN [3]
 RP SEQUENCE FROM N.A.

RA McMurray A.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 279600; CAB70221.1; -;
 DR EMBL; 275540; CAB70221.1; JOINED.
 DR EMBL; 275540; CAB70215.1; -;
 DR EMBL; 275540; CAB70215.1; JOINED.
 DR WormPep; F37D6.6; CE24960.
 DR InterPro; IPR001132; DwarfIn.
 DR InterPro; IPR003619; DwarfIn_A.
 DR Pfam; PF03166; MH2; 1.
 DR SMART; SM00523; DMB; 1.
 DR SMART; SM00524; DMB; 1.
 SQ SEQUENCE 436 AA; 49496 MW; E0C71263BC580FEE CRC64;

Query Match 40.9%; Score 51.5; DB 5; Length 436;
 Best Local Similarity 52.9%; Pred. No. 37;
 Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 5 WLRPE-DGGQGAEGDE 20
 I:III :II :I:II:
 Db 169 WIRPETNGDDGSEDK 185

RESULT 14

Q8XW90 ID Q8XW90 PRELIMINARY; PRT; 158 AA.
 AC Q8XW90;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein RSC2585.
 GN RSC2585 OR RS00797.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Siguler P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
 RL Nature 415:497-502(2002).
 DR EMBL; AL646070; CAD16292.1; -;
 DR InterPro; IPR002145; HTH_CopG.
 DR Pfam; PF01402; HTH 4; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 158 AA; 17814 MW; C9BA42BF9C10E1BC CRC64;

Query Match 40.5%; Score 51; DB 16; Length 158;
 Best Local Similarity 58.8%; Pred. No. 15;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALAGWLRLPEDGGQAEGA 17
 III III: I I I I
 Db 36 ALASWLSPDAGDQREAA 52

RESULT 15

Q90NL5 ID Q90NL5 PRELIMINARY; PRT; 201 AA.
 AC Q90NL5;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nickle D.C.;
 RT "A Persistent Reservoir for HIV-1 in Alveolar Macrophages."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF371104; AAK66503.1; -;
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR AIDS; Coat protein; Glycoprotein.
 KW NON_TER 1
 FT NON_TER 1
 FT NON_TER 201
 SQ SEQUENCE 201 AA; 22470 MW; E1993A2A412EC118 CRC64;

Query Match 40.5%; Score 51; DB 15; Length 201;
 Best Local Similarity 40.9%; Pred. No. 19;
 Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRLPEDGGQAEDELEV 23
 I:III :II :I:II:
 Db 179 ITGLLLTTRDGGGNGTNETEI 200

Search completed: September 11, 2003, 17:30:27
 Job time : 25.8449 secs

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03 ; Search time 3.46524 Seconds
(without alignments)
325.703 Million cell updates/sec

Title: US-09-853-253-4

Perfect score: 126

Sequence: 1 ALAGWLPRDPGQAEARDELEVR 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	126	100.0	117	1 GHRL_HUMAN	Q9ub33 homo sapien
2	95	75.4	117	1 GHRL_RAT	Q9qyh7 rattus norv
3	92	73.0	118	1 GHRL_PIG	Q9gky5 sus scrofa
4	91	72.2	117	1 GHRL_MOUSE	Q9eqx0 mus musculus
5	77	61.1	116	1 GHRL_BOVIN	Q9bdj6 bos taurus
6	73	57.9	117	1 GHRL_CANFA	Q9bef8 canis famil
7	54	42.9	200	1 NUPF_XENLA	P05221 xenopus lae
8	51	40.5	91	1 ACYP_BACSU	Q03031 bacillus su
9	50	39.7	653	1 APPI_MOUSE	Q03157 mus musculus
10	49	38.9	300	1 NKX1_BISBI	Q06383 bison bison
11	49	38.9	1216	1 NKX1_BOVIN	Q28139 bos taurus
12	48	38.1	668	1 SYM_METKA	Q8tx28 methanopyru
13	47.5	37.7	195	1 IGFB_HUMAN	P05019 homo sapien
14	47	37.3	380	1 OPRK_CAVPO	P41144 cavia porce
15	47	37.3	1168	1 DD88_ARATH	Q38953 arabidopsis
16	46.5	36.9	740	1 POLB_MAIZE	P15718 zea mays (m
17	46	36.5	516	1 SYM_AGR5	Q8ufa2 agrobacteri
18	45.5	36.1	580	1 MM14_PIG	Q9xt90 sus scrofa
19	45.5	36.1	582	1 MM14_HUMAN	P50281 homo sapien
20	45.5	36.1	582	1 MM14_MOUSE	P53690 mus musculus
21	45.5	36.1	582	1 MM14_RAT	Q10739 rattus norv
22	45.5	36.1	591	1 PAXI_HUMAN	P49023 homo sapien
23	45	35.7	190	1 RSPA_SCHPO	Q09757 schizosacch
24	45	35.7	242	1 HAP5_YEAST	Q02516 saccharomyc
25	45	35.7	349	1 WZEE_ECOLI	P25905 escherichia
26	45	35.7	494	1 KCF1_HUMAN	Q9h3m0 homo sapien
27	45	35.7	544	1 PYRG_DEIRA	Q9ru23 deinococcus
28	45	35.7	852	1 SRCH_RABIT	P16230 cryptotolagus
29	45	35.7	864	1 KLTK_HUMAN	P29376 homo sapien
30	45	35.7	992	1 SNXJ_HUMAN	Q92543 homo sapien
31	45	35.7	1059	1 SP8_VICFA	Q34876 vicia faba
32	44.5	35.3	777	1 RGL2_HUMAN	O15211 homo sapien
33	44.5	35.3	1233	1 VLI1_REOVD	P15024 reovirus (t

RESULT 1

ID	GHRL_HUMAN	STANDARD;	PRT;	117 AA.
AC	Q9UBU3: Q8TAT9; Q9H3R3;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).			
GN	GHRL OR MTLRP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.			
RX	MEDLINE=20067959; PubMed=10604470;			
Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;				
"Ghrelin is a growth-hormone-releasing acylated peptide from stomach.";				
RL	Nature 402:656-660(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Kojima M.;			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Stomach;			
RA	Tomasetto C., Karam S.M., Rio M.-C.;			
RT	"Identification of a novel gastric protein m46.";			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Wajhrach M.P., Ten I.S., Gertner J.M., Leibel R.L.;			
RT	"Genomic organization of the human Ghrelin gene.";			
RL	J. Endocrinol. Genet. 1:231-233(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Blood;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feilgenfeldt E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shervencko Y., Bouffard G.G.,			
RA	Blakeslee R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			

ALIGNMENTS

34	44	34.9	115	1 INS_VERMO	Q9w7r2 verasper mo
35	44	34.9	168	1 TCTP_BRAOL	Q944w6 brassica ol
36	44	34.9	273	1 NK22_MOUSE	P42586 mus musculus
37	44	34.9	301	1 TSA2_MOUSE	Q8vlg3 mus musculus
38	44	34.9	449	1 CMGA_BOVIN	P05059 bos taurus
39	44	34.9	4447	1 PKSK_BACSU	P40803 bacillus su
40	43.5	34.5	525	1 SYK_DEIRA	Q9rxel deinococcus
41	43.5	34.5	582	1 MM14_RABIT	Q95320 cryptotolagus
42	43	34.1	281	1 WS22_HUMAN	O43709 homo sapien
43	43	34.1	365	1 SYAP_MOUSE	Q9d5v6 mus musculus
44	43	34.1	380	1 OPRK_HUMAN	P41145 homo sapien
45	43	34.1	579	1 SYQ_XANAC	Q8pzn5 xanthomonas

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [6].
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RL hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RP [7].
 RP REVIEW.
 RP MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RL hormone secretagogue receptor.";
 CC Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect. Induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named Isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3.1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3.2; Sequence=VSP_003245;
 CC -1- PTM: O-n-octanoylation is essential for activity.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW='http://www.infobio-gen.fr/services/chromocancer/Genes/GhrelinID327.html'.
 CC -----
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 CC -----
 DR EXBL: AB029434; BAA89371.1; -.
 DR EXBL: AB035700; BAB19045.1; -.
 DR EXBL: AJ252278; CAB65733.1; -.
 DR EXBL: AF296558; AAG10300.1; -.
 DR EXBL: BC025791; AAH25791.1; -.
 DR PIR: A59316; A59316.
 DR MIM: 605353; -.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0005625; C:soluble fraction; TAS.
 DR GO: GO:0005331; F:growth hormone receptor ligand activity; TAS.
 DR GO: GO:0007267; P:cell-cell signaling; TAS.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
 DR InterPro: IPR006737; motilin_assoc.
 DR InterPro: IPR006738; motilin_ghrelin.
 DR InterPro: IPR005441; Preproghrelin.
 DR Pfam: PF04643; motilin_assoc; 1.
 DR Pfam: PF04644; motilin_ghrelin; 1.
 DR PRINTS: PR01624; GHRELIN.
 DR ProDom: PD332162; Preproghrelin; 1.
 KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23
 FT PEPTIDE 24 51 GHRELIN.
 FT PROPEP 52 117 REMOVED IN MATURE FORM.
 FT LIPID 26 26 N-OCTANOATE.
 FT VARSPIC 37 37 Missing (in Isoform 2).
 FT /FTID=VSP_003245.
 FT L -> M (IN REF. 5).
 FT CONFLICT 72 72

SO SEQUENCE 117 AA: 12911 MW: 39C0572BECA2755 CRC64;
 Query Match 100.0%; Score 126; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.8e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGGAEGAEDELEVR 24
 Db 52 ALAGWLRPEDGGGAEGAEDELEVR 75
 RESULT 2
 GHRL_RAT
 ID GHRL_RAT STANDARD: PRT; 117 AA.
 AC QOQYH7; Q9ET69;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide).
 GN GHRL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,
 RP AND ACYLATION OF SER-26.
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
 RX MEDLINE=20067959; PubMed=10604470;
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
 RT "Ghrelin is a growth-hormone-releasing acylated peptide from
 RT stomach.";
 RL Nature 402:656-660(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS
 RP SPECTROMETRY, AND ACYLATION OF SER-26.
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
 RX MEDLINE=20357315; PubMed=10801861;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Purification and characterization of rat des-Gln14-ghrelin, a second
 RT endogenous ligand for the growth hormone secretagogue receptor.";
 RL J. Biol. Chem. 275:21995-22000(2000).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=21092536; PubMed=11162448;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
 RT in gastrointestinal tissue.";
 RL Biochem. Biophys. Res. Commun. 279:909-913(2000).
 RN [4]
 RP STRUCTURE-ACTIVITY RELATIONSHIP.
 RX MEDLINE=21433488; PubMed=11549267;
 RA Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
 RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
 RT "Structure-activity relationship of ghrelin: pharmacological study of
 RT ghrelin peptides.";
 RL Biochem. Biophys. Res. Commun. 287:142-146(2001).
 RN [5]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RA "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect. Induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named Isoforms=2;

CC Name=1; Synonyms-Chrelin;
 CC ISOID-Q9QYH7-1; Sequence-Displayed;
 CC Name=2; Synonyms-del-Gln14-ghrelin;
 CC ISOID-Q9QYH7-2; Sequence-VSP_003248;
 CC TISSUE SPECIFICITY: Broadly expressed with higher expression in
 CC the stomach. Very low levels are detected in the hypothalamus,
 CC heart, lung, pancreas, intestine and adipose tissue.
 CC -1- PTM: O-n-octanoylation is essential for activity. The replacement
 CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.
 CC -1- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;
 CC RANGE=24-51.
 CC -1- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;
 CC RANGE=24-36, 38-51.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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 CC -----
 CC EMBL; AB029433; BAA89370.1; -;
 CC EMBL; AB035699; BAB11956.1; -;
 CC FIRM; B59316; B59316.
 CC InterPro: IPR006737; motilin_assoc.
 CC InterPro: IPR006738; motilin_ghrelin.
 CC InterPro: IPR005441; Preproghrelin.
 CC Pfam: PF04643; motilin_assoc; 1.
 CC Pfam: PF04644; motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom: PD332162; Preproghrelin; 1.
 CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW alternative splicing.
 FT SIGNAL 1 23 GHRELIN.
 FT PEPTIDE 24 51 REMOVED IN MATURE FORM.
 FT PROPEP 52 117 N-OCTANOATE.
 FT LIPID 26 26 Missing (in isoform 2).
 FT VARSPPLIC 37 37 /FTID-VSE_003248.
 FT SEQUENCE 117 AA; 13176 MW; 8857546F51A7691 CRC64;
 Query Match 75.4%; Score 95; DB 1; Length 117;
 Best Local Similarity 75.0%; Pred. No. 9.8e-07;
 Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 DB 52 ALEGWLHPEDRGQAGAEDELEIR 75
 RESULT 3
 GHRL_PIG.
 ID GHRL_PIG STANDARD; PRT; 118 AA.
 AC Q9GKY5; Q9BDG8; Q9GKY4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide).
 GN GHRL.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Kojima M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Stomach;

RA Rousselle J., Lacroix D., Dubreuil P.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms-Ghrelin;
 CC ISOID-Q9GKY5-1; Sequence-Displayed;
 CC Name=2; Synonyms-del-Gln14-ghrelin;
 CC ISOID-Q9GKY5-2; Sequence-VSP_003247;
 CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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 CC -----
 CC EMBL; AB035703; BAB19048.1; -;
 CC EMBL; AB035704; BAB19049.1; -;
 CC EMBL; AF308930; AAK19243.1; -;
 CC EMBL; AY028942; AAK30002.1; -;
 CC InterPro: IPR006737; motilin_assoc.
 CC InterPro: IPR006738; motilin_ghrelin.
 CC InterPro: IPR005441; Preproghrelin.
 CC Pfam: PF04643; motilin_assoc; 1.
 CC Pfam: PF04644; motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom: PD332162; Preproghrelin; 1.
 CC Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW alternative splicing.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT PEPTIDE 25 52 GHRELIN.
 FT PROPEP 53 118 REMOVED IN MATURE FORM (BY SIMILARITY).
 FT LIPID 27 27 N-OCTANOATE (BY SIMILARITY).
 FT VARSPPLIC 38 38 Missing (in isoform 2).
 FT SEQUENCE 118 AA; 12785 MW; 856D3E1D6DAB1A76 CRC64;
 Query Match 73.0%; Score 92; DB 1; Length 118;
 Best Local Similarity 66.7%; Pred. No. 2.7e-06;
 Matches 16; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
 DB 53 ALEGWLGPDSGEVEGDKLEIR 76
 RESULT 4
 GHRL_MOUSE
 ID GHRL_MOUSE STANDARD; PRT; 117 AA.
 AC Q9EQX0; Q9WU21;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide) (Motilin-related peptide) (M46 protein).
 GN GHRL OR MTLRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.

CC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Kojima M.;
 RL "Mouse mRNA for preproghrelin.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX STRAIN=C57BL/6J; TISSUE=Stomach;
 RC MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [5]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9EQX0-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9EQX0-2; Sequence=YSP_003246;
 CC -1- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
 CC with higher levels in the stomach, medium levels in the duodenum,
 CC jejunum, ileum and colon. Low expression in the testis and brain.
 CC Not detected in the salivary gland, pancreas, liver and lung.
 CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -----
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CC EMBL; AJ243503; CAB46500.1; -
 DR EMBL; AB035701; BAB19046.1; -
 DR EMBL; AB060078; BAB69857.1; -
 DR EMBL; AK008658; BAB25814.1; -
 DR EMBL; AK008860; BAB25934.1; -
 DR MG; MGI:1930008; Ghrl.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005576; C:extracellular; IDA.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR Pfam; PF04643; motilin_assoc; 1.
 DR Pfam; PF04644; motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 23
 FT PEPTIDE 24 51
 FT PROPEP 52 117
 FT LIPID 26 26
 FT VAPSPIC 37 37
 FT
 SQ SEQUENCE 117 AA; 13207 MW; EACB49D2E3CA7203 CRC64;
 Query Match 72.28; Score 91; DB 1; Length 117;
 Best Local Similarity 70.88; Pred. No. 3.6e-06;
 Matches 1; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
 Db 52 ALEGWLPEDRGQAEETEELR 75
 RESULT 5
 GHRL_BOVIN
 ID GHRL_BOVIN STANDARD; PRT; 116 AA.
 AC Q9BDJ6; Q9GKY6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ghrelin precursor (growth hormone secretagogue) (Growth hormone
 DE releasing peptide).
 GN GHRL.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kita K., Harada K., Yokota H.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 24-99 FROM N.A.
 RA Kojima M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -----
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CC -----
DR EMBL; AF350329; AAK18612.1; -.
DR EMBL; AB035702; BAB19047.1; -.
DR InterPro; IPR006737; motilin_ghrelin.
DR InterPro; IPR006738; motilin_ghrelin.
DR Pfam; PF04643; motilin_ghrelin; 1.
DR PRINTS; PRO1624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 50 GHRELIN (BY SIMILARITY).
FT PROPEP 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT CONFLICT 34 34 K -> E (IN REF. 2).
SQ SEQUENCE 116 AA; 12792 MW; F55536DAC5FA59B6 CRC64;

Query Match 61.1%; Score 77; DB 1; Length 116;
Best Local Similarity 69.6%; Pred. No. 0.00035;
Matches 16; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAGAEDELEVR 24
DB 52 LEGQFDPEVGSQAEGAEDELEIR 74

RESULT 6
GHRL_CANFA
ID GHRL_CANFA STANDARD; PRT; 117 AA.
AC Q9BEF8; Q9BEF7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide).
GN GHRL OR MTLRP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Gastric fundus;
RA Tomasetto C., Wendling C., Rio M.-C., Poitras P.;
RT Identification of cDNA encoding MTLRP/ghrelin precursor from dog
RT fundus.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9BEF8-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9BEF8-2; Sequence=VSP_003244;
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC -----
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CC -----
DR EMBL; AJ298295; CAC29155.1; -.

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DR EMBL; AJ298296; CAC29156.1; -.
DR InterPro; IPR006737; motilin_ghrelin.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; motilin_ghrelin; 1.
DR Pfam; PF04644; motilin_ghrelin; 1.
DR PRINTS; PRO1624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).
FT VARSPLIC 37 37 Missing (in isoform 2).
FT FTID=VSP_003244.
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Query Match 57.9%; Score 73; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 0.0013;
Matches 16; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 ALAGWLRPEDGGQAGAEDELEVR 24
DB 52 ALEGLSGPEDTSQVEAEDELEIR 75

RESULT 7
NUPL_XENLA
ID NUPL_XENLA STANDARD; PRT; 200 AA.
AC P05221;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nucleoplasmin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218476; PubMed=2884102;
RA Dingwall C., Dilworth S.M., Black S.J., Kearsey S.E., Cox L.S.,
RA Laskey R.A.;
RT "Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and a
RT cluster of sequences homologous to putative nuclear localization
RT signals.";
RL EMBO J. 6:69-74(1987).
RN [2]
RP SEQUENCE OF 7-200 FROM N.A.
RX MEDLINE=88112783; PubMed=3428591;
RA Buerglin T.R., Matta J.I.W., Newmeyer D.D., Zeller R.,
RA de Robertis E.M.;
RT "Cloning of nucleoplasmin from Xenopus laevis oocytes and analysis of
RT its developmental expression.";
RL Genes Dev. 1:97-107(1987).
CC -!- FUNCTION: NUCLEOPLASMIN IS AN ACIDIC, PENTAMERIC, THERMOSTABLE
CC PROTEIN WHICH IS ABLE TO ASSEMBLE NUCLEOSOMES BY BINDING HISTONES
CC AND TRANSFERRING THEM TO DNA.
CC -!- SUBUNIT: Homopentamer.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.
CC -----
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CC -----
DR EMBL; X04766; CAA28460.1; -.

```

	RA	Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetille D., Porwollik G., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tanakoshi A., Tanaka T., Terpsstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
	RT	Nature 390:249-256(1997).
	RL	-!- CATALYTIC ACTIVITY: An acyl phosphate + H(2)O -> a fatty acid anion + phosphate.
	CC	-!- SIMILARITY: BELONGS TO THE ACYLPHOSPHATASE FAMILY.
	CC	-----
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	CC	-----
	DR	EMBL; D86417; BAA22305.1; .
	DR	EMBL; Z99108; CAB12593.1; .
	DR	PIR; B69811; B69811.
	DR	HSP; P00818; IAPS.
	DR	Subtilist; BG12947; yfil.
	DR	InterPro; IP8001792; Acylphosphatase.
	DR	Pfam; PF00708; Acylphosphatase; 1.
	DR	PRINTS; PR00112; ACYLPHPHTASE..
	DR	ProDom; PD001884; Acylphosphatase; 1.
	DR	PROSITE; PS00150; ACYLPHOSPHATASE_1; 1.
	DR	PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.
	KW	Hypothetical protein; Hydrolase; Complete proteome.
	SQ	SEQUENCE 91 AA; 10318 MW; 50795631BF310F4 CRC64;
		Query Match 40.5%; Score 51; DB 1; Length 91;
		Best Local Similarity 44.0%; Pred. No. 1.4;
		Matches 11; Conservative 5; Mismatches 5; Indels 4; Gaps 1;
	QY	2 LAGWLRPEDGGQ----AEGAEDELE 22 :: :: :
	Dd	30 LAGWVKNRDGRVEILAEGPENALQ 54 :: :: :
	RESULT 9	
	APPL_MOUSE	
	ID APPL_MOUSE STANDARD; PRT; 653 AA.	
	AC Q03157; OSVC38;	
	DT 01-OCT-1993 (Rel. 27, Created)	
	DT 01-OCT-1993 (Rel. 27, Last sequence update)	
	DT 15-SEP-2003 (Rel. 42, Last annotation update)	
	DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].	
	OS Mus musculus (Mouse).	
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
	OX NCBI_TaxId=10090;	
	RN [1]	
	RP SEQUENCE FROM N.A.	
	RC TISSUE=Brain;	
	RX MEDLINE=93066322; PubMed=1279693;	
	RA Wasco W., Bupp K., Magendanz M., Gusella J.F., Tanzi R.E., Solomon F.;	
	RT Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer disease-associated amyloid beta protein precursor."	
	RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).	

RN [2] SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muny D.K., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettemann M., Madan A., Rodrigues S., Sanchez A.,
 Whiting M., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RX COLLAGEN-BINDING.
 RP MEDLINE=96139497; PubMed=8576160;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 mapping of the binding sites on APP and collagen type I";
 RT J. Biol. Chem. 271:1613-1620(1996).
 RN [4]
 RX INTERACTION WITH DAB1.
 RP MEDLINE=99389880; PubMed=10460257;
 RA Hameyouni R., Rice D.S., Sheldon M., Curran T.;
 RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
 protein 1";
 RL J. Neurosci. 19:7507-7515(1999).
 RN [5]
 RX INTERACTION WITH MAPK8IP1.
 RP MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niihara T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/Islet-brain-1
 scaffolds Alzheimer's amyloid precursor protein with JNK";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [6]
 RX GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
 TYR-641.
 RP MEDLINE=22313598; PubMed=12228233;
 RA Scheinfeld M.H., Gherzi E., Laky K., Fowlkes B.J., D'Adamio L.;
 RT "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
 secretase regulates transcription";
 RL J. Biol. Chem. 277:44195-44201(2002).
 CC -1- FUNCTION: May play a role in postsynaptic function. The C-terminal
 gamma-secretase processed fragment, ALDI1, activates transcription
 activation through APBB1 (Ref5) binding. Couples to JIP signal
 transduction through C-terminal binding. May interact with
 cellular G-protein signaling pathways. Can regulate neurite
 outgrowth through binding to components of the extracellular
 matrix such as heparin and collagen I.
 CC -1- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
 neuronal apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 cytoplasmic proteins, including APBB and APBA family members,
 MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
 serine phosphorylation.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
 processed in the Golgi complex.
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 phosphorylated proteins is required for the specific binding of
 the PID domain. However additional amino acids either N- or C-

CC terminal to the NPXY motif are often required for complete
 interaction. The NPXY site is also involved in clathrin-mediated
 endocytosis.
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal
 apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
 similarity).
 CC -1- PTM: N-glycosylated.
 CC -1- PTM: O-glycosylated.
 CC -1- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
 CC Zinc-binding increases heparin binding. No Cu(II) reducing
 activity with copper-binding.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
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 CC -----
 DR EMBL: L04538; AAA37247.1; -;
 DR EMBL: BC021877; AAH21877.1; -;
 DR FIR: A46362; A46362.
 DR HSSP: P05067; 1MWP.
 DR MGD: MGI:88046; Aplp1.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
 KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
 KW Glycoprotein.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 653 AMYLOID-LIKE PROTEIN 1.
 FT CHAIN 624 653 C30 (BY SIMILARITY).
 FT DOMAIN 38 583 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 584 606 POTENTIAL.
 FT DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 157 177 COPPER-BINDING.
 FT DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 263 271 POLY-GLU.
 FT DOMAIN 535 538 POLY-SER.
 FT DOMAIN 601 606 POLY-LEU.
 FT SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY
 SIMILARITY).
 FT SITE 607 618 BASOLATERAL SORTING SIGNAL (BY
 SIMILARITY).
 FT SITE 623 624 CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
 FT SITE 641 644 ENDOCYTOSIS SIGNAL.
 FT SITE 643 646 NPXY MOTIF.
 FT CARBOHYD 464 464 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 554 554 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOTAGEN 641 641 Y->G: REDUCED BINDING OF APBB1.
 FT CONFLICT 17 17 P -> PP (IN REF. 2).
 SQ SEQUENCE 653 AA; 72750 MW; 56516DC3EA40E4B0 CRC64;
 Query Match 39.7%; Score 50; DB 1; Length 653;
 Best Local Similarity 76.9%; Pred. No. 14;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 11 GGQAGGADEDELEV 23
 ||:|||||
 Db 233 GGRAGGEDDEEV 245
 RESULT 10
 NKX1_BISBI

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ID AC NKX1_BISBI STANDARD; PRT; 300 AA.
DT 046383;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Sodium/potassium/calcium exchanger 1 (Na(+)/K(+)/Ca(2+)-
DE SLC24A1 OR NCKX1.
OS Bison bison (American bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bison.
OX NCBI_TaxID=9901;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98138491; PubMed=9478004;
RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison
RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
CC -1- FUNCTION: Critical component of the visual transduction cascade,
CC controlling the calcium concentration of outer segments during
CC light and darkness. Light causes a rapid lowering of cytosolic
CC free calcium in the outer segment of both retinal rod and cone
CC photoreceptors and the light-induced lowering of calcium is caused
CC by extrusion via this protein which plays a key role in the
CC process of light adaptation. Transports one Ca(2+) and one K(+) in
CC exchange for four Na(+) (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q28139-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q28139-2; Sequence=VSP_006159;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Retina.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC
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CC
CC EMBL; AF025480; AAC13320.1;
CC Vision; Antiprot; Symport; Calcium transport;
CC Potassium transport; Sodium transport; Transmembrane.
CC NON_TER 1 1
CC TRANSNM 259 275 POTENTIAL.
CC DOMAIN 218 242 POLY-GLU.
CC NON_TER 300 300
CC SEQUENCE 300 AA; 31671 MW; 2BE592DA5AB9781E CRC64;
Query Match 38.98; Score 49; DB 1; Length 300;
Best Local Similarity 42.98; Pred. No. 8.8;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
Oy 4 GWLPRPDGGGAEGAEDELEVR 24
Db 84 GEIQAGEGGEVEDEGEIQ 104
RESULT 11
NKX1_BOVIN STANDARD; PRT; 1216 AA.
AC Q28139; Q46384;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-
DE exchange protein 1) (Retinal rod Na-Ca+K exchanger).
DE SLC24A1 OR NCKX1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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RP SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 66-88; 232-249;
RC 647-660 AND 1119-1136.
RC TISSUE-Retina;
RX MEDLINE=92258377; PubMed=1582405;
RA Rellaender H., Achilles A., Friedel U., Maul G., Lottspeich F.,
RA Cook N.J.;
RT "Primary structure and functional expression of the Na/Ca,K-exchanger
RL from bovine rod photoreceptors.";
RL EMBO J. 11:1689-1695(1992).
RN [2]
RP SEQUENCE OF 725-1216 FROM N.A. (ISOFORM 1).
RC TISSUE-Retina;
RX MEDLINE=98138491; PubMed=9478004;
RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.M.;
RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger:
RL comparison with a revised bovine sequence.";
RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
CC -1- FUNCTION: Critical component of the visual transduction cascade,
CC controlling the calcium concentration of outer segments during
CC light and darkness. Light causes a rapid lowering of cytosolic
CC free calcium in the outer segment of both retinal rod and cone
CC photoreceptors and the light-induced lowering of calcium is caused
CC by extrusion via this protein which plays a key role in the
CC process of light adaptation. Transports one Ca(2+) and one K(+) in
CC exchange for four Na(+) (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q28139-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q28139-2; Sequence=VSP_006159;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Retina.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X66481; CAA47108.1;
CC EMBL; AF025664; AAB88884.1;
CC PIR; S20969; S20969.
CC InterPro; IPR004817; K_NaCaexchang.
CC InterPro; IPR004481; K_NaCaexchng.
CC InterPro; IPR004837; NaCa_Exmemb.
CC Pfam; PF01699; NaCa_Ex; 2.
CC TIGRFAMS; TIGR00927; 2A1904; 1.
CC TIGRFAMS; TIGR00367; TIGR00367; 1.
CC Vision; Transport; Antiprot; Symport; Calcium transport;
CC Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
CC Phosphorylation; Signal; Repeat; Alternative splicing.
CC SIGNAL 1 38
CC CHAIN 39 1216 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
CC DOMAIN 39 446 EXTRACELLULAR (POTENTIAL).
CC TRANSNM 447 467 POTENTIAL.
CC DOMAIN 468 491 CYTOPLASMIC (POTENTIAL).
CC TRANSNM 492 512 POTENTIAL.
CC DOMAIN 513 518 EXTRACELLULAR (POTENTIAL).
CC TRANSNM 519 539 POTENTIAL.
CC DOMAIN 540 557 CYTOPLASMIC (POTENTIAL).
CC TRANSNM 558 578 POTENTIAL.
CC DOMAIN 579 579 EXTRACELLULAR (POTENTIAL).
CC TRANSNM 580 600 POTENTIAL.
CC DOMAIN 601 1024 CYTOPLASMIC (POTENTIAL).
CC TRANSNM 1025 1045 POTENTIAL.
CC DOMAIN 1046 1052 EXTRACELLULAR (POTENTIAL).
CC TRANSNM 1053 1073 POTENTIAL..
CC DOMAIN 1074 1088 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 1089 1109 POTENTIAL.
FT DOMAIN 1110 1127 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1128 1148 POTENTIAL.
FT DOMAIN 1149 1157 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1158 1178 POTENTIAL.
FT DOMAIN 1179 1185 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1186 1206 POTENTIAL.
FT DOMAIN 1207 1216 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 796 928 8 X 17 AA TANDEM REPEATS OF D-E-D-E-G-E-
I-Q-A-G-E-[CA]-G-E-V-[EK]-G.
1 (APPROXIMATE).
2.
3.
4.
5.
6.
7.
8 (APPROXIMATE).
ALPHA-1.
POLY-GLU.
PHOSPHORYLATION (POTENTIAL).
N-LINKED (GLNAC. . .) (POTENTIAL).
N-LINKED (GLNAC. . .) (POTENTIAL).
Missing (in isoform 2).
/FTID-VSP_006159.
MISSING (IN REF. 1; AA SEQUENCE).
MISSING (IN REF. 1; AA SEQUENCE).
MISSING (IN REF. 1; AA SEQUENCE).
A -> G (IN REF. 2).
SQ SEQUENCE 1216 AA; 131614 MW; 39F149A74D1D0523 CRC64;

Query Match 38.9%; Score 49; DB 1; Length 1216;
Best Local Similarity 42.9%; Pred. No. 36;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 4 GMLRPEDGGQAGAEDELEVR 24
I :: :::: :::: ::::
DB 816 GEIQAGEGVEGEDEGEIQ 836

RESULT 12
SYM_METKA
ID SYM_METKA STANDARD; PRT; 668 AA.
AC Q8TX28;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
DE (MTRS).
GN METG OR MK0850.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Shesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natalie D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -1- FUNCTION: Is required not only for elongation of protein synthesis
but also for the initiation of all mRNA translation through
CC initiator tRNA(fMet) aminoacylation (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
diphosphate + L-methionyl-tRNA(Met).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC MetG subfamily 1.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE010375; AA02063.1; -.
CC HAMAP: MF_00098; fused; 1.
CC InterPro: IPR004495; MetG_Cterm.
CC InterPro: IPR002300; tRNA-synt_1a.
CC InterPro: IPR001412; tRNA-synt_1.
CC InterPro: IPR002304; tRNA-synt_met.
CC InterPro: IPR002547; tRNA-bind.
CC Pfam: PF00133; tRNA-synt_1; 1.
CC Pfam: PF01588; tRNA_bind; 1.
CC PIRSF: PIRSF001528; MetRS_dimerising; 1.
CC TIGRFAMs: TIGR00398; metG; 1.
CC TIGRFAMs: TIGR00399; metG_C_term; 1.
CC PROSITE: PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
CC PROSITE: PS00886; TRSD; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW RNA-binding; tRNA-binding; Metal-binding; Zinc; Complete proteome.
FT SITE 11 21 "HIGH" REGION.
FT SITE 332 336 "KMSKS" REGION.
FT DOMAIN 567 668 tRNA-BINDING.
FT METAL 146 146 ZINC (BY SIMILARITY).
FT METAL 149 149 ZINC (BY SIMILARITY).
FT METAL 159 159 ZINC (BY SIMILARITY).
FT METAL 162 162 ZINC (BY SIMILARITY).
SQ SEQUENCE 668 AA; 77386 MW; FBC5734FF5FEF015 CRC64;

Query Match 38.1%; Score 48; DB 1; Length 668;
Best Local Similarity 53.3%; Pred. No. 27;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 LRPEGGQAGAEDE 20
I :: :::: ::::
DB 547 LUPESEGESEGGQDDE 561

RESULT 13
IGFB_HUMAN
ID IGFB_HUMAN STANDARD; PRT; 195 AA.
AC P05019;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Insulin-like growth factor IB precursor (IGF-IB) (Somatomedin C).
GN IGF1 OR IBP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168194; PubMed=2937782;
RA Rotwein P., Pollock K.M., Didier D.K., Krivi G.G.;
RT "Organization and sequencing of the human insulin-like growth factor I
gene. Alternative RNA processing produces two insulin-like growth
factor I precursor peptides.";
RL J. Biol. Chem. 261:4828-4832(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86094355; PubMed=3455760;
RA Rotwein P.;
RT "Two insulin-like growth factor I messenger RNAs are expressed in

```



```
Query Match          37.7%; Score 47.5; DB 1; Length 195;
Best Local Similarity 45.5%; Pred. No. 9.3;
Matches 10; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 4 GMLRPEDGG-QAEGAEDELEVR 24
   || | | | | | | | |
Db 151 GWPKTHPGGEQEGTEASLQIR 172

RESULT 14
OPRK_CAVPO STANDARD; PRT; 380 AA.
ID OPRK_CAVPO
AC P41144;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Kappa-type opioid receptor (KOR-1).
GN OPRK1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Brain;
RX MEDLINE=94224825; PubMed=8170987;
RA Xie G.X., Meng F., Mansour A., Thompson R.C., Hoversten M.T.,
RA Goldstein A., Watson S.J., Akil H.;
RT "Primary structure and functional expression of a guinea pig kappa
RT opioid (dynorphin) receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3779-3783(1994).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U04092; AAA67171.1; -.
DR PIR; A55259; A55259.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0362; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match          37.3%; Score 47; DB 1; Length 380;
Best Local Similarity 38.1%; Pred. No. 22;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 LAGWLRPEDGGQAEGAEDELE 22
   | | | | | | | |
Db 30 LPGWAEPDGNAGSAGPDEGLE 50

RESULT 15
DDX8_ARATH STANDARD; PRT; 1168 AA.
ID DDX8_ARATH
AC Q38953; O9LRV0;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative pre-mRNA splicing factor ATP-dependent RNA helicase.
GN AT3G26560 OR WPE16.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=97086699; PubMed=8932388;
RA Quigley F., Dao P., Cottet A., Mache R.;
RT "Sequence analysis of an 81 kb contig from Arabidopsis thaliana
RT chromosome III.";
RL Nucleic Acids Res. 24:4313-4318(1996).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty pl and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
CC -1- FUNCTION: COULD ACT LATE IN THE SPLICING OF PRE-MRNA AND MEDIATE
CC THE RELEASE OF THE SPLICED MRNA FROM SPliceosomes (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. DEAH
CC SUBFAMILY. DDX8/PRP22 ORTHOLOG.
CC -1- SIMILARITY: Contains 1 SL motif domain.
CC -1- CAUTION: Ref.1 sequences differ from that shown due to a
CC frameshift in position 57.
CC -----
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CC -----
DR EMBL; X98130; CAA66825.1; ALT_FRAME.
DR EMBL; X97970; CAA66613.1; ALT_FRAME.
DR EMBL; AB028611; BAB01838.1; -.
DR HSP; P05055; 1SRO.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002464; DEAH_box.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR003029; SL.
DR Pfam; PF00271; helicase_C; 1.
DR Pfam; PF00375; SL; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR SMART; SM00316; SL; 1.
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DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
DR PROSITE; PS0126; S1; 1.
KW Hypothetical protein; mRNA processing; mRNA splicing; Helicase;
KW ATP-binding; Nuclear protein.
FT DOMAIN 214 283 S1 MOTIF.
FT NP_BIND 538 545 ATP (POTENTIAL).
FT SITE 635 638 DEAH BOX.
FT DOMAIN 777 780 POLY-PRO.
SQ SEQUENCE 1168 AA; 134156 MW; B3632DE4A7A7690C CRC64;

Query Match      37.38; Score 47; DB 1; Length 1168;
Best Local Similarity 57.9%; Pred. No. 66;
Matches 11; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

Oy 9 EDGG-----QAEGAEDELEV 23
Db 372 EDGDMLYQEGAELEEI 390

```

Search completed: September 11, 2003, 17:21:44
Job time : 6.46524 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model
Run on: September 11, 2003, 17:21:03 : Search time 8.98396 Seconds
(without alignments)
256.908 Million cell updates/sec

Title: US-09-853-253-4
Perfect score: 126
Sequence: 1 ALAGWLRPEDGGQAGAEDELEVR 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126	100.0	117	1 A59316	ghrelin precursor
2	95	75.4	117	1 B59316	ghrelin precursor
3	54	42.9	200	2 A28169	nucleoplasmin - Af
4	52	41.3	232	2 G83609	probable transcript
5	51.5	40.9	249	2 T21920	hypothetical prote
6	51	40.5	91	2 B69811	conserved hypothet
7	51	40.5	604	2 AE2760	chloride channel p
8	51	40.5	604	2 C97541	chloride channel
9	50	39.7	131	2 B75433	hypothetical prote
10	50	39.7	653	2 A46362	amyloid precursor-
11	49.5	39.3	484	2 C75609	amino acid ABC tra
12	49	38.9	274	2 A26050	exfoliative toxin
13	49	38.9	1199	2 S20969	Na+/Ca2+,K+-exchan
14	48	38.1	114	2 T49338	hypothetical prote
15	47.5	37.7	195	1 IGRI1B	insulin-like growt
16	47	37.3	355	2 T09738	protein kinase PKI
17	47	37.3	380	2 A52559	kappa opioid recep
18	47	37.3	1273	2 C96767	unknown protein F2
19	46.5	36.9	80	2 T26398	hypothetical prote
20	46.5	36.9	740	2 T03975	hypothetical prote
21	46	36.5	163	2 T21674	hypothetical prote
22	46	36.5	259	2 A87377	hypothetical prote
23	46	36.5	287	2 C82965	hypothetical prote
24	46	36.5	491	2 H97088	protein containing
25	46	36.5	516	2 A82760	methionyl-tRNA syn
26	46	36.5	516	2 C97541	methionyl-tRNA syn
27	46	36.5	528	2 C84110	xylan beta-1,4-xyl
28	46	36.5	871	2 B71039	hypothetical prote
29	45.5	36.1	582	2 I38028	matrix metalloprot

30	45.5	36.1	582	2 I48673	matrix metalloprot
31	45.5	36.1	582	2 I84471	matrix metalloprot
32	45	35.7	69	2 C87574	cold-shock domain
33	45	35.7	184	2 T43321	ribosomal protein
34	45	35.7	191	2 S62409	40S ribosomal prot
35	45	35.7	195	2 T48728	hypothetical prote
36	45	35.7	242	2 S67270	CCAAT-binding fact
37	45	35.7	296	2 T15550	hypothetical prote
38	45	35.7	297	2 G71446	hypothetical prote
39	45	35.7	349	2 F91218	probable transport
40	45	35.7	349	2 H86064	probable transport
41	45	35.7	349	2 D65182	probable transport
42	45	35.7	479	2 A75353	mOCR protein - Del
43	45	35.7	494	2 JC5919	potassium channel
44	45	35.7	544	2 B75379	CTP synthase - Del
45	45	35.7	600	2 T17436	ATP-binding protei

ALIGNMENTS

RESULT 1

A59316
ghrelin precursor - human
N:Alternate names: preproghrelin
C:Species: Homo sapiens (man)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C:Accession: A59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: A59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-117 <KOJ>
A:Cross-references: GB:AB029434; NID:g6691571; PIDN:BAA89371.1; PID:g6691572
A:Experimental source: Tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gr
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 126; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAGWLRPEDGGQAGAEDELEVR 24
Db 52 ALAGWLRPEDGGQAGAEDELEVR 75

RESULT 2

B59316
ghrelin precursor - rat
N:Alternate names: preproghrelin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C:Accession: B59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: B59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA; protein
A:Residues: 1-117 <KOJ>
A:Cross-references: GB:AB029433; NID:g6691569; PIDN:BAA89370.1; PID:g6691570
A:Experimental source: strain SD; tissue stomach endocrine cells

A:Note: submitted to GenBank, June 1999
 C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone) from the hypothalamus
 C:Superfamily: motilin
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-51/Product: ghrelin #status predicted <MAT>
 F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 75.4%; Score 95; DB 1; Length 117;
 Best Local Similarity 75.0%; Pred. No. 2.6e-06;
 Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ALAGWLRPEDGGQAGAEDELEVR 24
 || ||| ||| |||| |||| |||| ||||
 Db 52 ALEGLHPEDRGQAEEAELEIR 75

RESULT 3
 A26169
 nucleoplasm - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 13-Aug-1999
 C:Accession: A26169
 R:Daniel, C.; Dilworth, S.M.; Black, S.J.; Kearsey, S.E.; Cox, L.S.; Laskey, R.A.
 EMBO J. 6, 69-74, 1987
 A:Title: Nucleoplasm cDNA sequence reveals polyglutamic acid tracts and a cluster of serine residues
 A:Reference number: A26169; MUID:87218476; PMID:2884102
 A:Accession: A26169
 A:Molecule type: mRNA
 A:Residues: 1-200 <DIN>
 A:Cross-references: GB:X04766; NID:g64939; PIDN:CAA28460.1; PID:g64940
 C:Superfamily: nucleophosmin
 C:Keywords: molecular chaperone; nucleus

Query Match 42.9%; Score 54; DB 2; Length 200;
 Best Local Similarity 55.6%; Pred. No. 2.8;
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 WLRPE-DGQAGAEDELE 22
 | || |||| |||| ||||
 Db 126 WAEEDSGEAGEEEEE 143

RESULT 4
 G83609
 probable transcription regulator PA0279 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: G83609
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brice, S.; Olson, M.V.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: G83609
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-232 <SPO>
 A:Cross-references: GB:AE004466; GB:AE004091; NID:g9946120; PIDN:AA03668.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA0279

Query Match 41.3%; Score 52; DB 2; Length 232;
 Best Local Similarity 72.7%; Pred. No. 6.2;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GWRPDEGGQA 14
 ||||| ||||
 Db 202 GWRPQDSRA 212

RESULT 5
 T21920
 hypothetical protein F37D6.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T21920
 R:McMurray, A.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: Z19487
 A:Accession: T21920
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-249 <WIL>
 A:Cross-references: EMBL:Z75540; PIDN:CAA99852.1; GSPDB:GN00019; CESP:F37D6.7
 A:Experimental source: clone F37D6
 C:Genetics:
 A:Gene: CESP:F37D6.7
 A:Map position: 1
 A:Introns: 41/1; 62/1; 115/1; 176/1; 209/1

Query Match 40.9%; Score 51.5; DB 2; Length 249;
 Best Local Similarity 52.9%; Pred. No. 7.8;
 Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy 5 WLRPE-DGQAGAEDE 20
 ||||| |||| ||||
 Db 73 WIREPNGDDGSGEDK 89

RESULT 6
 B69811
 conserved hypothetical protein yfif - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C:Accession: B69811
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 C.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
 tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lard
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma
 y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadaie, Y.; Sato, T.; Scan
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: B69811
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-91 <KUN>
 A:Cross-references: GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12593.1; PID:g26330
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yfif
 C:Superfamily: acylphosphatase

Query Match 40.5%; Score 51; DB 2; Length 91;
 Best Local Similarity 44.0%; Pred. No. 3.4;
 Matches 11; Conservative 5; Mismatches 5; Indels 4; Gaps 1;

Qy 2 LAGWLRPEDGGQ----AEGAEDELE 22
 ||||| | | | ||| | | |
 Db 30 LAGWKNRDRDGRVEILAEAGPENALQ 54

RESULT 7
 AE2760

chloride channel protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AE2760
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gilliet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AE2760
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AA42499.1; PID:gl71739917; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: clc
 A:Map position: circular chromosome

Query Match 40.5%; Score 51; DB 2; Length 604;
 Best Local Similarity 62.5%; Pred. No. 22;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAGWLRLPDPGGQAG 16
 I: ||||| || |
 Db 288 AIPGWLRLPTLGGVAVG 303

RESULT 8
 C97541
 chloride channel, clc (AE005067) [imported] - Agrobacterium tumefaciens (strain C58, Cer
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C:Accession: C97541
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: C97541
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-604 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK87284.1; PID:gl15156576; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C_2753
 A:Map position: circular chromosome

Query Match 40.5%; Score 51; DB 2; Length 604;
 Best Local Similarity 62.5%; Pred. No. 22;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAGWLRLPDPGGQAG 16
 I: ||||| || |
 Db 288 AIPGWLRLPTLGGVAVG 303

RESULT 9
 B75433
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
 C:Accession: B75433
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 . M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: B75433

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-131 <WHI>
 A:Cross-references: GB:AE001963; GB:AE000513; NID:g6458869; PIDN:AAF10714.1; PID:g645
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1139
 A:Map position: 1
 C:Superfamily: Deinococcus radiodurans hypothetical protein DR1139

Query Match 39.7%; Score 50; DB 2; Length 131;
 Best Local Similarity 47.4%; Pred. No. 6.7;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 ALAGWLRLPDPGGQAG 19
 || | || | | || |
 Db 101 ALLAWPPPPRGAQVOGA 119

RESULT 10
 A46362
 amyloid precursor-like protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
 C:Accession: A46362
 R:Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
 Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
 A:Title: Identification of a mouse brain cDNA that encodes a protein related to the A
 A:Reference number: A46362; MUID:93066322; PMID:1279693
 A:Accession: A46362
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-653 <WAS>
 A:Experimental source: brain
 A:Note: Sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIP:118684)
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
 C:Keywords: transmembrane protein

Query Match 39.7%; Score 50; DB 2; Length 653;
 Best Local Similarity 76.9%; Pred. No. 34;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGAAGAGADELEV 23
 ||: ||| || | |
 Db 233 GGRAEGGEDEEV 245

RESULT 11
 C75609
 amino acid ABC transporter, permease protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: C75609
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 . M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: C75609
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <WHI>
 A:Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12224.1; PID:g646
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DRA0136
 A:Map position: 2

Query Match 39.3%; Score 49.5; DB 2; Length 484;
 Best Local Similarity 61.1%; Pred. No. 29;
 Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 2 LAGWLRPEDGGQAEAGDELE 19
||||| | :||| |
Db 468 LAGWLTPR-GLRAEGGEE 484

RESULT 12
A26050
exfoliative toxin B precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 18-Nov-2002
C:Accession: A26050
R:Jackson, M.P.; Iandolo, J.J.
J. Bacteriol. 167, 726-728, 1986
A:Title: Sequence of the exfoliative toxin B gene of Staphylococcus aureus.
A:Reference number: A26050; MUID:86277939; PMID:3733674
A:Accession: A26050
A:Molecule type: DNA
A:Residues: 1-274 <JAC>
C:Superfamily: staphylococcal serine proteinase
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-274/Product: exfoliative toxin B #status predicted <MAT>

Query Match 38.9% Score 49; DB 2; Length 274;
Best Local Similarity 44.4%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 5 WLRPEDGGQAEAGDELE 22
||: |||| | ||: |
Db 86 WLKIQDGGDTTGQEEQE 103

RESULT 13
S20969
Na+/Ca2+, K+-exchanging protein - bovine
N:Alternate names: Na+/Ca2+, K+ antiporter; Na/Ca, K-exchanger
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S20969
R:Reilander, H.; Achilles, A.; Friedel, U.; Maul, G.; Lottspeich, F.; Cook, N.J.
EMBO J. 11, 1689-1695, 1992
A:Title: Primary structure and functional expression of the Na/Ca, K-exchanger from bovine
A:Reference number: S20969; MUID:92258377; PMID:1582405
A:Accession: S20969
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1199 <REI>
A:Cross-references: GB:X66481; NID:g505578; PIDN:CAA47108.1; PID:g505579

Query Match 38.9% Score 49; DB 2; Length 1199;
Best Local Similarity 42.9%; Pred. No. 86;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GWLRLPEDGGQAEAGDELEVR 24
|::: ||: || |||| |
Db 816 GEIQAGEGGEVGEDGEIQ 836

RESULT 14
T49338
hypothetical protein B13N20.230 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T49338
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <SCH>
A:Cross-references: EMBL:AL355925; GSPDB:GN00116; NCSP:B13N20.230
A:Experimental source: BAC clone B13N20; strain OR74A

C:Genetics:
A:Gene: NCSP:B13N20.230
A:Map position: 6
C:Superfamily: Neurospora crassa hypothetical protein B13N20.230

Query Match 38.1% Score 48; DB 2; Length 114;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 9 EDGGQAEAGDELEVR 23
||| | |||| |
Db 44 EDGFDDEGKEDQLEV 58

RESULT 15
IGHULB
insulin-like growth factor I precursor, splice form B [validated] - human
N:Alternate names: IGF-IB; somatomedin C
N:Contains: insulin-like growth factor IB-E1 amide
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-2000
C:Accession: A01611; A26181; S30540; B48960; A42664
R:Rotwein, P.; Pollock, K.M.; Didier, D.K.; Krivl, G.G.
J. Biol. Chem. 261, 4828-4832, 1986
A:Title: Organization and sequence of the human insulin-like growth factor I gene. A1
A:Reference number: A92581; MUID:86168194; PMID:2937782
A:Accession: A01611
A:Molecule type: DNA
A:Residues: 1-195 <ROT1>
A:Cross-references: GB:M14155; NID:gi83106; PIDN:AAA52537.1; PID:gi83109
R:Rotwein, P.
Proc. Natl. Acad. Sci. U.S.A. 83, 77-81, 1986
A:Title: Two insulin-like growth factor I messenger RNAs are expressed in human liver
A:Reference number: A26181; MUID:86094355; PMID:3455760
A:Accession: A26181
A:Molecule type: mRNA
A:Residues: 1-195 <ROT2>
A:Cross-references: GB:M11568; NID:gi83111; PIDN:AAA52539.1; PID:gi83112
R:Sandberg Nordqvist, A.C.; Stahlbom, P.A.; Lake, M.; Sara, V.R.
submitted to the EMBL Data Library, November 1990
A:Description: Nucleotide sequence of the human fetal brain IGF-1b.
A:Reference number: S30540
A:Accession: S30540
A:Molecule type: mRNA
A:Residues: 1-195 <SAN>
A:Cross-references: EMBL:X56774; NID:g32991; PIDN:CAA40093.1; PID:g32992
R:Sandberg Nordqvist, A.C.; Stahlbom, P.A.; Reinecke, M.; Collins, V.P.; von Holst, H.
Cancer Res. 53, 2475-2478, 1993
A:Title: Characterization of insulin-like growth factor 1 in human primary brain tumor
A:Reference number: A48960; MUID:93265440; PMID:8495408
A:Accession: B48960
A:Molecule type: mRNA
A:Residues: 1-195 <SA2>
A:Cross-references: GB:X56774; GB:S61860; NID:g32991; PIDN:CAA40093.1; PID:g32992
A:Experimental source: anaplastic oligodendroglioma
A:Note: sequence modified after extraction from NCBI backbone
A:Note: the authors translated the codon CAG for residues 124 and 133 as Glu
A:Note: sequence extracted from NCBI backbone (NCBIN:133058)
R:Siegfried, J.M.; Kasprzyk, P.G.; Treston, A.M.; Mulshine, J.L.; Quinn, K.A.; Cuttitt
Proc. Natl. Acad. Sci. U.S.A. 89, 8107-8111, 1992
A:Title: A mitogenic peptide amide encoded within the E peptide domain of the insulin
A:Reference number: A42664; MUID:92390398; PMID:1325646
A:Contents: annotation; IBE-1; amidated carboxyl end
C:Comment: For an alternative splice form, see PIR:IGHUL.
C:Genetics:
A:Gene: GDB:IGF1
A:Cross-references: GDB:120081; OMIM:147440
A:Map position: 12q22-12q24.1
A:Introns: 21/3; 74/1; 134/3
C:Superfamily: insulin
C:Keywords: alternative splicing; amidated carboxyl end; growth factor; plasma
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-48/Domain: propeptide #status predicted <PRO>

F:49-118/Product: insulin-like growth factor I #status predicted <MAT>
 F:49-77/Domain: insulin chain B-like #status predicted <CHB>
 F:78-89/Domain: insulin connecting C peptide-like #status predicted <CHC>
 F:90-110/Domain: insulin chain A-like #status predicted <CHA>
 F:111-118/Domain: D peptide #status predicted <CHD>
 F:119-195/Domain: carboxyl-terminal propeptide (E peptide) #status predicted <CHE>
 F:151-172/Product: insulin-like growth factor IB-EI amide #status predicted <MA2>
 F:54-96,66-109,95-100/Disulfide bonds: #status predicted
 F:172/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl

Query Match 37.7%; Score 47.5; DB 1; Length 195;
 Best Local Similarity 45.5%; Pred. No. 23;
 Matches 10; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 4 GWLRPEDGG-QAEGAEDELEVR 24
 II : II | II | | : I
 Db 151 GWPKTHPGGQKQEGTEASLQIR 172

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 Job time : 10.984 secs

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